Progress on the Prairie

2016 Beef Improvement Federation Annual Meeting & Symposium

June 14 - 17, 2016
Hilton Garden Inn
Manhattan, Kansas

K-STATE Research and Extension

www.BeefImprovement.org

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Research and Extension

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June 1, 2016

Welcome to 'Progress on the Prairie'!

On behalf of Kansas State Research and Extension and the Department of Animal Sciences and Industry it is my pleasure to welcome you to the 48th Beef Improvement Federation Annual Meeting and Research Symposium. We hope that you'll enjoy your time in the beautiful Flint Hills of Kansas and here in Manhattan, home to the K-State Wildcats!

This year's meeting is titled 'Progress on the Prairie.' The general sessions are designed to highlight some of the significant genetic improvements beef cattle producers have made over time and to help envision the future of the beef value chain. The speaker line-up features industry leaders and experts that will help us understand the changing beef consumer landscape here in the US and internationally. Recognizing the importance of the cow-calf sector in managing the landscape and building beef, speakers will highlight our current production capacity and needed improvements to ensure producer profitability and sustainability while satisfying consumers around the world.

Afternoon break-out sessions feature speakers covering a vast range of beef genetics topics including new genomics and genetic evaluation tools, improving feed efficiency, documenting the value of genomic testing and exploring genetic susceptibility to respiratory disease and heat stress.

Young producers should be sure to attend the young producer symposium on the afternoon of Tuesday, June 14. The session is designed to help young producers build, maintain and use their professional network, keep a healthy ranch work/family balance and design business plans that enable them to start a business or return to a family farm or ranch.

Sponsorship has played a substantial role in making this meeting possible. Please take a moment to thank representatives of these businesses and trade groups for their support of BIF. We truly appreciate their ongoing investment.

Please don't hesitate to contact one of the K-State hosts if we can be of assistance to you during your stay in Manhattan. We are delighted you are here! We hope you enjoy the meeting and social events, learn a lot, and engage your friends and colleagues in lively discussion about the genetic improvement of beef cattle!

Kind regards,

Robert L. Weaber, Ph.D.
Associate Professor, Cow-calf Extension Specialist

Knowledge for Life

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Schedule of Events

All events at the headquarters hotel unless noted.

Tuesday, June 14, 2016

7 a.m.	BIF Board Meeting
10:30 a.m. - noon	International Genetic Solutions Cattlemen's Seminar *(pre-conference event, no registration required)*
Noon - 5 p.m.	Registration opens, Hilton Garden Inn conference center foyer
1 - 4:30 p.m.	Young Producers Symposium and Reception Getting the most out of a meeting: building, maintaining and using your professional network *Dr. Michael Johll and Jeff Sleichter, Suther Feeds* Balancing ranch and family: keys to success *Debbie Lyons-Blythe, Blythe Angus, White City, KS* Growing a new or expanding a family business to make a place for YOU! Tips and strategies that have helped build businesses for these ranchers *C.J. Blew, Chairman, MKC Cooperative, and rancher/farmer, Castleton, Kansas* *Spencer Jones, Flint Hills Heifer Development/ Jones Family Angus, Wamego, Kansas* *Toby Jordan, Waukaru Polled Shorthorns, Rensselaer, Indiana* *Matt Perrier, Dalebanks Angus, Eureka, Kansas* *Don Schiefelbein, Schiefelbein Farms, Kimball, Minnesota*
6:00 - 8:30 p.m.	Registration, Weber Hall main west foyer
6:30 p.m.	Opening Dinner and Social, K-State Campus, Weber Arena *Shuttle buses depart Hilton Garden Inn east entrance at 6 p.m.; Last bus returns at 9:30 p.m.*

Wednesday, June 15, 2016

6:30 a.m. - 5 p.m.	Registration, Hilton Garden Inn conference center foyer
7 - 8:30 a.m.	Conference Breakfast, hotel foyer
8 a.m.	Opening Comments, Kansas Welcome
9:45 - 11:45 a.m.	Accompanying Persons Guided Tour of Flint Hills Discovery Center *(walk to tour location [1 block] depart as group from hotel lobby)*

General Session I: Opportunities for the Beef Value Chain: Can We Become More Efficient and More Profitable?
Moderator: Mr. Dave Weaber, VP of EMI Analytics, Beef, Express Markets, Inc.

8:15 - 8:45 a.m.	What will the North American beef market look like 20 years from now: opportunities for domestic and international growth *Dr. Glynn Tonsor/Dr. Ted Schroeder, Kansas State University*
8:45 - 9:15 a.m.	Beef as a consumer driven food business: Changing perspectives from cattle to food production *Dr. John Stika, Certified Angus Beef*
9:15 - 9:45 a.m.	Who's our consumer and what do they want 20 years from now? Trends in the protein landscape *Dr. Brad Morgan, Performance Food Group*
9:45 - 10:15 a.m.	Break
10:15 - 11 a.m.	Genetics of meat science: what traits can we improve that affect the value/palatability of beef? *Dr. Keith Belk, Colorado State University*
11 - 11:45 a.m.	Panel discussion of General Session I speakers

Noon — Awards Luncheon
Presentation of BIF Commercial Producer, Continuing Service and Ambassador Awards, Frank Baker and Larry Cundiff Scholarships

2 - 4 p.m. — Accompanying Persons Tour of Flint Hills Discovery Center, Education Symposia: "The role of fire and grazing management in the conservation of the tall grass prairie"
(walk to tour location [1 block] depart as group from hotel lobby)

2 - 5:30 p.m. — Break-out Sessions

Advancements in Emerging Technology
Chair: Dr. Megan Rolf, Kansas State University

2 - 2:45 p.m.	Comparative genomics and metagenomics: systems biology of bovine metabolism and of its ruminal symbionts *Dr. Gavin Conant, University of Missouri*
2:45 - 3:30 p.m.	RNA interference: will the overlooked nucleic acid be the new star among animal health technologies? *Dr. Barry Bradford, Kansas State University*
3:30 - 4 p.m.	Break
4 - 4:45 p.m.	Rumen microvirome *Dr. Samodha Fernando, University of Nebraska-Lincoln*
4:45 - 5:30 p.m.	Use of IVF technology and genomic selection for rapid beef cattle improvement *Dr. Mark Allen, TransOva*

Advancements in End Product Improvement
Chair: Dr. Tommy Perkins, International Brangus Breeders Association

2 - 3 p.m.	The beef yield grading system - it's history, current status and future *Dr. Ty Lawrence, West Texas A&M University*
3 - 4 p.m.	Live animal measures of tenderness *Dr. Rhonda Vann, Mississippi State University*
3:30 - 4 p.m.	Break
4 - 5:30 p.m.	Breeder panel - carcass cata, ultrasound data or DNA *Dick Beck, Three Trees Ranch, Sharpsburg, Georgia* *Jan Oleen, Oleen Brothers, Dwight, Kansas* *Vernon Suhn, Suhn Cattle Company, Eureka, Kansas*

Advancements in Selection Decisions
Chair: Dr. Bob Weaber, Kansas State University
Genetic Improvement of Feed Efficiency in Beef Cattle-Findings of a USDA Funded Integrated Project

2 - 2:30 p.m.	Project overview/objectives; genomics and RNA project discoveries *Dr. Jerry Taylor, University of Missouri*
2:30 - 3 p.m.	Gene set enrichment analysis for feed efficiency in beef cattle *Dr. Holly Neibergs, Washington State University*
3 - 3:30 p.m.	Effects of timing and duration of test period and diet type on intake and feed efficiency in Charolais-sired cattle *Dr. Dan Shike, University of Illinois*
3:30 - 4:00 p.m.	Feed efficiency and the microbiota of the alimentary tract *Dr. Harvey Freetly, US-MARC*
4 - 4:30 p.m.	Effects of diet digestibility on feed efficiency and impact of diet type and feeding phase on repeatability of feed efficiency phenotype *Dr. Stephanie Hansen, Iowa State University*
4:30 - 4:45 p.m.	Results of survey of stakeholders regarding knowledge of and attitudes towards feed intake, efficiency and genetic improvement concepts *Dr. Bob Weaber, Kansas State University*

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Schedule of Events

	4:45 - 5:15 p.m.	Extension demonstration project outcomes; Industry adoption and translation of project deliverables *Dr. Matt Spangler, University of Nebraska-Lincoln*
	5:15 - 5:30 p.m.	Question and answer session
6:30 p.m.		Evening Social/Dinner, Stanley Stout Livestock Marketing Center, K-State Campus *Shuttles depart Hilton Garden Inn east entrance beginning at 6 p.m.; Last bus returns at 9:30 p.m.*

Thursday, June 16, 2016

7 a.m. - noon	Registration, Hilton Garden Inn conference center foyer
7 - 8:30 a.m.	Conference Breakfast, hotel foyer
9 - 11:45 a.m.	Accompanying Persons Guided Tour of the Marianna Kistler Beach Museum of Art, K-State Campus. *(Depart from hotel lobby as group, board vans at east entrance of Hilton Garden Inn., refreshments served)*

General Session II: Protecting Producer Profit for the Future
Moderator: Dr. Matt Spangler, Associate Professor and Extension Specialist, University of Nebraska

8 - 8:15 a.m.	Call to order/housekeeping announcements
8:15 - 8:45 a.m.	The 2016 and the 2036 cow herd, what we do and what we need to do better *Dr. Dave Lalman, Oklahoma State University*
8:45 - 9:15 a.m.	Things a cow-calf producer learns when you own a feed yard: what drives profit *Chip Ramsay, Rex Ranch*
9:15 - 9:45 a.m.	Growing profit by understanding cow maintenance efficiency and maintenance requirement in an animal and systems context *Dr. Mark Enns, Colorado State University*
9:45 - 10:15 a.m.	Break
10:15 - 11 a.m.	Making the cow herd more efficient and profitable by 2036: Where do we focus our efforts for the biggest impact? *Dr. Clay Mathis, King Ranch Institute for Ranch Management*
11 - 11:30 a.m.	Panel discussion with General Session II speakers
11:30 a.m. - Noon	BIF Caucuses and Elections
Noon - 1:30 p.m.	Awards Luncheon *Conference wrap-up: call to action, Dr. Kent Andersen, Zoetis, Presentation of BIF Pioneer and Seedstock Producer Awards, Roy Wallace Scholarship, Introduction of newly elected BIF Board of Directors, Invitation to BIF 2017*

2 - 5:30 p.m.	Break-out Sessions **Advancements in Genomics and Genetic Prediction** *Chair: Dr. Mark Thallman, USDA-ARS-MARC*	
	2 - 2:45 p.m.	Bolt and an alternative approach to genomic EPDs *Dr. Bruce Golden, Theta Solutions, LLC*
	2:45 - 3:30 p.m.	EPDs and Risk *Dr. Dale Van Vleck, U.S. Meat Animal Research Center (retired)*
	3:30 - 4 p.m.	Break

4 - 4:45 p.m. Selection enhanced tenderness marker effects on means and variances of beef tenderness
Dr. J.R. Tait, U.S. Meat Animal Research Center

4:45 - 5:30 p.m. Accounting for discovery bias in genomic prediction
Jamie Parham, University of Nebraska

Advancements in Producer Applications
Chair: Dr. Darrh Bullock, University of Kentucky

2 - 2:45 p.m. Breeding objectives indicate value of genomics for beef cattle
Dr. M. D. MacNeil, Delta G

2:45 - 3:30 p.m. Using genomic tools in commercial beef cattle: taking heifer selection to the next level
Dr. Tom Short, Zoetis

3:30 - 4 p.m. Break

4 - 4:45 p.m. Genomics: return on investment - fact or fiction?
Dr. Tonya Amen, Dr. Michael Bishop, Dr. Andre Eggen, Illumina, Inc.

4:45 - 5:30 p.m. Panel Discussion

Advancements in Efficiency and Adaptability
Chair: Dr. Mark Enns, Colorado State University

2 - 2:50 p.m. Identifying genetic differences in susceptibility to BRD: Results from the USDA-NIFA CAP grant
Dr. Holly Neibergs, Washington State University

2:50 - 3:20 p.m. Guidelines for collection of bovine respiratory disease data
Dr. Larry Kuehn, USDA-Meat Animal Research Center
Dr. R. Mark Enns, Colorado State University

3:20 - 3:50 p.m. Break

3:50 - 4:10 p.m. Genetic Evaluation for Heat Tolerance in Angus Cattle
Heather L. Bradford, University of Georgia

4:10 - 4:30 p.m. Prototype Stayability Analysis using a Random Regression Approach
Dr. Scott E. Speidel, Colorado State University
Dr. Bruce L. Golden, Theta Solutions, LLC

4:30 - 5:15 p.m. Revised feed intake data collection guidelines
Dr. Robert Weaber, Kansas State University

5:30 - 6:30 p.m. BIF Board Meeting and Board Photo

6:30 - 8:30 p.m. Closing Reception on Blue Earth Plaza (adjacent to Hilton Garden Inn; hors d'oeuvres and drinks) and tour the Flint Hills Discovery Center (admission paid by conference)

Friday, June 17, 2016

7 a.m. Tour of Recent BIF Seedstock Producer of the Year Recipients
McCurry Angus, Mushrush Red Angus, Moser Ranch, Fink Beef Genetics

Tour of Recent BIF Seedstock Commercial Producer of the Year Recipients
Tailgate Ranch, Woodbury Farms, Kniebel Cattle Co.

Coach buses/vans for tours depart east entrance of Hilton Garden Inn. Tours include breakfast, lunch and dinner, beverages, and transportation. Tours will return to conference hotel by approximately 9 p.m.

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Speakers: General Session I

Session Moderator

Dave Weaber joined EMI Analytics and Express Markets Inc. in April 2016 as vice president and is responsible for leading and growing the company's efforts in beef supply chain analytics. This includes supply and demand side analysis and forecasting of cattle numbers and beef supplies as well as domestic and international trade impacts.

Before joining Express Markets, Dave served as economist, leading the Market Insights Team in the Strategic Sourcing and Supply Chain Analytics Group of Delhaize America, the eleventh largest grocery retailer in the U.S. From February 2005 through March 2007, Dave was employed by Swift & Co, as Director of Market Analysis. He was responsible for market research and forecasting in the cattle, beef, hog and pork markets as well tracking changes in the other commodity and competing meat markets. Dave also worked in the analysis of foreign markets and trade.

Prior to joining Swift & Co., Dave spent seven years at Cattle-Fax. Dave earned both his bachelor's and master's degrees from Colorado State University.

Glynn Tonsor is an Associate Professor in the Department of Agricultural Economics at Kansas State University (KSU). He grew up on a farrow-to-finish swine farm in Monroe City, Missouri. Tonsor obtained a B.S. from Missouri State University and Ph.D. from KSU. He was a faculty member at Michigan State University from May 2006 to March 2010 when he joined the KSU faculty.

Tonsor has broad interests and experiences which span issues throughout the meat supply chain. Through active research, engaged outreach with industry, and first-hand knowledge with livestock production, Glynn has economic expertise in an array of topics of importance to Kansas, U.S. and global stakeholders. These topics include animal identification and traceability, animal well-being and welfare, commodity market analysis, consumer demand, food safety, meat labeling policies, producer perceptions and preferences, risk management, and technology acceptance. Glynn's integrated research and extension program has resulted in multiple journal article publications and numerous outreach contributions.

Ted Schroeder knows that food for tomorrow depends on understanding the future of the livestock and grain industries.

Schroeder, an agricultural economist, studies livestock and meat marketing as well as price analysis to provide information and direction for the livestock and grain industries. His research focuses on improving commodity market efficiency by investigating price discovery methods, improving market coordinating mechanisms, evaluating market risk and understanding complexities of global meat demand.

He has received more than $4.2 million in funding from organizations such as the Department of Homeland Security, the Department of Agriculture, the U.S. Meat Export Federation and the National Cattlemen's Beef Association. He has more than 100 refereed journal publications. Schroeder is the founding director of the Kansas State University (K-State) Center for Risk Management Education and Research. He also teaches risk management and agricultural marketing courses.

Schroeder has a bachelor's degree in agricultural economics from the University of Nebraska and a doctorate in agricultural economics from Iowa State University. He began his career at K-State in 1986.

As president for the Certified Angus Beef® brand, **John Stika**, guides grassroots programs to deliver premium beef from family farmers and ranchers to consumers' dinner tables. He has led the brand through nine consecutive years of record sales, reaching 896 million pounds in fiscal 2015, to satisfy growing demand for great tasting beef in more than 15,000 restaurants and grocery stores worldwide.

John grew up on a small family farm in Kansas, and earned bachelor's and master's degrees from KSU and doctorate in meat science from the University of Kentucky. He joined the CAB LLC staff in February 1999 as director of feeder-packer relations, and then director of packing and supply development.

Moving on to vice president of business development, he led sales growth through retail, foodservice, international and value-added products before becoming president.

In 2010, John received the Outstanding Young Alumnus Award from K-State's College of Agriculture and the Achievement Award from the American Meat Science Association.

J. Brad Morgan was reared in the ranch and oil community of Antlers, Oklahoma. He received his bachelor's in animal science from Oklahoma State University (1985), his master's in meat science from the University of Nebraska–Lincoln (1988) and his Ph.D. in animal science from Texas A&M University (1991). Brad was an Assistant Professor and Extension Meats Specialist at Colorado State University from 1991 to 1995 where he was part of the inaugural National Beef Quality Audit.

In 1995, Morgan joined the Animal Science faculty at Oklahoma State University. He taught undergraduate and graduate meat science courses and conducts research on the quality, quantity, safety, and usefulness of meat and meat products. Morgan's research and expertise in meat tenderness and color is known nationally and internationally. He has conducted research for companies such as Wal-Mart, National Beef and the U.S. Meat Export Federation.

One of Morgan's last research interests focused on development, verification and implementation of the OSU Tenderness Prediction System. Morgan has attracted over $22.5 million in extramural funding, published more than 80 journal articles, given over 1,700 invited presentations, and conducted research in 29 countries. Morgan has received numerous research and teaching awards including the Outstanding Teaching Award from the American Meat Science Association along with the Outstanding Scientist in the Division of Agriculture at Oklahoma State University. Morgan is the past president of the American Meat Science Association and is currenlty the senior director of protein for Performance Food Group.

Keith Belk is a Professor and Holder of the Ken & Myra Monfort Endowed Chair in Meat Science with the Center for Meat Safety & Quality, Department of Animal Sciences, Colorado State University (CSU). He earned bachelor's and master's degrees from CSU, and his doctorate from Texas A&M University. He has been employed in the private sector as a buyer by Safeway, Inc., and by the USDA Agricultural Marketing Service in Washington, D.C., as an International Marketing Specialist.

At CSU since 1995, he has authored or co-authored 200 refereed scientific journal articles and more than 740 total publications, generated more than $18M in external funding, and was the primary inventor on two patents.

He served as the state Meat Extension Specialist between 1995 and 2000, on the Editorial Board for the Journal of Animal Science in 1997-2000, on the Board of Directors for the American Meat Science Association (AMSA) between 2003-2005, and as President of AMSA in 2009-2010.

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Who's Our Consumer and What Do They Want 20 Years from Now? Trends in the Protein Landscape

J. Brad Morgan, Performance Food Group

Introduction

It is no secret that the protein category has seen challenges over the last five years. The most recent Technomic Center of the Plate Beef and Pork Report (Technomic, 2014) reveals fresh meat shopping trips by today's consumer have declined. This may, to some degree, be attributed to a continual rise in red meat prices since 2010. Who knows, this may be a result of fuel prices, dual outside the home working families or simply just the number of hours in a day. However, don't be fooled, the slight dip in demand does not mean today's consumers have stopped craving red meat. With 97 percent household penetration, consumers still plan meals and special occasions around red meat proteins. One must remember that today's shopper in fact we must first understand and appreciate everything that has changed around them. While it is true that the millennial generation has driven this growth, these dynamic and interesting changes expand well beyond them. More than 80% percent of consumers, ages 18-64, have access to the internet, with that number growing to over 93 percent for those under the age of 50. For most easy access is strapped to their belt or carried in purse. In 2015, it is estimated that 78 percent of consumers have a smartphone and over 40 percent of consumers own a tablet device. With these advancements in technology, it becomes important to remember the **5 "M's"** associated with today's consumer and the protein that we are providing them.

MEAT LOVERS: According to findings of a propriety study (Cargill Proprietary Red Meat Consumer Study, 2015), true meat lovers have a passion for food, and they know what cuts to buy and how to prepare fresh meat. Quality is foundational for this segment. This group searches the meat case for beef cuts with high flavor and marbling and is willing to open their wallets to pay for the best. These consumers are primarily females' age 45-64 who are either retired or have higher household incomes and represent one-third of all dollars spent in the fresh red meat category. They have more time to prepare meals featuring red meat and have a tendency to bring people together to enjoy a high-quality dining experience. Baby Boomers (born 1946-1964) that prepare beef six or more times per month are considered true meat lovers and tend to be our most loyal consumers. Quality-conscious Baby Boomers mainly purchase red meat to connect with others through a special occasion. Confident in the kitchen, this group has a passion for food, knows what cuts to buy and knows how to prepare fresh red meat. Alternatively, value-conscious Baby Boomers often purchase red meat as part of their routine. Also experienced in the kitchen, they are very comfortable with shopping for, and preparing, red meat.

MILLENNIALS: What may be somewhat surprising is how important Millennials (born 1981-1996) are to the future growth of the red meat category. While Millennial budgets and kitchen experience is limited at the current moment, over the next 20 years, they are going to gain experience and confidence in purchasing and preparing red meat products. Some published reports suggest this group will be the only generational group that plan on spending more on all red meats next year compared to this year. This is certainly one of the reasons why many companies are directing their efforts at communicating with this particular group of consumers. This generational group shares similar motivations with Generation X (born 1965-1980), but because they are at a different income threshold and life stage, their behaviors do not always align. Millennials look for nontraditional sources of information about preparing food, complementing cuts and the latest trends that help support their busy lifestyles. Make no mistake, this younger fresh meat user thinks and acts differently than older, more confident users the industry knows. Keeping Millennials engaged in the fresh meat case will require a shift in thinking from product mix, rethinking the role brands play, how the case is merchandised and priced, and what role value added products play in helping get meals to the table to meet the demands of a busy lifestyle.

MOTIVATION: It is not enough to know our consumers, but we must also understand the motivations behind why they are buying red meat and what they want from the experience. Obviously, consumers desire a consistent eating experience and one way of motivating protein sales is creating a branded program that tells a story. This story (i.e., "brand") must not try to educate the consumer, but connect with the consumer and provide transparency associated with all aspects of the brand. A study conducted by Deloitte (Deloitte, 2015) revealed that consumers still want protein products that are affordable, taste good and convenient, but they are using a new set of evolving factors to make their protein purchases. These new motivational ideas include transparency factors that concentrate on social impact (It is not enough for a company to sell products consumers want at prices they are willing to pay, companies are now expected to demonstrate that they care about more than just profits), safety, health, animal well-being and sustainability. Additional research dealing with transparency (Maslansky and Partners, 2013) determined that 78% of consumers claimed it is very important for retail and foodservice entities to provide information on how food is raised. Many consumers – 40 percent – want this additional information but if they don't receive it they

are confident that the industry has something to hide (Maslanky and Partners, 2013). In a recent NCBA Beef Issues Quarterly publication (March, 2016), it was determined from the Consumer Image Index it was determined that only 1/3 of consumers claim to have knowledge about how animals are raised for food. This number becomes even more diluted when consumers are asked to focus on specific topics (i.e., antibiotics, factory farming, branding, dehorning, packing plant processes). Each year more and more consumers are becoming more interested in how animals are treated and raised for food production. So the dilemma on industry finds itself in is we are trying to be transparent to a group of people that do not have the knowledge base to understand.

MOMS: Women represent the largest market opportunity in the world, according to Forbes magazine. Globally, they control $20 trillion in annual consumer spending power. In the next five years, it is expected that this number will rise to nearly $30 trillion. In the United States, women have enormous control, and it's increasing. Reports range from $5-15 trillion, with Marketing Zeus citing sources that $7 trillion is contributed by women in the U.S. in consumer and business spending. Fleishman Hillard Inc. estimates that women will control two-thirds of the consumer wealth in the U.S. over the next 10 years. Women handle the bulk of purchasing decisions for everyday items like groceries and clothing — even for those items targeted at men. In fact, 50 percent of products marketed to men are actually purchased by women. That's why items for men are often marketed with women in mind, as well. In addition to being responsible for most of the day-to-day purchases, women are also heading up or influential in large ticket purchases like cars, homes and appliances. Women account for 85 percent of all consumer purchases including everything from autos to health care: 91% of New Homes, 66% of personal computers, 92% Vacations, 80% Healthcare, 65% New Cars, 89% Bank Accounts, 93% Food and 58% of Total Online Spending. A new generation of moms is rattling the baby care category. Here is some interesting information in that 83 percent of new moms are Millennials, making this generation the new target demographic purchasing all aspects of baby care. It has been established that selling to Millennials poses new, unique challenges not seen by generations past. Millennials are even more adamant about their unwaveringly high standards and need for instant gratification when shopping for their babies.

MARBLING: Although livestock producers have felt the pressures of economic change for considerably longer, the 2009 collapse in the U.S. housing market and following recession directly affected consumers and their meat purchasing habits. Even as late as 2013, among consumers who changed their meat purchases, 91 percent were spending less (FMI and AMI, 2014). Despite the recession, demand for high quality beef has continually risen and had obvious effects on the quality of the already low feeder cattle supply. Today, as a result of genetic tool implementation use as well as more affordable feed grains, the beef industry has seen a 12 percentage-point increase in carcass grading USDA Prime and Choice since 1995 (Dykstra, 2014). Currently a tremendous demand exists for high quality, storied beef programs at Performance Food Group. You can have all of the transparency in the world but the product has to check the box for consistent cooked beef flavor and tenderness.

Discussion

In a recent report (Deloitte, 2015) entitled, "Capitalizing on the Shifting Consumer Food Value Equation" underlined how widespread health and wellness and other "evolving value drivers" have become in influencing food sales in the U.S. The year-long study from Deloitte, Food Marketing Institute and Grocery Manufacturers Association included a survey of 5,000 prescreened American adults, fielded to more than 11,000. Survey data were weighed to represent U.S. food purchasers, based on U.S. Census data (age, gender, household income). Food purchasers were defined as adults 18 to 80 who are primary food/beverage shoppers for their households and eat dinner at home at least three times per week. Overall, 51% of those surveyed indicated that they weigh factors including health and wellness, safety, social impact, experience and transparency more heavily than the "traditional" value perception drivers of taste, price and convenience in their buying decisions. The other 49% said they give more weight to the traditional drivers. The shift toward the evolving drivers was "pervasive across region, age and income," meaning that "each and every consumer targeted by food manufacturers and retailers has changed in a fundamental way," stress the researchers. "It's not just Millennials or the most affluent putting these evolving drivers in the mix," summed up Jack Ringquist, principal, Deloitte Consulting LLP and global consumer products leader. Further, "preferences are becoming even more fragmented than the food industry may have anticipated," he said.

The survey also found a shift in how Americans define food safety. Nearly three-quarters (74%) said that a definition limited to foods or beverages not causing any "immediate, physical, harm" is insufficient. Instead, their definitions now include factors such as "free from harmful ingredients" (62%), clear and accurate labeling (51%), and "fewer ingredients, processing and nothing artificial" (42%). Consumers who place more value on the evolving drivers appear to be more likely to use social media, mobile apps and digital sources to research products and brands on the path to purchase. They're also more prone to distrust the food industry than those who put more stress on traditional drivers. Regarding food safety, companies need to ensure that they are satisfying consumers' broadened definition. Regarding "social impact" factors like food sourcing, sustainability, animal welfare, and fair treatment of employees, they are advised to "identify which issues have most opportunity or represent the greatest risk, and when to lead versus follow."

Consumers define the "experience" driver as including factors beyond the actual products offered, such as retail store layout and services, channel innovation, brand interaction, and personalized engagement spanning pre-, during and post-purchase. The survey found "transparency" to be an "overarching" evolving driver. Consumers define it as including clear labeling, certification by trusted third parties, and company attributes such as access and trust. Food companies and retailers should provide access to all relevant information, and "be prepared for two-way engagement to promote trust," sums up the report.

Figure 1. The Consumer Value Driver Plate (Deloitte, 2015)

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Genetics of Meat Science: What traits can we improve genetically that affect the value/sensory desirability of beef?

Keith E. Belk, Center for Meat Safety & Quality, Department of Animal Sciences, Colorado State University

As a young undergraduate Animal Science student working towards completion of a first animal breeding course (a long time ago), I recall the formula that, although perhaps oversimplified, helped students to understand how the genome related to phenotypic expression (please forgive inaccuracies of a Meat Scientist!):

Phenotype=Genotype+Envirnonment

Since that time, of course, computing power has improved exponentially and we became more quantitatively familiar with features of heritability, complementarity, hybrid vigor, pleiotropy, etc., which conspire to complicate basic Mendelian inheritance principles in complex organisms. We also now know that many events (often not yet explainable) during gene transcription, translation and protein synthesis/activity also contribute to the 'final' phenotypic expressions of genes in a given environment. My question then and now was/is: what is this 'environmental' component of the equation and how does it affect genomic expression? It now is more important than ever for scientists in biology and genetics to work hand-in-hand in a systems-based approach to help explain phenotypic expression.

Today, thanks in part to the Human Genome Project (1990-2003), we have more sophisticated and extensive tools to help us understand the previously un-understandable (is that a word?); one being Next Generation Sequencing (NGS). To elaborate on the power of this newer tool, and to put the advances that we have witnessed into perspective, let's for a moment consider this over-a-decade-long project. To sequence the first human genome using Sanger techniques, it took >13 years and approximately $3 billion, and the human genome is about 3.2 billion base pairs of DNA in length (NIH, 2010). In recent shotgun metagenomics studies conducted in our lab, our first sample took 7 days to sequence (Noyes et al., 2016; including extraction and library preparation), cost $900, and we generated >8 billion base pairs of DNA from that sample. So, we have witnessed incredible advancement in technology! Given access to, and declining costs of, using NGS to address modern questions, we may now actually have in our grasp the ability to explain the true phenotypic response of cattle given a bovine genome and a specific environment—but it still won't be a simple task.

As an example of why I believe that we must use NGS, coupled with a shift in Animal Science thinking, I will reference selection for beef eating quality, and particularly marbling scores. In discussion of this, it is important to note that—as scientists—we actually care about marbling scores per se only in the context that they are somewhat correlated to tenderness, flavor and juiciness of beef following processing and cooking (Tatum, 2016; the exception may be that we are also interested in marbling from a diet-health perspective); collectively referred to as 'eating satisfaction.' Marbling also is clearly important because it is used to some extent in value discovery. However, to be clear, marbling can only be partially associated with beef demand; the actual economic traits of primary relevance are tenderness, flavor, and juiciness. So, when attempting to improve marbling scores, one can say (in very simple terms) that we are attempting to predict (i.e., select for) a predictor of the attributes of actual value. When we select for ultrasonic or other measures of marbling scores, we are selecting for a predictor of a predictor of the traits of economic relevance. Hence, as geneticists, if you desire accuracy and true genetic improvement, you have two options: you can either select directly for the trait of interest (i.e., tenderness, flavor and/or juiciness), or you can do a more-perfect job of selecting for the predictive attribute(s) (i.e., marbling scores or, perhaps, ultrasound marbling scores).

How have we performed, as an industry, in taking the route of selecting for predictors of the economically relevant trait of importance? Consider USDA Quality Grade consists in 1974 through 2011 (last National Beef Quality Audit; NBQA-2011). Although there have been some changes to the USDA grade standards during that period of time, none really had a significant effect on the location of the lines which determine whether a carcass is graded U.S. Choice or not—and, if anything, grade lines are more liberal today than in 1974. Yet, the percentage of carcasses grading U.S. Choice in 1974 was 74%, while the percentage grading U.S. Choice in the last NBQA-2011 was 61%–and this value was up from 55% in 1991 when the first NBQA was conducted (Fig. 1). The cattle that did not meet strategic target-consist values for U.S. Quality Grades in NBQA-2011 accounted for 58% of lost opportunities (i.e., lost value per head slaughtered) to the U.S. cattle industry. Lastly, the percentage of the slaughter consist that was comprised of predominately black-hided cattle increased from 45.1% to 61.1% between 2000 and 2011—presumably to improve marbling scores and branding opportunities (NBQA-2011, 2012), but only marginally contributing to population-based improved U.S. Quality Grades. Considering the amount of investment in research and genetic selection inputs that were targeted towards improved ability of carcasses to grade U.S. Choice since 1974, data suggesting that we have not substantially improved U.S. Quality Grade consists are rather alarming!

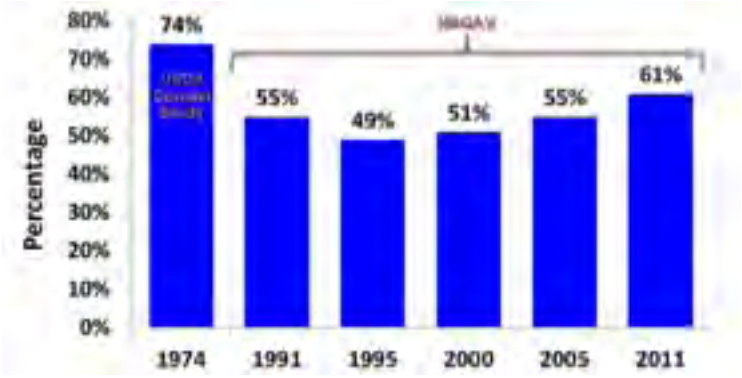

Fig. 1. USDA-AMS and National Beef Quality Audit-2011 U.S. Prime/Choice Consist by Year.

Given data associated with U.S. Quality Grade consists, is it even possible to make genetic progress in real-world phenotypic expression of, at least what we believe to be, important traits? The answer appears to be: absolutely! It seems that the industry responds quickly to price signals, but perhaps not strictly to beef demand signals. Take, for example, U.S. Yield Grade characteristics (Fig. 2) and weight; Yield Grades have improved while carcass weight has continued to increase at a substantial pace (mean carcass weight in NBQA-2011 was 818; it is much higher now).

When it comes to improving consumer demand for beef, is it perhaps time to begin to genetically select for the true traits of importance—those that affect purchasing decisions at retail (and, more importantly, re-purchasing decisions at retail)? This is a difficult assignment because the phenotypic outcome of importance in such a scenario is expensive and complicated to measure in the real world. Nonetheless, as we move forward, and if genetic selection is to have meaningful impacts on beef demand across breeds, it would seem that genetic selection directly for traits that affect demand will be important.

Given all of the modern EPD and genetic selection technology aimed at improved carcass U.S. Quality Grades, why have we not succeeded at improving U.S. Quality Grade consists? We know that selection for this trait must occur in the face of a faulty price discovery mechanism that does not adequately provide incentive for improved eating quality (marbling). But, is it also possible that—despite our best efforts—use of the genetic tools have been ineffective because we select for the wrong traits, the h2 is moderate at best, or that other factors play a greater role in determining phenotypic expression of marbling and eating satisfaction beyond the bovine genome alone? Could it be that the expression of the bovine genome is moderated or influenced by the expression of the microbiota genome?

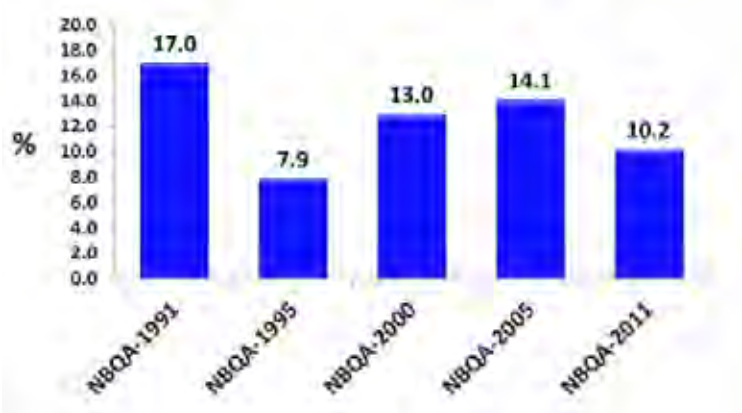

Fig. 2. National Beef Quality Audit-2011 U.S. Yield Grade 4's and 5's by Year.

My point is that an opportunity exists to estimate and select for phenotypic responses utilizing both the genetics of the animal AND the genetics of the microbiota—which may contribute a significant proportion to the equation factor of my youth that we call 'environment'! Such efforts at understanding the associations between human microbiota and genomic expression already have been underway in the Human Microbiome Project for some years (Foxman and Rosenthal, 2013), and it is time for us to start thinking about this more seriously in Animal Science. As stated by McFall-Ngai et al. (2013), "all biologists will be challenged to broaden their appreciation of these

interactions and to include investigations of the relationships between and among bacteria and their animal partners as we seek a better understanding of the natural world." Given that such relationships appear to truly exist and that they influence humans (Fig. 3), is it not reasonable to also believe that these interrelationships would influence expression of traits like marbling score, feed efficiency, U.S. Yield Grade, etc., in cattle?

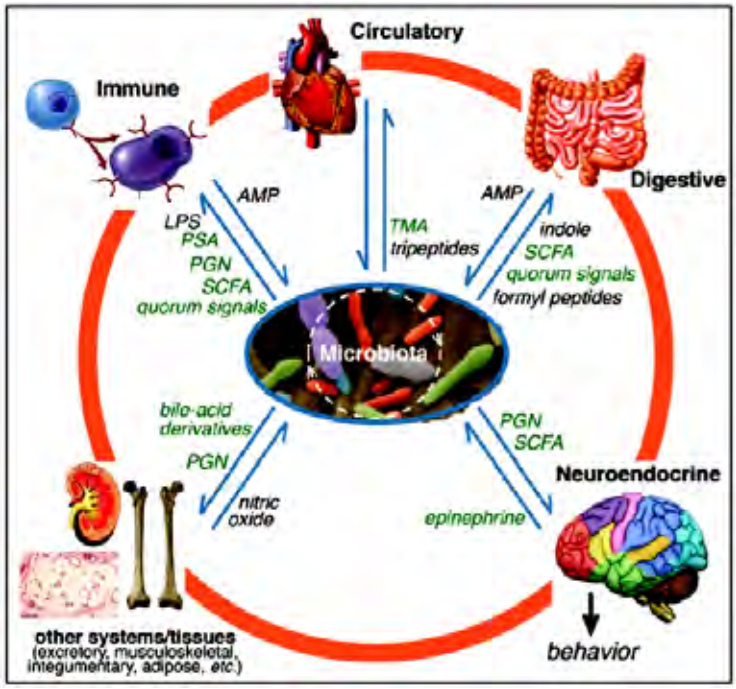

Fig. 3. Relationships among, and communication between, animals and their microbiome (from McFall-Ngai et al., 2013).

Recently, in a 16S rRNA-based analysis of 1,126 pairs of human twins, Goodrich et al. (2016) concluded that "A candidate gene approach uncovered associations between heritable taxa and genes related to diet, metabolism, and olfaction" and that "diet-sensing, metabolism, and immune defense are important drivers of human-microbiome co-evolution." In other words, the microbiota among twins was linked to the genetics of the twins, and those microbiota and phenotypes tended to develop together. So, it firstly is possible and even likely that the microbiome of cattle is at least partially dependent on cattle genetics and that the development of the cattle and the microbiota are associated with one another! But, in addition to this, a review by Soucy et al. (2015) suggested that there exists both a "core" and "pan" genome that are involved in phenotypic expression (Fig. 4), and that these genomes can each contribute to expression via horizontal gene transfer mechanisms—at least in plants (Fig. 5). So, is it also possible that similar sharing of genes occurs between livestock and their microbiota via horizontal transfer mechanisms?

It is time to begin the task of understanding relationships among, and the impacts of, microbiota of cattle on economically relevant traits and traits that ultimately influence consumer demand for beef at retail; things like tenderness, flavor, and juiciness. But also many additional traits.

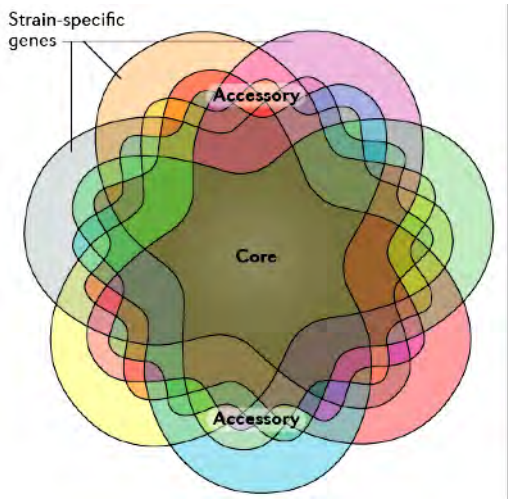

Fig. 4. "Core" (genes found in all members of a group of interest) and "pan" (the core genome plus the accessory genome—genes that are present in only one or a few members of the group) genomes. The concept of a pan-genome has led to the idea that steps in metabolic pathways may be distributed over several individuals within a community (from Soucy et al., 2015)

As the industry moves forward, and as beef demand (both domestic and global) becomes an increasingly important topic for sustainability of the industry in light of high production costs and subsequently high costs to consumers at retail (retail purchases of beef have declined by 39.3% since 1985), then a number of traits of interest emerge for consideration in genetic selection and animal husbandry. And, there also is the proposed Grand Challenge that we will need to feed, with an 80% likelihood, 9.6 to 12.3 billion people by the year 2100—albeit with all foods. These impending needs will likely need to be considered in relation to the microbiota of the cattle-raising and beef processing environment. The following are all of importance from a cattle industry economic viability, animal and public health, and food security perspective: (1) outlier cattle that are discounted, (2) carcass and offal condemnations, (3) effects of growth promotion (perhaps growth promotion technologies are not necessary when growth traits are selected for in conjunction with the microbiome!), (4) beef oxidative stability, color and display life, (5) immune response and animal diseases—particularly those that are zoonotic, (6) nutrient composition and density, (7) fatty acid composition, (8) transmission of foodborne pathogens, and (9) transmission of antimicrobial resistance.

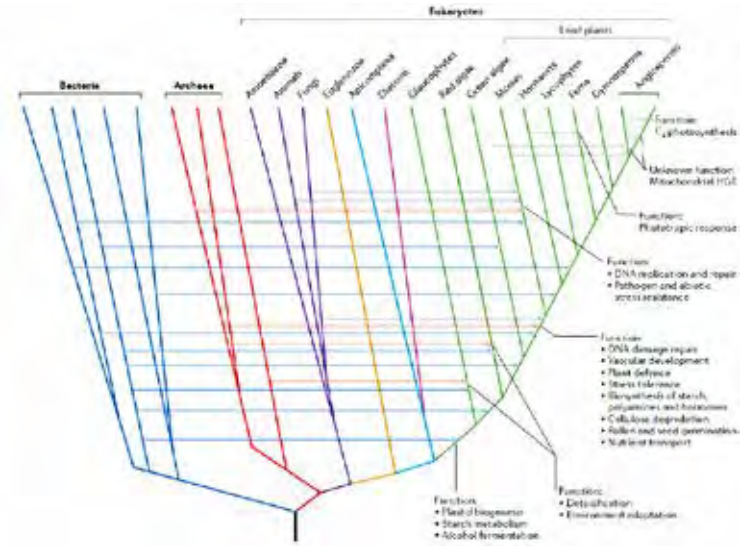

Fig. 5. Horizontal gene transfer has resulted in unique capabilities in plants (from Soucy et al., 2015).

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Speakers: General Session II

Session Moderator

Matt Spangler grew up on a diversified crop and livestock farm in Kansas. He received degrees from K-State (BS; 2001), Iowa State University (MS; 2003), and the University of Georgia (PhD; 2006) and is currently an Associate Professor and Extension Beef Genetics Specialist at the University of Nebraska.

He works as part of a team with colleagues at UNL and US MARC to improve genetic/genomic selection tools and methods and is currently part of an effort funded by the USDA to develop genomic predictors for feed efficiency in beef cattle.

Dave Lalman is a professor in the Animal Science Department at Oklahoma State University. He serves as the Extension Beef Cattle Specialist with primary responsibilities in cow-calf and stocker cattle nutrition and management.

Lalman's extension and research program emphasis is on increasing profitability and/or reducing cost of production through improved forage utilization, defining optimal management practices and evaluating beef production systems.

Kenneth (Chip) Ramsay was born and raised on a corn, soybean and cattle operation in central Indiana. He received an associate's degree in beef cattle management from Ricks College, a bachelor's degree in business finance from Brigham Young University and a master's in feedlot management from Texas A&M.

Ramsay has served in various management positions in cattle production and retained ownership for Deseret Ranches in Florida and Oklahoma from 1991 to 2006. He is currently general manager of Deseret Ranches' Nebraska operation known as Rex Ranch.

Clay Mathis was named director and endowed chair of the King Ranch® Institute for Ranch Management in July 2010. As director, Mathis leads faculty and staff appointed to the King Ranch Institute for Ranch Management and oversees teaching and outreach efforts of the Institute.

He maintains and develops curriculum for the master's in ranch management degree program, which includes more than 42 hours of business and animal production coursework and intensive project work tackling issues on large partnering ranches across the U.S.

Mathis works closely with the KRIRM Management Council to identify topics and speakers for the entire suite of KRIRM lectureships and the annual Holt Cat Symposium on Excellence in Ranch Management.

A native of New Braunfels, Texas, he received a bachelor's degree in animal science and master's in the physiology of reproduction from Texas A&M University.

In 1998, he earned a doctorate from K-State in ruminant nutrition where his research focused on supplementing grazing cattle. From 1998 to 2010, Mathis worked as a professor and extension livestock specialist at New Mexico State University.

Conference Wrap-up

Kent Andersen was raised on a diversified livestock and farming operation in central Nebraska. Following graduation from the University of Nebraska (B.S., 1985) and Colorado State University (M.S., 1987 and Ph.D., 1990), Andersen served as director of education and research (1990 to 1999) and executive vice president (2000 to 2009) for the North American Limousin Foundation.

During his career, he has been active in various beef industry organizations, including the Beef Improvement Federation, the National Pedigreed Livestock Council, and the U.S. Beef Breeds Council.

In his position with Zoetis, Andersen serves as director of genetics for cattle and equine technical services. Andersen is active in his family's commercial cow-calf and farming operation in Nebraska.

The 2016 and the 2036 cowherd, what we do and what we need to do better.

David Lalman, Damona Doye, Megan Rolf, Mike Brown, Miles Redden, Adam McGee, Corbit Bayliff, and Courtney Spencer

Oklahoma State University and Kansas State University

Introduction

Tools and benchmarking data are readily available to monitor changes over time in post-weaning performance, finishing phase profitability and carcass characteristics. For example, in most breeds the genetic trend for yearling weight and marbling EPD continues to steadily increase over time (Kuhn and Thallman, 2015). Finished cattle weights and carcass weights are increasing at the rate of about 9.4 and 5.7 lb per year since 2007 (LMIC, 2016). Likewise, percent of federally inspected cattle grading USDA Choice and above has increased from 48% in 1995 to 78% for the 2015 calendar year (LMIC, 2016).

In contrast, documenting production and financial performance of the commercial cow/calf sector continues to be a challenge. Programs designed to simultaneously evaluate economic and animal performance are necessary because production outcomes are influenced by the production environment and management. In other words, one can increase production by accelerating input costs resulting in a higher per unit cost of production. Consequently, cost per unit of land or per unit of production ($/cwt of calf produced, for example) are better indicators of ranch efficiency…at least through the weaning phase. Obviously, this picture is complicated further if calves are retained through a post-weaning phase and especially considering dramatic differences in carcass value. Benchmarking data in the commercial cow/calf industry is scarce. Numerous commercially available programs are available to record and evaluate cow/calf enterprise production records (Lalman et al., 2015), although few of these provide the capability to benchmark against other similar enterprises. Fewer programs with the capability to simultaneously evaluate economic and performance outcomes are available. For the purpose of evaluating the current "state" of the commercial cow/calf sector and identifying areas of low hanging fruit through the next 20 years, we reviewed production and economic performance of commercial cow/calf enterprises over time. This data was provided by the Kansas Farm Management Association (Herbel, 2016), Southwest Cow-Calf SPA (Bevers, 2016), Cow Herd Appraisal Performance (CHAPS) program (Ringwall, 2016), and FINBIN, Center for Farm Financial Management (University of Minnesota, 2016).

Cost of Production

Figures 1 and 2 show the annual cost per cow in the SPA and KFMA data sets, respectively. Using simple linear regression to evaluate the trend over time, the cost to maintain beef cows has increased at the rate of $22.45 per year in the southern Great Plains (Texas, Oklahoma and New Mexico) as determined using the SPA methodology. In the KFMA system, annual cow cost escalation has averaged $34.35 per year since 1994. Methodology may differ between these

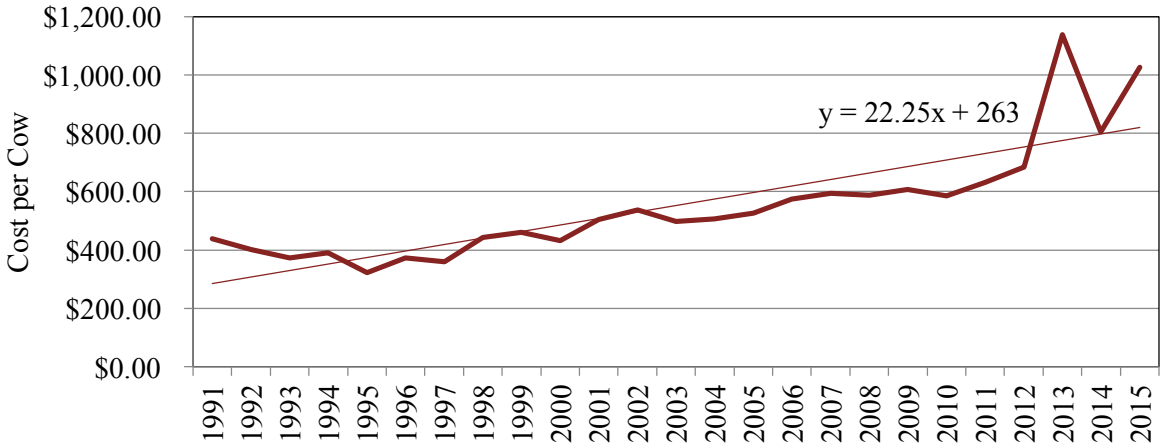

Figure 1. SPA (Texas, Oklahoma and New Mexico) total cost per cow.

programs, therefore, the costs should not be compared directly, but both clearly document increasing annual cost of production.

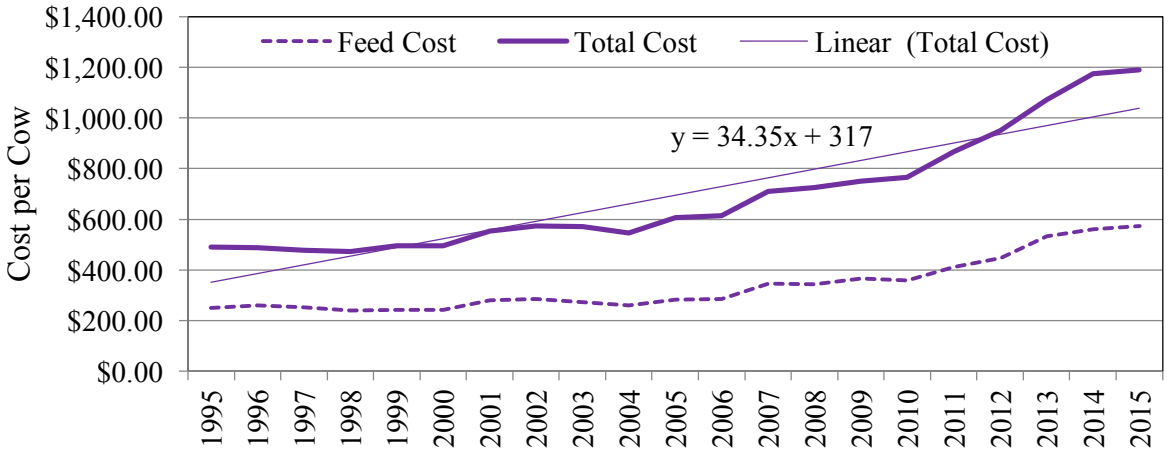

Figure 2. KFMA (Kansas) total cost and feed cost (pasture and non-pasture) per cow

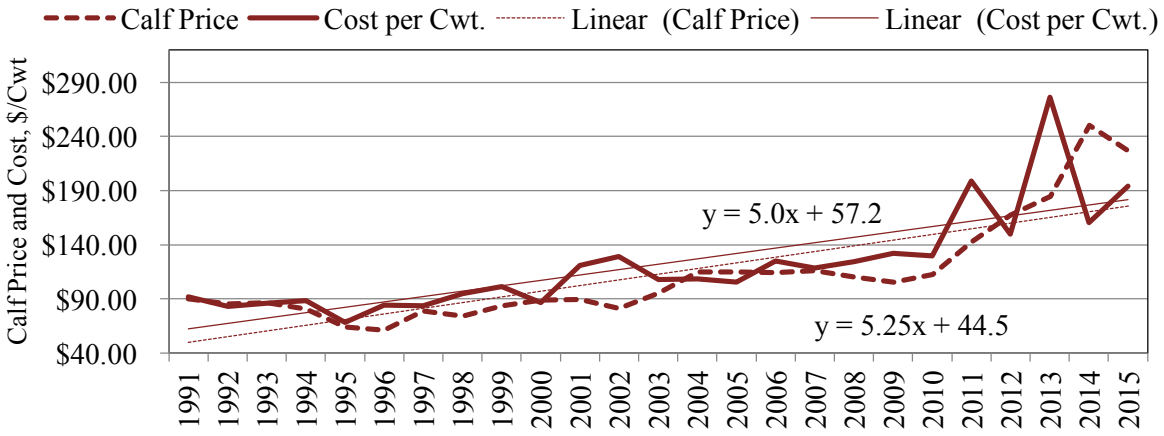

Figure 3. SPA (Texas, Oklahoma and New Mexico) calf price versus cost of production over time

Using the SPA data, cost per cwt of calf produced has accelerated at the rate of $5.00 per year. During the same time period, calf prices have accelerated at an average rate of $5.25 per cwt per year (Figure 3). These data suggest that the relationship between the cost of production and the value of weaned calves has not changed much when viewed from a general "trend over time" perspective.

Pendell et al. (2015) reported characteristics influencing profitability and cost in 79 Kansas cow/calf enterprises participating in the program between 2010 and 2014. Even though average cow/calf enterprise profitability has not changed much over the last 20 years, the variation in profitability from year to year remains lower than the variation in profitability among operations within any given year. In other words, in "bad" years, some cow/calf operations remain profitable and some continue to be unprofitable in "good" years. Cattle producers have little influence on macroeconomic factors driving year-to-year differences in industry-wide profitability. However, this data confirms older reports suggesting that management decisions and production systems, which are within the producers' influence or control, can have a dramatic impact on profitability.

In Pendell et al. (2015), the 79 operations were divided into high, medium and low profitability groups. The high profitability 1/3 ranches averaged $415.03 more net return per cow than the low 1/3 profitability group. When comparing the characteristics driving differences in profitability between the high 1/3 and the low 1/3 groups, they found that 67.8% of this difference was due to lower cost of production in the high profit group. The remaining 32.2% difference in profitability was due to differences in gross income per cow. As one would expect, higher profitability herds had slightly higher average weaning rate, weaning weight and calf sale price. However, controlling cost was substantially more important in driving profitability than was increasing pounds of cattle sold (calves and cull cows) or price for cattle sold.

In this same study, the Kansas group reported results from multiple regression analyses designed to explore factors explaining variation in profitability among these 79 operations. In the profit model, neither calf weight nor calf price were significant factors. However, in the cost ($/cow) model, increased calf sale weight (weaning weight) was highly significant. In fact, for

every one-pound increase in calf weight, total cost per cow increased by $0.86. Considering the weaning rate during this time period in these operations averaged about 90%, the cost to increase one pound of weaning weight was about $0.96.

To quantify the value of additional weaning weight, we evaluated 234 weekly sales reports from the Oklahoma National Stockyards in Oklahoma City (Livestock Marketing Information Center) from 2010 through 2014. The mean value of added weight in the 550 lb to 650 lb weight range was $85.90 with a standard deviation of $33.20. On average, the cost associated with increasing weaning weight in the Kansas data was slightly greater than the value of increased weaning weight. The relative value of additional weaning weight is highly variable over time, and therefore, the profitability of managing to achieve greater weaning weight will be highly variable over time.

Clearly, in a "sell at weaning" enterprise context, there is more low hanging fruit in cutting or managing cost than there is in increasing production. Fortunately, selection indexes as well as relatively new EPD's more directly related to profitability, input costs and fertility are becoming available. Over the next 20 years, these tools should help curb the appetite for traits that result in increased cow costs such as increased mature cow weight, milk yield, and extremes in growth (Lalman, 2013).

Reproductive Efficiency

Genetic trend data (Kuehn and Thallman, 2015) indicates that tremendous changes have occurred in the seedstock sector over time in conjunction with continued proliferation and refinement of genetic selection tools. However, tools to assist in improving the genetics of fertility or reproductive efficiency, which are low in heritability, have been scarce and relatively recent in terms of implementation (heifer pregnancy EPD's for example). Perhaps it is no surprise that advancing such a difficult trait has been a challenge in the commercial cow/calf segment. Weaning percent, also described as weaning rate or percent calf crop weaned, is the calculation used to evaluate overall reproductive efficiency according to Beef Improvement Federation (BIF) guidelines (BIF, 2010). This calculation includes losses due to cows failing to become pregnant, pregnancy losses, calf death loss prior to weaning and cow death loss. Mean herd average weaning percent is shown for each of the last 24 years in figure 4 for commercial cow/calf operations contributing to KFMA (Kansas), SPA (Texas, Oklahoma and New Mexico), CHAPS (North Dakota) and FINBIN (upper Midwest) programs. The Kansas data represents percent of calves weaned from number of pregnant cows. Consequently, weaning rate in this data set would be a few percentage units lower than those reported in figure 4 (due to open cows and early embryonic losses not being included in the calculation).

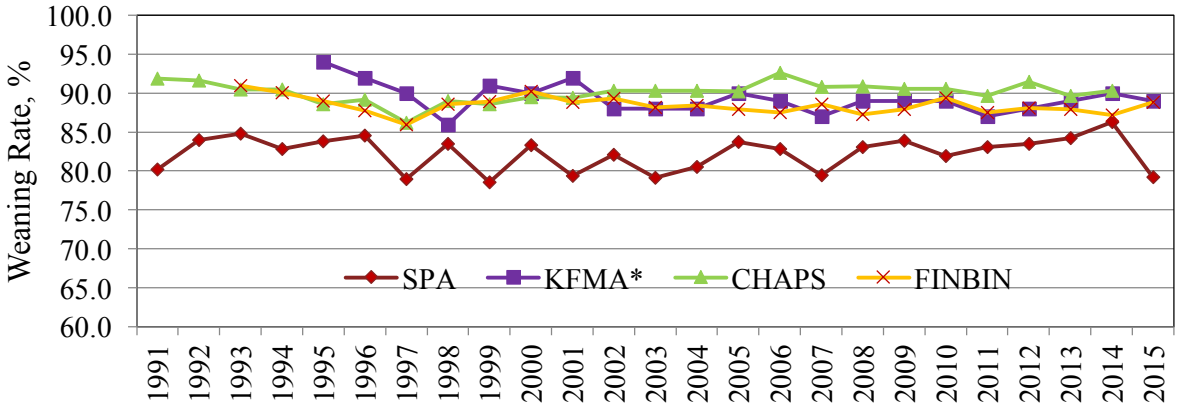

Figure 4. SPA, KFMA, CHAPS weaning rate over time
*KFMA data represents % calves weaned from pregnant cows

Overall reproductive efficiency has not changed significantly throughout this time period in these four datasets. For the ten-year period from 2005 through 2014, weaning rate has averaged 90.7, 88.7, 88.0 and 83.2 for North Dakota, Kansas, upper Midwest and the southern states of Oklahoma, Texas and New Mexico, respectively. True weaning rate in the Kansas data would be lower than 88.7, although how much lower is unknown. This data suggests a substantial reproductive efficiency gradient declining from the northern to the southern Great Plains region of the United States.

This discrepancy in fertility and (or) calf survival has been consistent over time. Many factors may contribute to reduced weaning rate in the South including heat stress, parasite burden, lower forage quality, an increase in proportion of non-adapted cattle (dark hide and hair color in particular), and reduced utilization of *Bos indicus* cattle in planned crossbreeding systems …to name a few. In general, it appears that room for economically beneficial improvement in overall fertility in the northern Great Plains is limited. On the other hand, there seems to be an opportunity for a major breakthrough in reproductive efficiency in the southern U.S. Obviously, the potential to improve fertility through maternal heterosis, planned crossbreeding systems, and use of composite populations have been known for a long time. In particular, it would seem that the southern cow/calf region as a whole should reconsider the rapid evolution away from use of planned crossbreeding systems or composite systems utilizing *Bos indicus* breeds and other regionally adapted cattle.

Consider a quote from Dr. Ron Randel, Texas A&M University in a recent conversation, "F1 females, out of Hereford bulls and Brahman cows, gives you North Dakota-like fertility in the Gulf-Coast region. You have a well-adapted, low-maintenance female that can take the heat, the parasites, and nutritional stress during tough drought years or in cases of marginal management. If you mate those females to an Angus bull with growth, feed efficiency, marbling and muscle, you have an animal that can compete in today's feeding industry and perform well in a grid marketing program." Obviously, there are challenges associated with creating and maintaining an F1 cow herd. These challenges along with market discounts for feeder cattle and carcasses have

contributed a great deal to the decline in use of similar breeding systems. The same breed structure and crosses will not work in every region and each producer should choose a planned crossbreeding system that would work for their management and marketing goals. However, the use of planned crossbreeding or composite populations to create maternal heterosis and regional adaptability, paired with traditional selection on fertility-related EPDs, has the potential to dramatically increase reproductive performance in the southern U.S.

A significant proportion of the number of cows failing to wean a calf are due to failure to become pregnant and embryonic mortality (loss of pregnancy). Just recently, the American Hereford Association initiated the use of the Sustained Cow Fertility EPD (Northcutt and Bowman, 2015) designed to address these fertility components in genetic selection. Hopefully, whole-herd reporting will continue to expand across the seedstock sector allowing further development and implementation of similar tools directly related to reproductive efficiency.

Production at Weaning

Average weaning weights over time from the four benchmarking programs, along with Angus weaning weights for bull calves are shown in figure 5. Angus data is shown as an example of phenotypic changes over time in the seedstock sector. It should be recognized that the three commercial data sets represent actual weaning weights for both steers and heifers. Adjusted weights are not available in the SPA, KFMA or FINBIN programs. Logically, one primary factor that could lead to these results (no increase in actual weaning weight) would be a wide-spread evolution to earlier age at weaning in commercial operations. In other words, we are assuming that age at weaning has not changed substantially during this time period. The Angus data in the graph represents adjusted weights for bulls only. Consequently, the relative differences in weaning weights are not comparable. Rather, our objective is to observe change over time in large datasets that have used consistent guidelines in collecting and reporting weaning weight data.

Simple linear regression was applied to each dataset independently. The regression coefficient for the SPA ($P = 0.65$), CHAPS ($P = 0.80$) and FINBIN ($P = 0.74$) data did not differ from zero, indicating that, on average, there has been no change in weaning weight for herds participating in these programs during this time period. The regression coefficient for the KFMA data was positive and significantly different from zero ($P = 0.016$) suggesting that, on average, weaning weight in these herds have increased at the rate of about 1.1 lb per year since 1995. There is a highly significant ($P < 0.01$) positive linear coefficient in the Angus dataset, indicating that adjusted weaning weights have increased at a rate of about 2.6 lb per year. Although the Angus heifer data is not shown in Figure 5, a similar positive, linear coefficient ($P < 0.01$) was observed at the rate of 2.1 lb per year.

Based on the limited data available, we submit that commercial cow/calf and seedstock phenotypic changes in weaning weight may be uncoupled. Either the producers in these datasets are not selecting for increased weaning weight or lower nutrient availability and (or) less intense management restrict the expression of genetic potential for weaning weight growth in commercial operations. Genetic improvement would be expected to lag in the commercial segment by several years. Regardless of the reason, commercial operators should be asking the question, “Does

continued aggressive selection for growth improve my bottom line?" Certainly, potential antagonisms of continued aggressive selection for growth should be considered (increased appetite and maintenance requirements in retained females, for example).

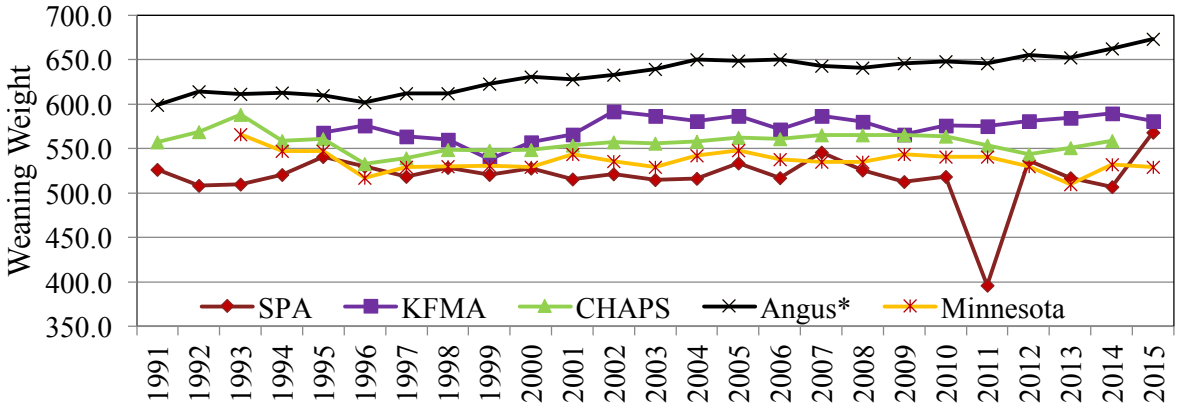

Figure 5. SPA, KFMA, CHAPS and Angus weaning weights over time.
*Angus values represent adjusted weaning weights for bulls

Summary

Long-term trends in cost of production appear to be keeping pace with increased calf prices while there has been no substantial change in productivity of the nation's commercial cow herd over the past 24 years when viewed from a "sell at weaning" enterprise context. In contrast, changes in post-weaning growth, carcass weight and marbling has been dramatic. This is both good and bad news. While overall cow/calf segment year-to-year profitability has not changed substantially, well-managed operations remain profitable even during financially difficult years. At the same time, some cow/calf enterprises continue to lose money in relatively "good" years. While increased calf prices, weaning weight and reproduction are features of profitable cow/calf enterprises, controlling or minimizing cost of production is more important. On average, minimal improvement in weaning weight and no improvement in reproductive efficiency has been achieved in the nation's commercial cow herd over the 24-year time period evaluated. This is surprising because genotypic and phenotypic trends indicate substantial positive change in breed association data. Although certainly not new or revolutionary, a shift towards more emphasis on minimizing production cost in the cow/calf enterprise is appropriate. This shift should not come at the expense of industry gains made in post-weaning characteristics over the past 20 years. The toolkit to convey the costs (antagonists) associated with increasing growth, milk yield and carcass weight genetics has expanded in recent years. This trend in development of genetic selection tools is vital to assist the commercial cow/calf sector in balancing genetic selection for controlling production cost versus increasing post-weaning phase performance, post-weaning phase profitability and carcass value.

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In Search of Beef Production Nirvana
Things a cow-calf producer learns when you own a feedyard: what drives profit?

Chip Ramsay, Rex Ranch

Executive Summary

The increasing volatility of market price and weather patterns are two major challenges that pose serious threats to profitability in our "betting on the come" segmented management systems. We hope to counteract some of that risk through further integration in the beef industry which can increase opportunity to add value and efficiency to the whole system thus increasing long term profitability. Added value can be recognized through increased revenues generated from producing a more targeted, consistent product and then marketing that product to those who desire it most. Added efficiency can be realized through the cost-side of the profitability equation. As trust between segments increase, unneeded redundancies will be discarded. A greater understanding of how each segment affects the system as a whole will cause inputs to be used in an increasingly additive fashion rather than the traditional "I am going to get mine" approach. Beef production's competitive advantage over swine and poultry is our ability to turn roughage into protein. Thus, the profitability measure in an integrated system should become more focused on a "return per acre" as opposed to "return per cow", which should intensify our focus on optimizing the use of the whole system's capacity.

Although the challenges facing this industry are not for the faint of heart, we can adapt and prosper. The speed of our progress will be highly correlated to the cohesiveness of our approach as opposed to trying to do it all within our own little segmented operational vacuums. Ranchers, feedyards, packers, retailers, researchers, associations and allied partners taking the time to develop the pertinent questions and coordinating their approach so as to not waste intellectual and financial resources on stuff that has little effect on sustainable profitability will be key to our future success.

What we have learned since owning a feedyard:

The organization that I work for is in beef production because we want to own agricultural land. Owning good land is a wholesome food producing investment that can feed people in a time of need which also can provide a hedge against inflation. Consequently, some of that land is best suited for beef production. So when talking about profitability, we are much more concerned with a sustainable return per acre rather than return per cow. Thus, owning a feedyard and/or entering into an agreement with a packer to develop a branded product are further attempts to return more dollars to the original land investment. We also hope the closer we get to the consumer dollar the more we will lessen the price volatility of our final product. Within that framework, the following observations are provided to encourage thought more than to provide absolute answers.

1. Market price for our calves or our fed cattle has more influence on our profitability than anything else we do. Unfortunately, our company doesn't have a system that can accurately forecast what our calves are going to be worth or whether those calves will make money in the feedyard or not ($P < .000001$). In fact, market variability has been quite pronounced over the last few years as shown in Table 1 and Table 2. Table 1 shows the actual prices and Table 2 defines the year on year variation. Table 2 shows that from 2012 to 2016, calf prices have changed up or down from the previous year by an average of 20% or $241 per head. That is all fine and good when it is going up, as it did in 2013 and 2014. However, coming down may present some real problems if you haven't been thrifty with previous profits and are not willing to adapt. Consequently, Table 2 also shows the volatility appears to be slightly less on fed cattle over that same period.

Table 1. Average of Weekly Market Price ($ / head)

	2011	2012	2013	2014	2015	2016
Jan-Mar 550 lb. Steer [a]	842	974	957	1,210	1,551	1,089
Jan-Mar Fed Steer [b]	1,430	1,625	1,638	1,885	2,106	1,768
Jul-Sep Fed Steer [c]	1,482	1,560	1,586	2,067	1,885	1,560 [d]

[a] Nebraska average of weekly prices from Jan to Mar
[b] Kansas average of weekly prices from Jan to Mar (assumed 1300 lbs.)
[c] Kansas average of weekly prices from Jul to Sept (assumed 1300 lbs.)
[d] Not actual; based on an estimated price of $120/cwt.

Table 2. Percentage variation in revenue per head from one year to the next							
	2012	2013	2014	2015	2016	5 year avg.[d]	Avg. $/head [e]
Jan-Mar 550 lb. Steer [a]	16%	-2%	26%	28%	-30%	20%	$ 241
Jan-Mar Fed Steer [b]	14%	1%	15%	12%	-16%	11%	$ 203
Jul-Sep Fed Steer [c]	5%	2%	30%	-9%	-17%	13%	$ 218

[a] Formula for 2012 = From Table 1 (2012 price / 2011 price) – 1 (rounded to nearest percent)
[b] Formula = From Table 1 (2012 price / 2011 price) – 1 (rounded to nearest percent)
[c] Formula = From Table 1 (2012 price / 2011 price) – 1 (rounded to nearest percent).)
[d] Sum of absolute values of the year to year percentage changes from 2012 to 2016 divided by the 5 years
[e] Sum of absolute values of the year to year dollar changes from 2012 to 2016 divided by the 5 years

2. Weather extremes can also wreak havoc on profitability by rapidly increasing the cost of production. We cannot predict the weather so as to plan optimum stocking rate; we can only react to it. Table 3 shows the effects of the extreme drought of 2012-2013 which nearly doubled our cost of production on the Rex Ranch. Fortunately, the increase in the 2014 market price baled us out of what could have been a severe loss on the 2013 calf crop.

Table 3. Rex Ranch Annual Calf Cost ($/head)						
	2011	2012	2013	2014	2015	Average Variation
Calf Cost	453	635	876	591	579	
Variation from previous year	(20)	182	241	(285)	(12)	148

3. A feedyard when used as a hotel to rent space makes a nice return on investment as long as you keep occupancy up. However, the profitability of owning the cattle is extremely volatile. Since 2010 feeding returns have ranged from $600 to ($600) per head when viewing the feedyard as an isolated segment. When viewing the system as a whole (ranch and feedyard together) during the last few years, the $600 losses were more than compensated for by the cow/calf profitability on the ranch.

4. We learned quite a bit from 1995 to 2010 custom feeding our calves in multiple feedyards and harvesting the cattle at multiple packing plants. However, since feeding our cattle in one yard for the past six years and harvesting at only two plants, we feel we are learning at a much faster pace than before.

5. We are learning how to feed cattle differently from different parts of the country.
   o Florida calves fed a higher roughage ration than previously for first 60 days in the feedyard caused dry matter intake to increase from 1.6% to 1.9% of body weight and decreased founders from 7% to 0%. Whereas, the western calves never really exhibited an intake problem or founder problem to begin with.

6. We are adjusting how we implant cattle based on genetic make-up
   o Holstein calves from our dairy in Utah require a less aggressive implant protocol than we originally assumed. The less aggressive protocol decreased dry matter feed conversion (DM lbs. per lb. of gain) from 6.7 to 6.2, increased ADG (lbs. per head per day) from 2.8 to 3.1 and increased hot carcass yield from 58.5% to 61.5%.

7. Animal handling/disposition plays a role in feedlot performance. For years, Rex Ranch has focused on animal handling technique because our grazing philosophy requires that we move often and we choose not to increase labor (one man moving 850 pair every 3 to 4 days). We have also culled the poor attitudes (I am only talking about the cattle; fortunately, they have allowed me to stay on.). Consequently, the Rex cattle' disposition is noticeably different in eyes of the feedyard cowboys and they appear to have a slight edge on feedyard performance in terms of dry matter feed conversion (DMC) and average daily gain (ADG) when compared to cattle of similar genetics from our other ranches. In addition, another one of our operations has made an intensive effort to decrease hotshot use. The resulting difference in the way the cattle handled and came up on feed was noticed immediately at the feedyard. We fully expect the differences of cattle disposition between ranches to dissipate as we focus on improving our animal handling skills company wide.

8. You can improve genetics within a genetic interval using EPDs and it will translate into added feedyard performance and profitability.

   o Prior to 1999, we were still using ratios to select our bulls on our Florida operation. Finally, in the year 2000, all the hard work and foresight over the prior years of data collection culminated in us being able to run EPDs on our ranch raised bulls. As you can imagine, those EPDs had very low accuracies but we used the EPDs and a disposition score to cull the bottom third of our bull battery. We had been custom feeding our calves for the last 5 years so we had a pretty good idea of what they were. The next two calf crops from the improved bull battery showed significant improvement in feedyard performance. Calf fed ADG improved from 2.6 to 2.9 and DMC improved from 6.7 to 6.2. This added performance jump has been retained and improved upon to this day through the consistent use of EPDs.

   o In the early to mid1990's calves raised on the Rex Ranch were sold and fed to repeat buyers and those buyers reported that they graded 70 to 80% choice. Prior to 2007, the Rex Ranch was using ratios to select their bulls off test. In addition, the ranch raised bulls with the highest ratios were collected and used along with a few proven AI sires to expose the seedstock cows for the next bull crop. Since marbling wasn't seen as a problem, selection focus for several years had been on creating the best cow for the environment that produced a calf that grew well post weaning. Consequently, pregnancy rate and weaning percentage both improved from 92% to 94% and ranch cost of production held steady. However, quality grade by early 2006 had decreased by 40% and dystocia rate on our 1st calf heifers was around 25%. In 2007, we made bull and seedstock cow selections based on our first in-herd EPD run and we used only high accuracy industry proven AI sires on the seedstock cows. Using EPDs, we intensified our focus on improving marbling and calving ease and tried not to give up too much growth or ruin the cow in the process. In 2015, our dystocia rate on our 1st calf heifers that had been exposed to our ranch raised bulls had decreased from 25% to 8%. Our feedyard performance had held steady while quality grade had risen back to 80% choice or better. ADG and DMC on comparable sets of cattle across years has held steady or improved. 1737 head of open yearling heifers placed in the yard in September 2015 at 761 lbs. closed out in January and February of 2016 with 841 lb. hot carcass weight, 3.76 lb. ADG, 6.23 DMC, 87% choice or higher, 44% Y1&Y2s and 10.4% Y4s. Clearly, progress can be made if we use the technology and tools available to us in a sound fashion.

Table 4. Calves weaned from two different ranches experiencing extreme drought [a]

	2012 Preg Rate	2013 Preg Rate	In Wt.	Out Wt.	HCW	Death Loss	DoF	ADG	DMC	COG
Ranch A	91%	92%	621	1,408	901	1.1%	209	3.74	5.57	$ 1.03
Ranch B	93%	91%	538	1,382	885	10.5%	288	2.71	6.34	$ 1.23

[a)] Both ranches calves had been weaned in growyards prior to entering the feedyard. Ranch A's calves stayed in the growyards 45 days longer.

9. The nutritional environment absolutely matters from conception to carcass.
   o Two of the ranches in our system that experienced serious drought conditions had drastically different feedyard performance from the calves weaned during the drought. However, both ranches had similar conception rates during the drought so you couldn't see the nutritional effects in cow condition. Table 4 shows the differences in feedyard performance.

10. For better or worse, owning a feedyard has narrowed our focus and decreased our marketing options allowing us to spend more time on improving operational efficiency. The following points indicate some of the changes that have occurred.

    o Our marketing options have been greatly simplified. We no longer sell calves or yearlings just fed cattle on a carcass basis. This change greatly simplifies the revenue equation.
    o If it doesn't make logistical sense on the ranch to ship the cattle from a set of scales, we can just add back the historical shrink to the off truck weight at the feedyard for the ranch's data.

    o In the dead of winter with extreme weather, we no longer worry about an early morning gather for weigh up purposes. Instead, we gather the cattle later to make sure they have watered and eaten to lessen the stress of the haul and arrival.

- Since our cattle are sold on a carcass weight basis, we have foregone the weighing of our fat cattle prior to hauling them to the plant to decrease stress, labor and dark cutters.

- We are streamlining our processing protocols so as to not unnecessarily repeat vaccinations.

- We have quit sorting off and haggling on the value of what appears to be lower quality cattle. What few head of cattle that are lighter weight, off color, rat tails, long ears, humps, etc… ship together and feed right along with the others of their same weight class.

- It is exciting to see our people in the field moving beyond being cowboys to becoming beef producers.

11. "In Search of Beef Production Nirvana" what kind of title is that? Wikipedia defines Nirvana in the following ways (I am partial to the Hindu philosophy):

    - In the Buddhist tradition, nirvana is described as the extinguishing of the fires that cause suffering and rebirth.[29] These fires are typically identified as the fires of attachment (raga), aversion (dvesha) and ignorance (moha or avidya).

    - In Hindu philosophy, it is the union with Brahman, the divine ground of existence, and the experience of blissful egolessness.[8]

The overall question for our industry should be: In our quest to achieve Beef Production Nirvana, what is the most efficient, cost effective way to provide a constant flow of quality beef to various targeted markets? Individually, each of us need to ask: What role do I play in adding value to that system, how can I improve and how do I get compensated properly for my contribution?

Growing Profit by Understanding Cow Maintenance Efficiency and Maintenance Requirement in an Animal and Systems Context

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Introduction and Background

A statistic often used to illustrate the importance of cow maintenance requirements is that the feed associated with maintaining the cow herd accounts for roughly 60% to75% of the total feed used in the cow calf herd and in some cases for overall beef production—a range that is well supported by scientific literature (Ferrell and Jenkins, 1984; Gregory, 1972; Heitschmidt et al., 1996; BIF, 1981). Given the magnitude of the costs associated with cow herd maintenance, cow feed intake is clearly an economically relevant trait—a trait directly related to the costs and therefore profit of beef production. In addition to its economic importance, differences in maintenance requirements have been shown to be heritable ($h^2 = 0.52$; Hotovy et al., 1991), which allows reduced maintenance requirements to be a clear target for selection and genetic improvement. Yet, the availability of these selection tools for genetic improvement of cow maintenance requirements is limited due to the expense associated with measuring maintenance requirements directly. Even with this difficulty, there are tools currently available that aid in the selection for improved maintenance requirements.

Tools for Selection

Cow energy needs can be divided up into four general categories: energy for gestation of the calf, growth, lactation, and maintenance (e.g. locomotion, temperature regulation, protein turnover, etc). Literature evidence also suggests the latter 2 items (lactation and maintenance) are not completely independent (Jenkins and Ferrell, 1983; Ferrell and Jenkins, 1984). Currently available expected progeny differences (EPD) useful for genetic improvement of maintenance requirements are largely comprised of those categories. These EPD focus on "maintenance energy" and make the assumption that a relationship between lactation and maintenance requirements exists.

The EPD related to maintenance energy requirements are based primarily on mature cow weight, height and body condition score, leveraging data on traits easily recorded and reported by breeders. Given the relationship between lactation requirements and maintenance energy, milk EPD are also often used as a piece of the maintenance energy puzzle. In most cases, EPD for mature weight and height are available to use in selection with increases in mature weight indicating greater maintenance requirements. In some instances information on mature weight and the resulting mature weight EPD are combined with the milk EPD to produce the $EN (American Angus Association, 2016) and the maintenance energy EPD (e.g. Red Angus Association of America, 2016). However, one of the challenges associated with the calculation of these EPD is the relative low reporting rate for mature weight and body condition score observations. Often the number of mature weight observations may represent only 2 to 5% of the number of weaning weights stored in breed association databases. Admittedly, weaning weight numbers include observations on both male and female calves, yet given the opportunity to leverage repeated mature weight and BCS measures on cows, increased reporting rates would greatly enhance the accuracy of these evaluations.

One of the other challenges associated with genetic evaluation of ME is the time required for observations to be collected and the amount of time needed for EPD accuracy increases to be realized. The most useful data for the evaluation of ME comes from 2 year old and older cows, although in some instances weaning and yearling weights are used in multiple trait analyses as a correlated trait to provide some indication of mature size at an earlier age. An alternative to "waiting" for mature cow observations would be the development of genomic markers predictive of maintenance requirements. Markers associated with maintenance requirements could be used to increase accuracy of selection at younger ages and to identify maintenance energy requirement differences not expressed through mature weight alone. These markers would provide information earlier in an animal's life span, but given the current state of knowledge, they would not eliminate the need to weigh and body condition score females. Research is underway to identify DNA and protein markers predicative of differences in maintenance energy requirements such as reported by Cooper-Prado et al. (2014) and as indicated in the USDA-NIFA funded National Program for Genetic Improvement of Feed Efficiency in Beef Cattle (see: http://www.beefefficiency.org/).

Interpretation and Use

The EPD for improvement of maintenance energy requirements must be used in the context of the beef production system and never independent of that context or as the focus of single trait selection. With that perspective, EPD representing maintenance energy would be much like birth weight. Continued downward selection pressure on birth weight would ultimately result in calves with lowered survival rates. As with many traits maintenance energy likely has an intermediate optimum, where too low or too high is not a preferred outcome and is liable to result in reduced profitability.

Interpretation of mature weight and mature height is relatively straightforward with units in pounds (kg) or inches (cm) depending upon location (e.g. American Hereford Association and American Angus Association). However interpretation of maintenance energy EPD can be less straightforward with the particular breed deciding on the appropriate unit for interpretation. For instance, the Red Angus Association of America has chosen to express that EPD (I.e. ME EPD) in terms of Mcal/month where animals with lower EPD produce progeny requiring less feed input for maintenance than animals with higher EPD. This EPD combines knowledge of mature cow metabolic weight (thru the EPD for that trait) with knowledge of the milk production level of the cow as indicated by her milk EPD using an approach similar to that reported by MacNeil and Mott (2000), with increases in milk EPD resulting in increases in overall maintenance requirements. In the end, mature size accounts for approximately 91% of the variability in maintenance energy requirement while milk production level accounts for roughly 9%. The differences represent expected differences in the metabolizable energy requirements of daughters at a body condition score of 5. Translating the ME EPD into an amount of a specific feed source requires knowledge of the net energy of that feedstuff. However, no matter the feed source, animal ranking will not change for both ME EPD and predicted differences in metabolizable energy requirements. The American Angus Association has taken a slightly different approach, combining knowledge of genetic differences in mature weight and milk production with the economics of production into a dollar value, $EN. Representing the "an expected dollar savings difference in future daughters of sires" (http://www.angus.org/Nce/ValueIndexes.aspx) with larger values associated with larger savings in feed costs.

In the end, selection for maintenance requirements is undertaken with the goal of increasing profitability. The American Angus Association has taken the next step. Generally, maintenance energy is related to overall body size with heavier cattle having greater maintenance requirements. The challenge for cattle breeders is to balance lowering feed costs/input with the increased salvage value of larger cull cows. This balance is typically accounted for in the development of maternal-focused indexes where the value of changes in maintenance energy requirements is balanced with the increased income associated with larger cows and greater salvage value. Application of this knowledge in the public domain is limited with Melton (1995) and a few others reporting specific values for selection for improved efficiency or maintenance energy requirements. As adoption of economic selection indexes and the genetic and economic research increases, valuing differences in maintenance energy requirements will become more straightforward and likely use more precise genetic predictors than only mature weight alone.

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Making the cowherd more efficient and profitable by 2036: where do we focus our efforts for the biggest impact?

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Introduction

The future of the beef industry is encouraging. Recent years have yielded exceptional prices that have allowed unprecedented profits, especially for the cow-calf sector of the beef supply chain. At the same time, great advancements in production and genetic technologies have improved the production potential of cow-calf enterprises. The future holds expectations for continued global population growth and rising demand for protein. As a result, the beef industry's outlook for the next 20 years is bullish. The biology of beef production will not change, but there are numerous external factors to which cow-calf producers must adapt to remain profitable. In general, the challenges ahead are not new. A growing population with evolving social norms and interests in agriculture, increasing costs of production, labor challenges, and an uncontrollable pattern of precipitation would have topped the list of concerns for beef producers 20 years ago, and still do today.

This paper will take an over-the-shoulder look back in time to identify important changes and challenges the beef industry has dealt with over the past twenty years. Recent history will be used to illuminate factors of importance for the cow-calf sector in the future. Even though the prevalence and magnitude of external factors affecting the beef industry will remain largely unpredictable, there are enough trends to speculate where cow-calf managers should focus their efforts to maintain or improve efficiency and profitability through 2036.

Looking Back

Financial. Revenues and expenses have changed greatly over the past few decades. According to CattleFax (Troy Applehans, personal communication), weekly 550-pound calf price from 1988 to 1995 averaged $90/cwt, and increased to $165/cwt from 2008 to 2015 – an 88% increase. However, when adjusted for inflation the difference is only 18%. The influence of the cattle cycle does marginalize the value of prices between any two points in time, but considering that each value is an 8-year average, the influence of the cycle is lessened. Surely calf prices of 2014 and 2015 were exceptional, such that even without an improvement in performance, commercial cow-calf enterprises have been highly profitable.

The revenue portion of the profit equation is primarily a function of weaning rate and weights, calf price, and cull cow value, whereas the expense component is much more complicated. Figure 1 shows that over half of the expenses for a cow-calf enterprise can be categorized as depreciation, labor, or feed. Other expenses like repairs and maintenance, fertilizer, fuel, leases, and veterinary services are important when taken together, but independently are less important. In general, business expenses are influenced by broader economic factors like minimum wage, and the costs of energy, grains, and land. These external factors have also changed over time, and in some cases the change was dramatic. Figure 2 illustrates the relative change in corn, oil, land value, and minimum wage over the past 20 years. Each of these is important because they strongly influence major cost categories in a cow-calf enterprise. Table 1 shows the actual average prices for the same commodities and costs. The magnitude of inflation adjusted increase in oil and land values is remarkable, 284% and 134%, respectively. So remarkable that the more moderate increases of 9% for labor and 24% for feed appears less significant. However, when considering the proportional contribution of feed and labor to the total cow calf budget these smaller increases may be equally impactful.

Performance. Since the mid 1990s, the beef industry has embraced technology like never before. The seedstock sector has led the charge to develop improved data-driven tools for genetic selection. For example, residual feed intake as a measure of efficiency is now relatively common, and genomically-enhanced expected progeny differences (EPD) are available to the industry. Use of genetic tools for selection has yielded measurable gains in performance, particularly in the easily quantified growth traits. The average reported 205-day adjusted weaning weight of bulls and heifers entered in the American Angus Association in 1995 and 2015 are 581 and 638 pounds, respectively, indicating a 2.9-pound average annual increase. Data from the American-International Charolais Association shows a 31-pound increase in adjusted weaning weight over the same time period. It is safe to assume that the same upward trend in weaning weight is also evident in most other major breed associations. There are many other traits that must be considered to quantify overall genetic improvement, but in general, performance advancement has occurred in the seedstock sector.

On the other hand, translation of seedstock improvement to the commercial cow-calf operation performance is not as apparent. Availability of information documenting performance changes within the cow-calf sector over the past two decades is limited; however, Standardized Performance Analysis (SPA) data does shed some light. Table

2 shows Southwest SPA summary production date from 1993-1995 compared to 2013-2015 for ranches in Texas, Oklahoma, and New Mexico. Interestingly, during this time period when seedstock weaning weights were increasing, no change was evident among the commercial operations in the SPA dataset. In fact, there was essentially no change in reproductive performance or pounds of calf weaned per cow exposed. Table 3 demonstrates that this is also true in the northern plains region. Given the resources and climate, it is not surprising performance is higher on average among North Dakota cow-calf operations than those in the southwest, but it is interesting that over the past 20 years in these separate regions productivity per cow has not increased in parallel with clear growth trait advancement in the seedstock sector.

Why has there not been phenotypic change in the commercial cow-calf sector paralleling the seedstock increase in weaning weight? Why has reproductive performance also not improved? These are two very important questions to ponder. It may be that genetic potential for production of the seedstock sector has simply advanced beyond what the environment/resources will allow in these regions. It is possible that the SPA summaries from the southwest and northern plains simply show optimization, and that resources are dictating an upper limit to cost-effective performance.

Looking Forward to 2036

Understanding the changes that have occurred over the past 20 years provides context for identifying where producers should focus their efforts to ensure profitability in the future. The historic data should be viewed holistically in that future efficiencies and profits will not be mutually exclusive efforts to controlling costs and increasing revenues. Instead, success will come from optimizing expenses and performance by building a production system that will yield the lowest unit cost of production for the most valuable calf that can be produced in the operational environment. Excellent genetics exist, and there is opportunity to better utilize advanced genetics across most of the commercial cowherd in the U.S; however, there is greater opportunity for improving efficiency and profit for most operations through management.

Financial. Consider the price data in figure 1 and table 2. If the same trend in prices and inflation over the past 20 years continue for the next 20 years, then prices of oil, corn, ag land, and minimum wage in today's dollars would approximate $307/barrel, $5.77/bushel, $6,786/acre, and $7.90/hour, respectively, in 2036. It is difficult to speculate these trends over 20 years, and seems likely that this extrapolation over-estimates oil, and underestimates corn and especially labor. However, these values are still concerning. Producers should ask themselves if their current cow-calf production system can remain financially successful in such a volatile price environment. Using the same approach to extrapolate the 18% inflation adjusted increased calf prices from the past 20 years equates today's $175/cwt calf price to $206/cwt in 2036. Global population growth will increase food demand and beef price; however, the same influence will elevate the cost of grains and energy. The most successful cow-calf operations in 2036 will employ production systems that minimize labor, purchased feed and depreciation costs to realize the lowest unit cost of production possible.

Independent of the cost of production, calves and cull cows of the most profitable 2036 cowherds will be aggressively marketed. In an effort to gain the highest possible price for the most valuable calves that the efficient production system will allow, successful managers must capitalize on market seasonality when marketing calves and culls, and capture premiums through branded programs that are compatible with the production system.

Performance. The demonstrated lack of performance change in the commercial cow-calf sector over the past 20 years causes one to question how managers should focus their effort in achieving or exceeding animal performance targets in the future. It is likely that for most operations some improvement in both genetics and management will be necessary, but even where good genetics are present such potential will not be realized to the fullest without great management. There is opportunity to improve pregnancy rate and weaning rate, but the marginal cost of higher performance may be prohibitive. In operations that are already well-managed, performance improvement will come in very small increments. However, among operations below 90% pregnancy rate, there may be an opportunity to gain another 5%. The marginal cost for weaning a calf crop greater than 85 to 90% is likely not warranted. This is especially true in extensive range conditions or harsh subtropical environments where a practical upper limit to pregnancy percentage may fall below 90%. In these same environments current genetic potential for milk production and preweaning growth can exceed the resource's ability to support such potential. Managers in these environments must use caution in genetic selection and pursuit of increased animal performance.

Performance gains may be made through long-term selection or strategic inputs to yield small improvements, but managers of the 2036 cowherd should seek high leverage change for greatest impact. The best managed operations do these things already and utilize strategic inputs well. Nevertheless, across the U.S. cowherd there is still opportunity for commodity beef producers to better utilize technologies like calfhood growth-promoting implants

that increase gain and efficiency at a low cost, and properly timed and administered vaccines and anthelmintics that improve health and minimize performance losses.

The greatest opportunity and leverage to cost-effective performance improvement may exist at the production system level. Many of the best managed cow-calf operations in the U.S. do a very good job of capitalizing on hybrid vigor, but unfortunately too many continue to overlook this opportunity. Crossbreeding is a management decision that is high leverage because by improving fertility, calf age at weaning, calf weaning weight and cow longevity is enhanced. Greater cow longevity decreases the percentage of replacements needed annually and increases the proportion of forage consumed by producing cows. Ultimately, this can have a big effect on the efficiency of production. This is not a new concept, but somehow crossbreeding remains underutilized. The most efficient and profitable commercial cow-calf operations of 2036 will maximize the benefits of heterosis by being predominately crossbred, and they will utilize terminal sires to the fullest potential within the constraints of meeting replacement female needs. These same characteristics exist today among the most profitable commercial cow-calf operations.

Focusing Efforts for the Biggest Impact

Neither currently nor in the future will producers individually be able to control commodity prices, the price of grazing land, or the compensation rate of adequately skilled labor. Also outside of producer control are the biological limitations to cow performance in any given environment. As world population grows, demand for food and energy will increase as well, elevating both revenues and expenses to the cow-calf operation. Considering the proportional changes in calf prices and expense category indicators over the past 20 years, cow-calf producers should prepare for these trends to be somewhat similar in the future. In order to make the cowherd more efficient and profitable by 2036, producers should focus on high leverage interventions at the production system level. There is no silver bullet to success, but cow-calf producers interested in making improvement will adapt their production system with a focus on optimizing labor, purchased feed, and depreciation in a way that minimizes unit cost of production. Successful operations will employ proven technology with a positive return on investment, diligently market calves and cull cows to their highest value, and manage price risk effectively. Producers should focus on maintaining or improving genetics of the cowherd with reasonable expectations for improved performance and a careful consideration for the marginal value of performance change. Central to the decisions for optimizing performance of the cowherd should be an effort to maintain a high level of heterosis.

The overarching philosophy of management in the future will be of paramount importance to success in the years ahead. The interconnectedness of a cow-calf enterprise to other agriculture and nonagricultural enterprises and activities on farms and ranches will be inescapable. As production systems are adapted to the changing business and social pressures in the years ahead, focus on the habitat, wildlife, and societal views on production methods will be warranted.

Figure 1. Proportional contribution of expense categories for a cow-calf enterprise (2010-2015 Southwest SPA data)

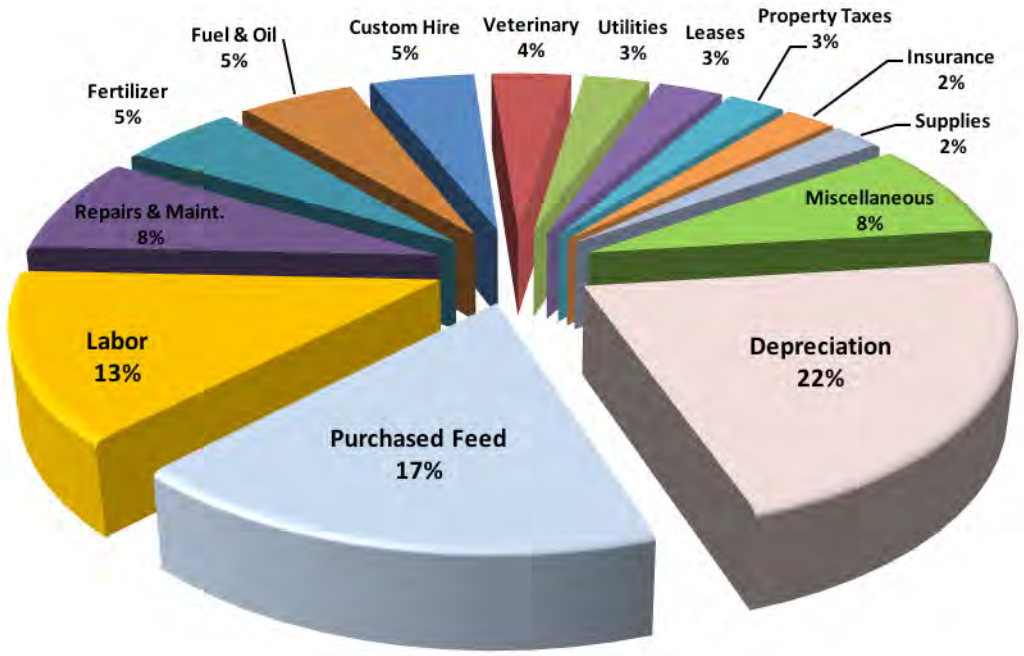

Figure 2. Inflation adjusted 20-year relative price change in corn, oil, ag land, and minimum wage

Table 1. Twenty-year price change in corn, oil, ag land, and minimum wage

Item	1993-1995	2013-2015	%[a]
Corn ($/bushel)	2.40	4.65	24
Oil ($/barrel)	18	80	284
Ag Land ($/acre)	793	2900	134
Minimum wage ($/hour)	4.25	7.25	9
Dollar	1.00	1.56	56

[a]Percent change after adjustment for inflation; shown graphically in figure 1

Table 2. Southwest Standardized Performance Analysis (SPA) summaries comparing average cow-calf performance measures separated by 20 years.

Measure	1993-1995[a]	2013-2015[b]
Pregnancy rate/cow exposed (%)	89	90
Weaning rate/cow exposed (%)	84	84
Weaning weight (lb.)	525	525
Lbs. of calf weaned/cow exposed	439	439

[a]64,881 cows
[b]12,291 cows

Table 3. Northern Plains Standardized Performance Analysis (SPA) summaries comparing average cow-calf performance of CHAPs producers separated by 17 years.

Measure	1993-1997[a]	2010-2014[b]
Pregnancy rate/cow exposed (%)	93	94
Weaning rate/cow exposed (%)	89	90
Weaning weight (lb.)	557	554
Lbs. of calf weaned/cow exposed	490	495

[a]111,583 cows; Ringwall and Helmuth, 1998
[b]88,000 cows; www.ag.ndsu.edu/DickensonREC/chaps-software-1

RNA interference:
Will the overlooked nucleic acid be the new star among animal health technologies?

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Introduction

The "central dogma" of modern biology, since its adoption in the mid-20th century, has been the basis for our understanding of how genetics impacts animal phenotypes. However, discoveries in the past 20 years have greatly complicated this simple storyline. Among these new discoveries, RNA interference is exciting not only because it allows us to more fully understand the inheritance of complex traits, but also because it is allowing for the development of an entirely new class of pharmaceuticals.

What is RNA interference?

In genetics, it is common to think of DNA as containing sequences that encode for proteins (genes) and a bunch of other DNA that is unimportant. This thinking is based on the central dogma of biology, which states that DNA serves as a template for RNA production, and RNA serves as a template for protein production, ultimately driving the form and function of the organism. Unfortunately, this elegantly simple paradigm has been muddied by the discovery of a number of very important non-coding RNA species. Scientists working with the roundworm in the early 1990s discovered short segments of RNA that did not code for protein at all (Lee et al., 1993). Instead, these segments (now called microRNA) could align with a longer RNA strand containing a complementary sequence, and cause it to be degraded, blocking protein production (Figure 1). This biological phenomenon was later verified to occur in many other species, including plants, animals, and humans.

Scientists began to realize the importance of this mechanism in normal development and function, partly because of the sheer number of genes that are regulated in this manner. The number of potential target genes varies between species, but recent estimates are that about 50% of human genes can be regulated by microRNA.

Further groundbreaking work, resulting in a Nobel Prize in 2006, was the discovery that introduction of synthesized double-stranded RNA into the cell could mimic the naturally occurring process, bind to RNA of a specific gene, and prevent protein production (Fire et al., 1998). Not only has this provided scientists with a superior research technique to determine the function of specific genes, but this technology also has exciting potential to be developed as a tool to treat disease or affect physiological function.

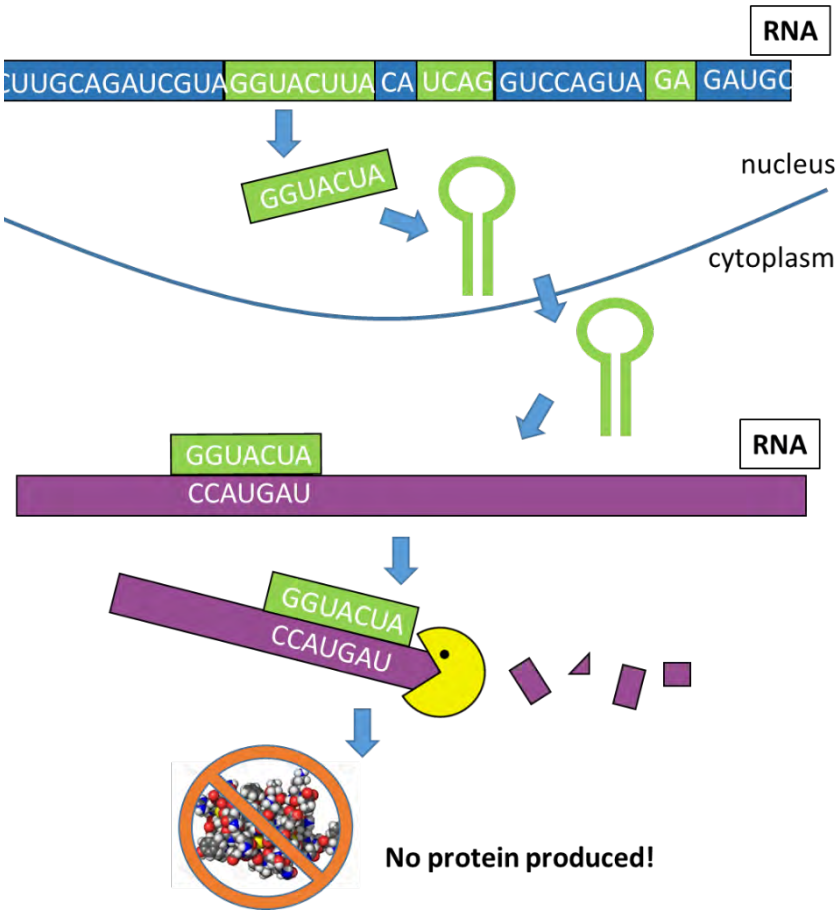

Figure 1. Mechanism underlying gene silencing by microRNA-mediated RNA interference. MicroRNA encoded by the genome is often found in introns that are excised from messenger RNA after transcription. The excised microRNA typically forms a hairpin loop that triggers post-transcriptional processing. The resulting short interfering RNA strand is complementary to a portion of a messenger RNA sequence, or often to several mRNA targets. The formation of double-stranded RNA causes the activation of an enzyme complex known at the RNA-induced silencing complex that degrades the mRNA. As a result, the protein encoded by the mRNA is not produced, resulting in a change in cellular function.

Micro RNA and inherited traits

One intriguing aspect of this new knowledge around RNA interference is the idea that introns (the non-protein coding "junk" DNA found within the coding sequences for proteins) may actually be the key genetic element underlying some selected traits. A single nucleotide polymorphism at a critical place within a microRNA sequence could, in theory, impact many proteins by creating or eliminating regulatory suppression by the microRNA through improved or impaired complementarity (Li et al., 2011; Li et al., 2015).

Epigenetics, though not the primary focus of this paper, has also turned traditional genetics on its head. The premise of this field of study is that environmental factors (i.e. diet, social interactions, physical activity) can lead to changes in animal function that can be passed on to the next generation, *without* an alteration in DNA sequence (Gonzalez-Recio et al., 2015). These

changes are typically driven by altered chemical states of DNA that influence its accessibility for transcription. Interestingly, microRNA play a key role in regulating epigenetic mechanisms (Holoch and Moazed, 2015), and therefore may be involved in inherited traits that are not encoded by DNA sequences. Conversely, epigenetic modification of DNA induced by butyrate (an end-product of ruminal carbohydrate fermentation) lead to alterations in microRNA expression (Li et al., 2010), suggesting a bidirectional link between epigenetics and RNA interference.

RNA interference as a next-generation pharmaceutical tool

In the same way that genetically-encoded microRNA can target mRNA sequences for destruction, synthetically-produced RNA molecules can be designed to silence proteins in a cell with great specificity (Bradford et al., 2016). This offers a number of exciting opportunities for addressing big problems in animal agriculture. For example, modern laboratory tools allow for the rapid genomic sequencing of new pathogens that can devastate livestock sectors; however, this information is currently put to use in a months-long process of creating vaccines. With continued developments in RNAi, it should be possible to rapidly (days or weeks) design and deploy small RNA molecules targeting the pathogen directly, allowing for a much more rapid counter-attack. Also, the active compound in RNAi is simply an RNA molecule (consumed daily by everyone), which makes this platform appealing from a food safety / residue perspective.

There are significant challenges to address before RNAi-based therapies will be practical for use in livestock. One hurdle that must be addressed for *in vivo* application of RNAi is the delivery of RNA molecules into cells of target organs. This is challenging because most cells do not normally take up RNA molecules. Secondly, the RNA molecules have to be protected from degradation while in transit to the organ of interest, which generally means using a nanoparticle with its own set of challenges. Finally, in light of recent survey data suggesting that 80% of consumers want mandatory labeling of food that contains DNA (Lusk, 2015), it is likely that consumers will initially be apprehensive about agricultural uses of RNAi.

Although the use of RNA interference to promote animal health may not come to fruition soon, it may be impacting human health already. The first phase 3 clinical trial utilizing RNAi is currently underway, targeting the elimination of a mutant protein that can cause a form of amyloidosis (http://clinicaltrials.gov/ct2/show/NCT01960348). More broadly, there is growing evidence that animal-source foods may impact human health in part by delivering biologically-active microRNA (Zempleni et al., 2015). Among the hundreds of microRNA found in cow's milk, one sequence known as miR-29b was shown to increase in circulation follow human consumption of the milk, and the downstream targets of this microRNA were altered in blood cells (Baier et al., 2014). Because miR-29b has been shown to promote the growth of cells that create bone matrix, these findings implicate cross-species RNAi as a likely factor in the beneficial effects of milk consumption on bone density. It is entirely possible that humans have been affected by diet-derived RNAi "nutraceuticals" for millennia!

Conclusions

We are in the very early stages of understanding the role of microRNA in inheritance of traits in livestock, and we are also likely decades away from seeing commercial application of

RNAi therapeutics. Nevertheless, the growing understanding of this fascinating biological process, and its implications across species, has opened up exciting possibilities in both fields.

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BEEF YIELD GRADING: *History, Issues, and Opportunities*

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Beef grading history

The United States beef yield grade arose from industry interest in yield measurement beginning in the 1950's. The landmark data from which the yield grade is derived was presented at the American Society of Animal Production meetings in Chicago in 1960 and consisted of 162 beef carcasses representative of the period (Murphey et al., 1960). Those data were used to develop a multiple-linear prediction equation using 12th rib fat depth, percentage kidney-pelvic-heart fat, hot carcass weight and ribeye area to estimate percentage boneless closely trimmed round loin rib and chuck (BCTRLRC). A second equation, the calculated yield grade, was developed as a 1 through 5 index using the same four carcass variables to estimate ranges of BCTRLRC. Yield grading began as a one-year trial in July 1962 and was put into effect on June 1, 1965.

Since the industry began using the yield grade equation, much research (Abraham et al., 1968; Abraham et al., 1980; Reiling et al., 1992; Farrow et al., 2009) has evaluated the ability of the four chosen variables to estimate boneless lean yield. Subcutaneous fat depth measured at the 12th rib is most closely related (r = -0.53 to -0.66) to boneless lean yield, followed by percentage kidney-pelvic-heart fat (r = -0.18 to -0.58), ribeye area (r = -0.18 to 0.51), and hot carcass weight (r = -0.03 to -0.53).

At inception, the yield grade was either determined from objective measures of 12th rib fat depth (using fat ruler) and ribeye area (using dot grid) or subjectively assessed. By 1978, the GAO reported to the U.S. Congress that yield grade needed to be assessed more accurately (Woerner & Belk, 2008). Development of an electrical instrument grading system began in 1980 and through several iterations of improvement and validation, instrument grading became a reality in 2007. No industry standard exists concerning subjective human versus objective instrument grading; instrument grading use ranges from none to the sole determinant of yield and quality grade.

Economics of yield grading

Value-based sales in which yield grade premiums and discounts may alter the final carcass value are an ever-increasing proportion of beef cattle/carcass marketings. The maximum premium offered for a yield grade 1 equals $8/cwt. whereas a yield grade 5 carcass carries up to a $20/cwt. discount (USDA 2016a). When the maximum reported yield grade premium or discount is applied to a 900-pound carcass, carcass value is altered by +$72, +$45, -$135, and -$180 for yield grades 1, 2, 4, and 5, respectively. Application of the previous values to the annual fed beef population indicates the potential industry value for yield grade valuation is +$108 million, +$326 million, -$309 million, and -$61 million for yield grades 1, 2, 4, and 5, respectively (USDA, 2016a; USDA, 2016b).

Inconsistencies and challenges

The era in which the yield grade was developed was dominated by small-framed early maturing cattle which were primarily purebred Herefords. In contrast, the current fed beef population is a kaleidoscope of genetic diversity that is medium and large in frame; the greatest population of purebred animals is now represented by the Holstein breed. Moreover, cattle feeding technology including growth promoting implants and beta-adrenergic agonists offer cattle feeders the opportunity to maximize growth and manipulate composition of gain. Improvements in genetic selection and growth technology have resulted in annual hot carcass weight gains of 5 pounds for steers and 6 pounds for heifers. Continuation of the current trend suggests that mean hot carcass weights will reach 1000 pounds in the years 2040 and 2046 for fed steers and heifers, respectively. In contrast, the population of cattle from which the yield grade equation was derived ranged from 350-900 pounds with a mean hot carcass weight of approximately 600 pounds.

The relationship between hot carcass weight and rib eye area has been assumed to be linear as denoted in the yield grade equation (USDA, 1997) and displayed on a rib eye measurement dot grid. In contrast, we have demonstrated that relationship is quadratic in total, with a linear portion that is represented by a lesser rate of longissimus muscle growth than assumed (Lawrence et al., 2008). When yield grades derived from the multiple-linear equation are compared to red meat yield, 40% of the variation in red meat yield can be accounted for in beef-type carcasses (Lawrence et al., 2010). However, 0% of the variation in red meat yield can be accounted for when the yield grade equation is applied to Holstein steers (Lawrence et al., 2010). The lack of relation is Holstein steers is most likely due to limited or disproportional subcutaneous fat deposition as compared to other lipid depots combined with a lesser muscle to bone ratio.

Potential modifications and other systems

Camera grading technology has the ability to redefine appropriate linear measures to predict red meat yield of beef carcasses. However, today camera systems continue to use the equation generated from 162 carcasses harvested in the 1950's. Farrow et al. (2009) demonstrated that other variables could be generated to improve predictability of red meat yield. Although no official changes are slated to be made to alter the yield grade equation, this author suspects that individual beef processors have gathered and are using such information in-house.

In considering how to improve upon the USDA system, it is imperative that we reflect on what other nations are doing. Our Canadian neighbors developed their current beef yield system in 1992; that system uses metrics of muscle width (dorsal-ventral distance), muscle length (medial-lateral distance), and subcutaneous fat depth to predict percentage carcass lean. Notably, the Canadian system does not include hot carcass weight or percentage kidney-pelvic-heart fat. Similarly, a system developed to predict yield of Japanese beef carcasses measures subcutaneous fat depth, intermuscular fat depth, and rib eye area – albeit at the 6th rib location as well as a cold carcass weight specific to the left carcass side. Beef producers in Europe have still another method of lean prediction, a subjective evaluation of carcass muscle conformation combined with a subject evaluation of fat deposition.

In summary, we continue to use a yield estimation system developed from a small population of cattle that no longer exist to predict red meat yield of cuts that are increasing leaner. We apply that estimate to carcasses that weigh beyond the inference of which it was designed and we have ignored the opportunity to develop new yield estimates afforded by camera grading. Leadership within the beef community must decide if the status quo is acceptable, or if improvement is warranted.

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Our goal is to sustainably reduce feed resources required to produce beef via the rapid development and deployment of novel nutritional, genomic and genetic improvement technologies.

We will strengthen the international competitiveness of US agriculture and enable increased food production by increasing the animal protein produced without additional feed inputs and with a reduced greenhouse gas footprint.

What is the project?

✓ The project involves a consortium of scientists, industry partners, breed associations, and cattle producers who will collect DNA samples and feed intake, growth and carcass composition data from over 8,000 animals (8 breeds).

✓ Over 2,400 animals will be genotyped to generate across-breed molecular expected progeny differences (**MEPDs**) for feed efficiency, feed intake, growth and carcass traits.

✓ In addition to creating and validating selection tools for producers, we will also be examining the DNA of efficient animals and seeking straightforward methods to identify efficient animals without measurement of individual intakes.

✓ This project involves developing tools for marker assisted selection (MAS) and also for marker assisted management (**MAM**). MAM is application of specific management practices (e.g. diet, days on feed, etc.) based on an animal's genotype so that it reaches a given outcome group (i.e. choice) with the least feed inputs.

Why is this important?

A 1% improvement in feed efficiency has the same economic impact as a 3% increase in rate of gain.

The traits that beef producers routinely record are outputs which determine the value of product sold and not the inputs defining the cost of beef production. The inability to routinely measure feed intake and feed efficiency on large numbers of cattle has precluded the efficient application of selection despite moderate heritabilities (h^2 = 0.08-0.46). Feed accounts for approximately 65% of total beef production costs and 60% of the total cost of calf and yearling finishing systems. The cow-calf segment consumes about 70% of the calories; 30% are used by growing and finishing systems.

Table 1 shows the potential cost savings to the US beef cattle industry that could occur with selection for feed intake, feed efficiency, growth, and carcass traits. Calves and yearlings selected for residual feed intake (RFI) have the same ADG but eat less feed thus saving feedlot operators money. Assuming 27 million cattle are fed per year and that 34% of cattle in the feedlot are calves and 66% are yearlings, the beef industry could save over a billion dollars annually by reducing daily feed intake by just 2 lb. per animal.

Table 1. Estimated cost savings to the US beef cattle industry from selection for a 2 lb reduction in residual feed intake.

In Wt.	Out Wt.	Lb. Gain	ADG	Days on Feed	RFI	Reduced Feed Intake (lb)	Feed Cost Savings $/hd	% of Fed Mix	Total Feed Cost Savings
Calf Feds									
600	1250	650	3.5	186	0.0	0			
600	1250	650	3.5	186	-2.0	-372	(54.72)	34	$ 502,620,656
Yearling Feds									
775	1300	525	4.0	131	0.0	0			
775	1300	525	4.0	131	-2.0	-262	(38.67)	66	$ 689,539,820
								Total Savings:	**$ 1,192,160,476**
Annual fed slaughter cattle: 27 million head; Delivered feed cost: $ 294.62 as fed									

Weaber, 2011

How will this benefit me?

You will have genetic selection tools and techniques (**MEPDs**) that will allow you to create a cow herd that is more efficient at converting nutrients to calf gain. Additionally, the steers and heifers you send to a feedlot will use less feed to produce the same amount of high quality protein for human consumption.

Will this really work?

✓ MEPDs have been successfully employed for output traits (i.e. growth and carcass) on a within-breed basis in beef cattle. Results from the dairy industry have shown tremendous advantages, particularly in evaluating young sires, through the use of MEPDs.

✓ A large demonstration project that aims to illustrate the efficacy of tools developed from this project includes a group of approximately 20 seedstock producers from seven states representing the seven major U.S. beef breeds along with a large commercial ranch. Producer owned sires will be used to generate crossbred progeny that will have growth, feed intake and carcass data collected. These steer progeny and their sires will be genotyped.

✓ The demonstration component enables a validation of discovery work from the project and a visible demonstration utilizing academic and industry resources working towards a common goal, the development and employment of genomic tools to improve feed efficiency.

✓ Producer collaborators will provide DNA samples on females within their herds to examine the relationship between female fertility/longevity and feed efficiency. Inclusion of fertility/longevity traits in the project enables selection decisions to be made with a more complete understanding of potential genetic antagonisms across a suite of economically important beef production traits.

How can I keep up to date?

✓ Go to: www.beefefficiency.org

✓ Watch for episodes on NCBA's Cattlemen to Cattlemen television show.

✓ Attend meetings or presentations by members of the research team.

Producer Resources

Website
www.beefefficiency.org

Broadcast Media
NCBA's Cattlemen to Cattlemen

Multimedia Presentations
Webinars

2-day Conferences
Research updates
Feed efficiency component traits
Strategies for genomic selection
Commercial herd sire selection
Feedlot marker-assisted management (MAM)

Youth Leadership Conferences

Educational materials
Powerpoint™ presentations
eXtension materials

Software
Decision support software for sire selection and evaluation of economics of implementing MAM

Field demonstration projects

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Gene set enrichment analysis for feed efficiency in beef cattle

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Abstract

Selection for improved feed efficiency in cattle would decrease the amount of feed consumed for the same or greater levels of production resulting in enhanced profitability and sustainability. Selection for feed efficient cattle has been hampered by a lack of phenotypic data on feed intake and weights from cattle in production due to the cost and difficulty in collecting these data. The aim of this study was to better understand the molecular functions and biological processes associated with residual feed intake (RFI) by identifying gene sets (biological pathways) associated with RFI in Hereford cattle and to use this information to facilitate genomic selection for RFI. Feed intake and body weight were measured on 847 Herefords at Olsen Ranches in Harrisburg, NE. Animals were genotyped with the Illumina BovineSNP50 or BovineHD Bead Chips. Genome-wide association analysis was conducted with GRAMMAR mixed model software as part of the gene set enrichment analysis (GSEA). Single nucleotide polymorphisms were mapped to 19,723 genes based on the UMD 3.1 reference genome assembly based on coordinates within 8.5 kb either side of each gene. Gene sets (4,389) were compiled from Gene Ontology (GO), Kyoto Encyclopedia of Genes and Genomes (KEGG), Reactome, Biocarta and Panther for the GSEA. Gene sets associated (Normalized Enrichment Score > 3.0) with RFI after 10,000 permutations in GenABEL were centrosome (5) (GO:0005813), cytoskeleton organization (4) and peroxisome (KEGG:04146). Most (191) of the identified genes enriched within the gene set for RFI (leading edge genes) were unique to a single gene set although 15 leading edge genes were shared between centrosome (5) and cytoskeleton organization (4) and one gene was shared between cytoskeleton organization and peroxisome gene sets. Further GSEA are being conducted with Angus, Angus x Simmental and crossbred beef cattle to validate these results.

Introduction

Great strides have been made in improving cattle traits that are easily measured and associated with performance or output measures such as weaning and yearling weights. These traits also determine the value of beef products that are sold. Less improvement has been made in traits that are more difficult and costly to measure that are associated with inputs or cost of production. The expense and difficulty in measuring these traits has hampered improvement even though the majority of the costs associated with raising cattle reside in feed (Anderson et al. 2005). Residual feed intake (RFI) is often used as a measure of feed efficiency in beef cattle because it is phenotypically independent of growth and body weight (Koch et al., 1963). Residual feed intake is defined as the difference between the amount of feed actually consumed and the expected feed requirement based on body size and production level of the animal over the period feed consumption was measured. Cattle with low RFI are efficient animals that

consume less feed than expected for their level of performance. An advantage of using RFI as a measure of feed efficiency is that it is not correlated with the traits that are included in its calculation, unlike some other measures such as feed conversion ratio, that may have unintended selection consequences such as large mature cow size (Archer et al., 1999). The failure to measure RFI and use it as an evaluation tool to improve feed efficiency in cattle has largely been due to the cost and difficulty in measuring feed intake.

In the past decade, genomic resources for identifying regions of the genome associated with economically important traits have become available that have accelerated genetic improvement in cattle. As the genetics community has enjoyed these new genomic tools, the impediment to greater genetic improvement has become the collection of cattle phenotypes. The ability to economically collect a full set of phenotypes on cattle lags behind our ability to analyze genomes. This has been particularly true in collecting phenotypes on traits that occur late in life, are expensive or require specialized equipment. Traits such as these are therefore typically not used for routine calculation of estimated progeny differences (EPD), or if used are associated with low EPD accuracies due to the limited number of phenotypes collected on the breeding stock as well as their progeny.

The genotype-phenotype relationship for feed efficiency in cattle is complicated by stage of life, diet, breed, weather and a host of other factors. The use of phenotype-focused approaches to study the genetic basis of feed efficiency may be very helpful in identifying and validating loci that explain a large fraction of genetic variance. The National Program for Genetic Improvement of Feed Efficiency in Beef Cattle has collected RFI data on over 8,000 cattle in several cattle breeds (Angus, Charolais, Gelbvieh, Hereford, Limousin, Red Angus, Wagyu and crossbreds of Charolais x Angus, Piedmontese x Angus x Simmental, Simmental x Angus) to identify quantitative trait loci associated with RFI. To compensate for the lack of RFI phenotypic data on the majority of cattle in the US, the use of genetic markers predictive of RFI could be used to select animals for improved feed efficiency.

Just as breeds of cattle differ in their abilities to use dietary energy, so do individuals within breeds differ in their ability to convert forages or concentrates into usable energy to grow, maintain their body condition, successfully maintain a pregnancy or raise a calf. Some of the differences in feed intake that are not explained by differences in weight or growth rate are the result of genetic variation (Carstens and Tedeschi, 2006; Herd and Bishop 2000, Basarab et al., 2003). The reported heritability for RFI is moderate (18-49%) suggesting that there is an opportunity to make significant genetic gains in feed efficiency through selection (Bolormaa et al., 2011; Saatchi et al., 2014). There is evidence that measurement of RFI in cattle post-weaning, in mature cows, or across different feeding regimes is repeatable (Herd et al., 2003; Durunna et al., 2011). The consistency of RFI over time and across feedstuffs suggests that it may be a good measure to include in selection indexes for multiple-trait selection of cattle that are feed efficient and productive. It would also be an excellent candidate trait for marker-assisted or genomic selection.

To identify markers for marker-assisted or genomic selection, genome-wide association studies have been conducted to identify genomic regions with major effects on RFI (Barendse et al., 2007; Sherman et al., 2008; Bolormaa et al., 2011; Mujibi et al., 2011; Rolf et al., 2012; Serão et al., 2013; Abo-Ismail et al., 2014; Saatchi et al., 2014). A complementary approach to identify markers for selection is to identify genes that are differentially expressed between cattle

with high and low RFI (Chen et al., 2011; Al-Husseini et al., 2015; Paradis et al., 2015; Tizioto et al., 2015; Xi et al. 2015, Weber et al., 2016). The identification of genes that are differentially expressed would potentially identify genes with large or modest effects on variation in RFI. Genetic markers or single nucleotide polymorphisms (SNPs) within or near these genes could be used for selection.

The use of gene expression data can also be integrated into a third approach; the use of pathway, network or gene set enrichment analysis (GSEA). Pathway, network or GSEA aim to provide insights into genes that individually may have more modest individual effects but may be interacting with one another to cumulatively elicit a large effect on phenotype. The study of pathways or gene networks allows us to better understand the molecular functions and biological processes that are associated with a trait such as RFI. As GSEA has matured, it has used associations with SNPs within or near genes to substitute for gene expression data to identify gene pathways important to a trait. More recent enhancements have combined both SNP and differentially expressed gene data together to identify important gene pathways. Gene set enrichment analysis has previously been conducted with RFI for five breed groups consisting of Angus, ¾ Angus, crossbred Angus and Simmental and purebred Simmental (Serão et al., 2013). Nine clusters of Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways were associated ($p < 0.001$, enrichment score > 3.0) with feed efficiency. Those pathways included GO molecular functions of nucleotide binding, protein kinase activity and metallopeptidase activity, and GO biological process of ion transport, phosphorus metabolic process, membrane invagination and proteolysis. The KEGG gene set associated with RFI was the *MAPK* signaling pathway (Serão et al., 2013). The glycogen synthase kinase 3 beta (*GSK3B*) gene was the leading edge gene in the KEGG gene set and is involved as a regulator of nutrient storage in adipose tissue and skeletal muscle (Hoehn et al., 2004). Abo-Ismail and colleagues (2014) identified 35 biological process gene sets that were associated with RFI. Of these gene sets, ion transport and cation transport contained the largest number of leading edge genes although proteolysis, protein complex biogenesis and protein amino acid glycosylation were also identified. Ion transport, *MAPK* signaling, and proteolysis were gene sets that had also been identified by Serão et al. (2013) as associated with RFI in beef cattle. Pathway or network analysis can also be performed using other approaches as has been described by Rolf et al. (2012), Saatchi et al. (2014), and Weber et al. (2016). Several pathways (adherens junction, adipocytokine signaling, apoptosis, long-term depression, calcium signaling, melanogenesis, pancreatic cancer, pathways in cancer and *MAPK* signaling) were identified in more than one pathway and/or GSEA study as being important in RFI (Rolf et al., 2012; Abo-Ismail et al., 2014; Xi et al., 2015). Although, the specific pathways differed, Weber et al. (2016) identified pathways associated with RFI that are involved in the activation of the immune response and in the down regulation of fat deposition in adipose and muscle tissue in eight steers produced from one high and one low RFI Angus bull.

The aim of this study was to identify genes and gene sets that were associated with RFI to better understand the molecular functions and biological processes that are associated with RFI and to exploit this information through genomic selection to improve the efficiency of beef cattle production.

Materials and Methods

Eight hundred seventy Hereford cattle were sampled while on feed at Olsen Ranches, Inc. in Harrisburg, Nebraska where they were fed a concentrate ration as previously described (Saatchi et al., 2014). Phenotypes and DNA samples were collected over a three year period (2009-2011). Date of birth (DOB), date of weaning, sex (S), breed composition, days on feed (DOF), feed intake (DMI) and weights were collected. All cattle were fed a minimum of 70 days. Feed intake and body weight gain were measured with a GrowSafe (Airdrie, Alberta Canada) system. There were nine male contemporary groups that consisted of a total of 824 steers and one female contemporary group that consisted of 23 heifers. Four hundred eighty-nine cattle were genotyped with the BovineHD and 358 were genotyped with the BovineSNP50 assays. BovineSNP50 genotypes were imputed with Beagle 4.1 to the density of the Illumina BovineHD BeadChip using the 489 BovineHD genotyped Hereford cattle as a reference. Animals were removed from the analysis if the genotype call rate was less than 90%, if they were predicted to be Klinefelter (XXY) individuals or if phenotypic information (average daily gain [ADG], mid test metabolic weight [MMWT] or DMI) used to calculate RFI was missing. Heterozygosity of > 0.2 for non-pseudoautosomal region markers on the X chromosome was evaluated to confirm anatomical gender. A total of 847 Hereford cattle remained for the GSEA-SNP. Single nucleotide polymorphisms were removed if less than 90% of the genotypes were successfully called, if the minor allele frequency was less than 1% or if they failed the Hardy-Weinberg equilibrium ($p < 1.0x10^{-100}$) test.

Genome-wide association analysis (GWAA) was performed using the GRAMMAR mixed model software in GenABEL (http://www.genabel.org/; Aulchenko et al., 2007). Residual feed intake was calculated by subtracting expected DMI (dependent variable) from the actual DMI. Expected DMI was calculated by incorporating covariates for ADG, MMWT, contemporary group (CG), S, DOB and DOF to estimate RFI (*Animal* + *e*) as shown in equation 1.

Equation 1. Calculation of residual feed intake

$$DMI = \beta_o + \beta_1(ADG) + \beta_2(MMWT) + \beta_3(CG) + \beta_4(S) + \beta_5(DOB) + \beta_6(DOF) + Animal + e$$

The most significantly associated SNPs for each of the 19,723 annotated genes in the UMD3.1 reference assembly (http://bovinegenome.org/?q=node/61) were selected as a proxy for each gene and used for the GSEA-SNP. Gene proxies were only considered for SNPs that were located within 8.5 kb of a gene as this was representative of the average haplotype block size in Herefords as determined by a haplotype block analysis performed in the SNP Variation Suite 8.1 software (Golden Helix, Bozeman, MT) and finding the average distance between the beginning and ending nucleotide positions for each haplotype block. The GSEA-SNP analysis was conducted using a composite of 4,389 gene sets taken from Gene Ontology (GO; http://geneontology.org/) (n= 3,147), Kyoto Encyclopedia of Genes and Genomes (KEGG; http://www.genome.jp/kegg/) (n=186), Reactome (http://www.reactome.org/) (n=674) , Biocarta (http://www.genecarta.com/) (n=217), and Panther (http://www.pantherdb.org/) (n=165). Significance was calculated using the null distribution estimated from 10,000 permutations for each gene set using GenABEL in R (Holden et al., 2008). An enrichment score was calculated for each pathway using a modified Kolmogorov-Smirnov statistic, and these were normalized

(NES) based on the size of each gene set. Gene sets with NES > 3.0 were identified as associated with RFI.

Results and Discussion

Two GO gene sets, centrosome (5) (GO:0005813) and cytoskeleton organization (4) (GO:0007010) and one KEGG gene set, peroxisome (KEGG:04146) were associated with RFI (Table 1). The centrosome gene set is a member of the cellular component ontology tree. Centrosomes are critical in mitosis and meiosis as the spindle apparatus of the cell is organized by the centrosomes. Disruption of the centrosome affects the proper segregation of chromosomes in the dividing cell and the stability of the genome (Lerit and Poulton, 2016). Centrosomes are cell organization centers around which hundreds of proteins are found that regulate the cell cycle (Conduit et al., 2015). The centrosome gene set consists of 99 genes, and 37 of those genes are leading edge genes or genes that are enriched among those associated with RFI (Table 1). Fifteen of the leading edge genes in the centrosome gene set were also leading edge genes in the cytoskeleton organization gene set (Table 1). In addition to these genes being involved in centrosome and cytoskeleton organization in the cell, many of these genes play a role in tumor growth in a host of cancers. Of the leading edge genes, *CEP120* has been associated with abdominal obesity as measured by waist circumference in humans, although no direct associations with feed efficiency have been reported (Wen et al., 2016).

The cytoskeleton organization gene set is part of the biological process ontology tree. The cytoskeleton is responsible for maintaining the shape of the cell and is involved in cellular movement, cell division, and endocytosis. The cytoskeletal organization gene set has previously been associated with feed efficiency traits in poultry. Cytoskeletal genes have been downregulated in breast muscle in high feed efficiency broiler chickens (Kong et al., 2011). Others have identified the role of regulation of actin cytoskeleton as an important component of feed efficiency and compensatory gain in cattle (Rolf et al., 2012; Keogh et al., 2016). The regulation of actin cytoskeleton organization shares some similarity (3.84%) to that of the cytoskeleton organization gene set in that it is involved in the processes that disassemble cytoskeleton structures or their proteins. The cytoskeleton organization gene set consists of 246 genes of which 97 were associated with RFI.

Table 1. Gene Sets and Leading Edge Genes Associated with Residual Feed Intake.

Gene Set	NES[1] (nominal p value)	Gene set size (# leading edge genes)	Leading Edge Genes shared between gene sets[2]
Centrosome (5) (GO:0005813)	3.19 (p=0.0010)	99 (37)	Centrosome & cytoskeleton organization gene sets: *SLC9A3R1, CEP120, BIRC5,HEPACAM2, TUBG1, MAP10, USP33, BBS4 TBCCD1, CSNK1D, CEP57, LZTS2, CTNNB1, CYLD, SLAIN2*
Cytoskeleton organization (4) (GO:0007010)	3.07 (p=0.0011)	246 (97)	Cytoskeleton organization & peroxisome gene sets: *SOD1*
Peroxisome (KEGG:04146)	3.05 (p=0.0016)	73 (30)	

[1]Normalized enrichment score; [2]Leading edge genes are those that are enriched (significant) within the gene set.

Thirty leading-edge genes were associated with RFI in the peroxisome gene set and one gene (*SOD1*) was shared between the cytoskeleton organization and peroxisome gene sets. The peroxisome gene set is part of the cellular process ontology tree and is involved in cellular transport and catabolism. Peroxisomes are small organelles whose functions are essential in free radical detoxification, lipid homeostasis and hydrogen peroxide metabolism. The peroxisome transports medium chain fatty acids to the mitochondria where most of the β-oxidation occurs. The efficiency and ability of the peroxisome to function in lipid metabolism and to neutralize free radicals is essential in maintaining cellular membrane integrity and animal health. Mitochondrial biogenesis may play a role in shifts of muscle fiber types which may also impact feed efficiency (He et al., 2016). Although peroxisome proliferator activated protein gamma (*PPARG*) was not a leading edge gene in this study, it has been identified as an important regulator of food intake and energy homeostasis in rodents (Larsen et al., 2003; Festuccia et al., 2008).

Conclusion

Costs incurred with feeding constitute the major portion of the expense of raising cattle. Cattle that are able to develop, grow and maintain their body weight with less feed are more feed efficient. Identifying cattle that are more resource efficient through collection of daily feed intake and body weights is expensive and requires specialized equipment which has limited the collection of these data. The use of genomic markers to identify efficient cattle will provide a means of selecting breeding stock without the collection of expensive phenotypes on all animals. This study evaluated which biological pathways are involved in those cattle that were more feed efficient using RFI as the phenotype. Three pathways, centrosome (5), cytoskeleton organization (4) and peroxisome were associated with RFI, representing 191 unique genes. These genes are positional and functional candidates for use as genomic markers for RFI in beef cattle. Gene set enrichment analysis of Angus, Angus x Simmental and crossbred cattle are also being conducted to examine and compare in other beef cattle breeds.

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Effects of timing and duration of test period and diet type on intake and feed efficiency in Charolais-sired cattle

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Introduction

Profitability, within all sectors of beef production, is a function of inputs and outputs. In production systems, individual feed consumption represents the greatest financial burden (Miller et al., 2001). However, a majority of the intake evaluations performed in beef cattle have been conducted in cattle fed grain-based diets rather than those grazing forages. Furthermore, regulation of feed intake is influenced largely by diet type; thus, there may be limitations of using feedlot intake information in heifer development systems. For example, intake of grain-based, high energy feeds is controlled metabolically or chemostatically (NRC, 1996), whereas when poor quality, roughage-based diets are fed, intestinal capacity, "gut-fill", limits intake (Mertens, 1994). In addition, Durunna et al. (2011; 2012) discovered that feed efficiency reranking occurs in cattle fed different diet types at different biological stages. Therefore the regulation of feed intake of these different diet types may influence their efficiency of feed utilization, and some calves may be more efficient on different diet types.

Considering intake of forage and grain is regulated by different mechanisms, the hypothesis is that intake and efficiency will not be correlated across differing diet types, suggesting that feed intake and efficiency measures on differing diet types cannot be used interchangeably. We also hypothesize that intake evaluations can be shortened without losing accuracy; and feed efficiency can be measured at different stages of maturity in growing feedlot calves. This experiment has two objectives: 1) determine appropriate test length, timing, and repeatability of DMI, ADG, and efficiency over different biological time points; and 2) determine the relationship between forage-and grain-fed efficiency measures.

Materials and Methods

Two separate postweaning intake and performance evaluations were conducted on Charolais X SimAngus calves (n = 628; initial BW = 238 ± 46 kg, age = 211 ± 32 d). The 2 performance and intake tests represent the 2 major biological periods in the feedlot: growing and finishing. Upon arrival at the feedlot and prior to the growing period, steers were transitioned over 3 wk to a grain-based growing diet consisting of 50% corn, 15% corn co-products, 25% corn silage, and 10% supplement. Heifers were fed a forage-base diet consisting of 47.5% corn silage, 47.5% alfalfa haylage, and 5% supplement. After completion of the 70 d growing period, heifers were transitioned over 3 wk from the forage-based diet to the grain-based diet. All cattle were fed the common, grain-based diet for the 70 d finishing period.

Growing/Finishing Intake and Performance Data Collection

Upon arrival, cattle were stratified by sire and allotted to pens equipped with a GrowSafe® automated feeding system (Model 4000E, GrowSafe Systems Ltd., 86 Airdrie, Alberta, Canada) so individual intakes could be recorded. For each performance and intake test (growing and finishing) a minimum of 70-d were required each year to calculate individual animal ADG and DMI. This complies with Beef Improvement Federation (**BIF**)

recommendations for performance data and intake collection (BIF, 2010). At the conclusion of the 70d finishing period test, individual feed intakes were no longer recorded using the GrowSafe system, as cattle were bunk fed for 60 ± 30 d until slaughter.

Performance data collection remained consistent for both years during both the growing and finishing performance tests. Initial and final BW for each test was the average of 2 consecutive d BW measurements prior to morning feeding. All cattle were weighed every 2 wk. Individual animal ADG was calculated by regressing each individual weight of all time points during both the growing and finishing evaluation period. Individual mid-test metabolic BW (**MW**) was determined by the linear regression coefficients for each animal for the growing and finishing evaluation period.

At the conclusion of each test period, 12th rib fat thickness was measured via ultrasound, to account for the variation in residual feed efficiency measures due to body composition. Ultrasound measurements were taken by trained personnel using an Aloka 500SV (Wallingford, CT) B-110 mode instrument equipped with a 3.5-Mhz general purpose transducer array. Twelfth rib fat thickness measurements were taken in transverse orientation between the 12th and 13th ribs approximately 10 cm distal from the midline. Images were analyzed using CPEC imaging software (Cattle Performance Enhancement Company LLC., Oakley, KS).

Total Intake Period Performance and Intake Data Collection

Individual feed intakes were recorded during the growing, transition, and finishing periods of this experiment for steers fed grain throughout the study; therefore, the combination of recorded individual DMI during these periods was identified as the 161-d total intake period DMI (**161DMI**). Initial and final BW represented the average of 2 consecutive days BW measurements during the growing and finishing periods, respectively. Individual animal ADG was calculated by regressing all weights taken over the course of the growing, transition, and finishing periods and was identified as (**161ADG**). One hundred sixty-one d total intake period mid-test metabolic BW (**161MMW**) was calculated using the ADG regression coefficients.

Total Feeding Period Performance Data Collection

For steers fed the grain-based diet during both test periods, performance was evaluated for the duration of time on feed from feedlot arrival to slaughter. This method was used to determine total feeding period BW gain. Initial BW represented the BW of calves at arrival at the feedlot (age = 180 ± 29 d). Individual final BW was calculated by dividing HCW by a standard dressing percentage of 63%. Two total feeding period performance measures were calculated to test the relationship between traditional and regressed measurements of performance during an animal's time on feed. Total feeding period ADG (**FPADG**) was calculated by the difference between initial and final BW, divided by the number of days between feedlot arrival and harvest. Regressed individual feeding period ADG (**R_FPADG**) was determined via regression of all weights taken from feedlot arrival to adjusted final BW.

Test Duration for DMI

To test the effects of intake evaluation period timing and duration, individual animal DMI during the growing period was divided into 10 total sections. Sections of intake during the growing period included: the final 7 d of intake (**70_63DMI**), the final 14 d of intake (**70_56DMI**), the final 21 d of intake (**70_49DMI**), the final 28 d of intake (**70_42DMI**), the

final 35 d of intake (**70_35DMI**), the final 42 d of intake (**70_28DMI**), the final 49 d of intake (**70_21DMI**), the final 56 d of intake (**70_14DMI**), the final 63 d of intake (**70_7DMI**), and the final 70 d of intake (**70_0 DMI**).

Calculation of Feed Efficiency

Feed efficiency traits were determined for all cattle during the growing and finishing periods. Feed conversion ratio (**FCR**) represented the ratio of individual animal feed:gain, and was calculated by dividing individual average daily DMI by regressed ADG. Contemporary groups were assigned for each individual animal according to year born and sex. Individual animal residual feed intake (**RFI**) and residual BW gain (**RG**) were calculated for both growing and finishing periods. Residual feed intake was calculated using the PROC MIXED procedure of SAS (SAS Institute Inc., Cary, NC), and was assumed to represent the residuals of a multiple regression model regressing DMI on MW, ADG, and 12th rib fat thickness using pen as a random effect. Likewise, RG was calculated using the PROC MIXED procedure of SAS, and was assumed to represent the residuals of a multiple regression model regressing ADG on DMI, MMW, and BF using pen as a random effect.

To test the concept of RFI using decoupled performance and DMI information, 35 d of recorded intake were evaluated along with FPADG as the measurement of individual animal BW gain, and mid-test BW was calculated by the average of calves' initial and final BW, raised to the 0.75 power. The 35 d of recorded intake evaluated in this measure of feed efficiency represented the first and final 35 d of each feeding period. Residual feed intake represented the residuals of a multiple regression equation regressing 35 d of recorded DMI on FPADG, feeding period mid-test metabolic weight, and carcass BF using pen as a random effect.

Statistical Analysis

Simple pearson correlations were calculated for ADG, DMI, and efficiency for the growing, finishing, 160-d total intake period, and total feeding periods using the PROC CORR procedure of SAS. Pearson correlations were used to test the number of days required for accurate DMI estimates using the PROC CORR procedure of SAS. All rho values were considered significant when $P \leq 0.05$. Correlations were considered strong when rho values were greater than or equal to 0.70; moderate when rho values were between 0.30 and 0.69; and weak when less than 0.29.

Results and Discussion

Relationships between grain-fed steer DMI, ADG and feed efficiency are presented in Table 1. Steers that consumed more feed during the growing period also had greater DMI during the finishing phase (r = 0.56; $P < 0.05$). The moderate association of DMI during the growing and finishing periods of this experiment reflects the results of Kelly et al. (2010), who reported a correlation of 0.61 between DMI when heifers were fed a 70:30 pelleted concentrate:corn silage diet during consecutive feeding periods. However, ADG was not repeatable in steers between the growing and finishing periods (r = 0.11; $P = 0.06$). Although this was a surprise, because DMI was repeatable and related to ADG in both periods, this phenomenon was also observed by Kelly et al. (2010); who also reported the same correlation of 0.11, and suggested that cattle ADG may re-rank compared to their contemporaries. Growing period RFI was moderately correlated (r = 0.63; $P < 0.05$) to finishing period RFI. Although RG during the growing period was correlated

(r = 0.24; $P < 0.05$) to RG in the finishing period, the relationship was much weaker compared to RFI. Calculated FCR during the growing and finishing periods were also moderately correlated (r = 0.41; $P < 0.05$). The repeatability of these feed efficiency traits suggest that steers that had more desirable growing period feed efficiency were also more efficient during the finishing period.

Table 1. Simple phenotypic correlations between postweaning traits for steers fed grain[a]

Item	Grow DMI	Grow ADG	Grow RFI[1]	Grow RG[2]	Grow FCR[3]	Finish DMI	Finish ADG	Finish RFI[1]	Finish RG[2]	Finish FCR[3]
Grow DMI	**1**	**0.64**	**0.49**	0.00	**0.51**	**0.56**	-0.02	**0.27**	**-0.30**	**0.44**
Grow ADG		**1**	0.00	**0.71**	**-0.31**	**0.29**	0.11	-0.04	-0.04	0.11
Grow RFI[1]			**1**	**-0.42**	**0.59**	**0.38**	-0.06	**0.63**	**-0.39**	**0.34**
Grow RG[2]				**1**	**-0.76**	-0.04	**0.19**	**-0.28**	**0.24**	**-0.22**
Grow FCR[3]					**1**	**0.38**	**-0.13**	**0.37**	**-0.30**	**0.41**
Finish DMI						**1**	**0.49**	**0.66**	0.00	**0.22**
Finish ADG							**1**	0.00	**0.77**	**-0.72**
Finish RFI[1]								**1**	**-0.51**	**0.49**
Finish RG[2]									**1**	**-0.84**
Finish FCR[3]										**1**

[a] |R| values in bold are significant ($P < 0.05$)
[1] Residual feed intake
[2] Residual BW gain
[3] Feed conversion ratio expressed as feed:gain

The fact that ADG was not repeatable across test period was not expected. However, there were moderate associations ($0.69 \geq r \geq 0.58$; $P < 0.05$) between growing and finishing ADG when compared to R_FPADG and FPADG (Table 2). This suggests that regardless of timing of the evaluation of postweaning gain, both periods can serve as similar proxies in determining the performance of a growing animal during its entire time spent on feed. The stronger correlation ($0.96 \geq r \geq 0.81$; $P < 0.05$) between 161ADG and R_FPADG and FPADG suggests that longer periods of performance evaluation may result in more accurate determinations of ADG over an animal's entire lifespan. The strong, positive correlation (r = 0.85; $P < 0.05$) between R_FPADG and FPADG suggests that cattle performance may be accurately predicted by dividing the difference of an animal's final BW and feedlot arrival weight by the number of days on feed. This is important, because FPADG is a measure of performance that is widely accepted within the industry. When FPADG is calculated by dividing

the difference between adjusted HCW and feedlot arrival BW by the number of d on feed, FPADG can be an effective proxy for individual ADG over the lifespan of calves, which is supported by Retallick et al. (2015).

Table 2. Simple phenotypic correlations between measurements of ADG during different feeding periods and biological timepoints[a]

Item	Growing	Finishing	161ADG[1]	R_FPADG[2]	FPADG[3]
Growing	**1**	0.11	**0.57**	**0.58**	**0.58**
Finishing		**1**	**0.76**	**0.69**	**0.58**
161ADG[1]			**1**	**0.96**	**0.81**
R_FPADG[2]				**1**	**0.85**
FPADG[3]					**1**

[a] |R| values in bold are significant ($P < 0.05$)
[1] 161 d intake period
[2] Total feeding period (regressed ADG)
[3] Total feeding period

As the number of recorded d of DMI increased, the association between number of d of recorded DMI and overall period DMI increased (Table 3). Due to a strong correlation of 0.95 ($P < 0.05$), this experiment suggests that only 35 d of recorded intake are sufficient for predicting 70d test period DMI. However, *when* DMI intake is recorded for those 35 d makes a difference. Recorded DMI during the end of the growing period was a more accurate predictor of DMI during the finishing period. This study showed that in order to accurately predict DMI across different time points in life, not only is it important to record a sufficient amount of d, but the proximity of the different test periods being compared is an important factor to consider as well.

Table 3. Simple phenotypic correlations during different durations of mean DMI observations from the end of the 70d growing period in grain fed steers[a]

Item	70-0DMI	FDMI[1]	161DMI[2]
70-63DMI	**0.88**	**0.58**	**0.86**
70-56DMI	**0.87**	**0.62**	**0.87**
70-49DMI	**0.89**	**0.62**	**0.88**
70-42DMI	**0.92**	**0.61**	**0.89**
70-35DMI	**0.95**	**0.61**	**0.90**
70-28DMI	**0.97**	**0.58**	**0.89**
70-21DMI	**0.98**	**0.56**	**0.89**
70-14DMI	**0.99**	**0.56**	**0.90**
70-7DMI	**1**	**0.56**	**0.90**
70-0DMI	**1**	**0.56**	**0.90**
FDMI[1]		**1**	**0.85**
161DMI[2]			**1**

[a] |R| values in bold are significant ($P < 0.05$)
[1] Finishing period DMI (d91-161DMI)
[2] 161 d intake period total DMI (d0-161DMI)

Minimal work has been done investigating the idea of decoupling performance and intake information when determining the feed efficiency of a feedlot steer during its entire time on feed. Interest in this concept is due to the fact that accurate measures of DMI and ADG require substantially different durations, and performance and intake evaluation tests are costly. Total beef production efficiency can be improved when a greater number of animals are tested annually; therefore, more cost effective ways to test growing animals are needed. In our trial, comparisons were made between RFI values using short duration intake test periods (35 d) with FPADG; and RFI measures calculated by the standards set forth by the BIF (Table 4). Relationships ranged from strong to weak ($0.85 \geq r \geq 0.28$; $P < 0.05$) between these measures of RFI using decoupled DMI and ADG and 70 d test period RFI. This suggests that there is a possibility that these alternative measurements of RFI may have efficacy to the industry and should be further investigated.

Table 4. Simple phenotypic correlations between measures of feed efficiency for grain fed steers during the growing, finishing, and total feeding period using decoupled DMI and ADG variables in the predicted DMI model in the total feeding period[a]

Item	Growing RFI[1]	Finishing RFI[1]
0-35RFI[2]	**0.70**	**0.28**
36-70RFI[3]	**0.54**	**0.62**
90-125RFI[4]	**0.56**	**0.85**
126-161RFI[5]	**0.46**	**0.79**

[a] |R| values in bold are significant ($P < 0.05$)
[1] Residual feed intake
[2] Total feeding period residual feed intake when predicted total feeding period DMI is a linear function of the first 35d of recorded DMI during the growing period, FPADG and mid-test metabolic BW, and carcass BF.
[3] Total feeding period residual feed intake when predicted total feeding period DMI is a linear function of the final 35d of recorded DMI during the growing period, FPADG and mid-test metabolic BW, and carcass BF.
[4] Total feeding period residual feed intake when predicted total feeding period DMI is a linear function of the first 35d of recorded DMI during the finishing period, FPADG and mid-test metabolic BW, and carcass BF.
[5] Total feeding period residual feed intake when predicted total feeding period DMI is a linear function of the final 35d of recorded DMI during the finishing period, FPADG and mid-test metabolic BW, and carcass BF.

Regulation of feed intake may differ when cattle are fed differing diet types, and DMI is related to energy content of the feed delivered (NRC, 1996) or physical fill. Since DMI plays a vital role in feed efficiency, mechanisms of intake regulation for divergent diet types may confound the accuracy of comparing RFI of cattle when fed grain or forage. Minimal research has been conducted comparing RFI values when cattle are fed differing diet types. Comparisons of feed intake and efficiency when two different diet types are fed are presented in Table 5. The correlation between forage and grain DMI was 0.58 ($P < 0.05$). This linear relationship of DMI closely parallels the relationship of DMI during the growing and finishing period of grain fed steers (0.56), and in this study, suggests mechanisms of intake regulation on these diet types may

not differ. The moderate, positive correlation (r = 0.40; $P < 0.05$) between RFI values derived from forage and grain based diets suggested that growing cattle that were more efficient when fed forage were also more efficient when fed grain. This is an important discovery, as most feed intake and subsequent efficiency tests are done in feedlot-like test stations.

Table 5. Simple linear phenotypic correlations between postweaning traits in heifers fed different diets[a]

Item	Forage DMI	Forage ADG	Forage RFI[1]	Forage RG[2]	Forage FCR[3]	Grain DMI	Grain ADG	Grain RFI[1]	Grain RG[2]	Grain FCR[3]
Forage DMI	**1**	**0.25**	**0.69**	0.00	**0.24**	**0.58**	-0.01	**0.24**	**-0.26**	**0.43**
Forage ADG		**1**	0.00	**0.53**	**-0.72**	**0.16**	**-0.30**	-0.03	**-0.17**	**0.42**
Forage RFI[1]			**1**	**-0.29**	**0.39**	**0.25**	0.00	**0.40**	**-0.17**	**0.17**
Forage RG[2]				**1**	**-0.53**	-0.08	**-0.11**	**-0.15**	-0.10	0.05
Forage FCR[3]					**1**	**0.14**	**0.27**	**0.17**	0.06	**-0.16**
Grain DMI						**1**	**0.36**	**0.65**	0.00	**0.38**
Grain ADG							**1**	0.00	**0.82**	**-0.70**
Grain RFI[1]								**1**	**-0.36**	**0.46**
Grain RG[2]									**1**	**-0.79**
Grain FCR[3]										**1**

[a] |R| values in bold are significant ($P < 0.05$)
[1] Residual feed intake
[2] Residual BW gain
[3] Feed conversion ratio expressed as feed:gain

Conclusions

Relationships existed between measures of feed efficiency and intake across diet type and test period. Accurate feed efficiency measures can be obtained in either the growing or finishing period of feedlot cattle. The relationship of forage and grain DMI and efficiency in heifers suggests that measures of DMI and feed efficiency in heifers are relevant, regardless of diet fed. This suggests that DMI and efficiency information derived from the feedlot may have application to the cowherd. Limitations on test period length are due to the number of d to accurately assess individual ADG. Since intake evaluation periods can be shortened without losing accuracy in predicting individual animal DMI, decoupling performance from DMI information may be the most cost effective way to test a greater number of animals annually.

More research is needed to further investigate novel methods of testing for feed efficiency with the vision of improving beef production efficiency as a whole.

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FEED EFFICIENCY AND THE MICROBIOTA OF THE ALIMENTARY TRACT

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Introduction

There is considerable variation in the efficiency that cattle convert feed for maintenance and product (body weight gain, milk, and conceptus). Both intake and gain are polygenic traits and to better understand factors that contribute to variation in feed efficiency more defined phenotypes are needed. Several studies have associated differences in the microbiota of the alimentary tract between obese and non-obese rodents (Turnbaugh et al., 2006), obese and non-obese humans (Ley et al., 2006), and energy metabolism in birds (Torok et al., 2008 and Stanley et al., 2013). These finding suggest that there is a potential relationship between the microbiota of the alimentary tract and feed efficiency in beef cattle. Considerable research has been conducted on the rumen microbiota, but less consideration has been given to the rest of the alimentary tract.

Changes in the microbial community of the rumen-reticulum complex with changes in diet as well as across species of ruminants have been documented. The observed diversity in the microbiota has been limited to those organisms that can be cultured. The rumen is an anaerobic environment and many of the strict anaerobes are difficult to culture in vitro. The concern has been that relative differences in microbial species may have been a function of the ease of culturing some species in vitro and that the ability to grow in vitro is not indicative of their relative proportion of the rumen-reticulum microbiota. Using next-generation sequencing provides a tool to estimate the makeup of the microbiota by identifying bacteria by their DNA sequence rather than enumerating them through culture techniques.

Two studies were conducted as part of the Agriculture and Food Research Initiative Competitive Grant 2011-68004-30214 from the USDA National Institute of Food and Agriculture to determine the relationships between the microbiota and feed efficiency. The results of this research have been reported by Myer et al. (2015a, 2015b, 2015c, and 2016) and Freetly et al. (2015).

Study 1 – Microbial community profiles of the rumen-reticulum, jejunum, cecum, and colon of steers differing in feed efficiency.

Steers for this study were selected from two contemporary groups that individual feed intake and body weight were measured for a 63-d period. Group 1 (n = 148) was comprised of spring-born calves that were 371 ± 1 d of age and weighed 522 ± 4 kg at the start of the feed intake measurements. Group 2 (n = 197) was comprised of fall-born calves that were 343 ± 1 d of age and weighed 448 ± 4 kg at the start of the feed intake measurements. Steers were fed a ration that on a dry matter basis consisted of 57.35% dry-rolled corn, 30% wet distillers grain with solubles, 8% alfalfa hay, 4.25% supplement (containing 772 mg monensin/kg), and 0.4% urea. At the end of each feeding period, steers were ranked based their standardized distance

from the bivariate mean for average daily gain (**ADG**) and average daily feed intake (**ADFI**) assuming a bivariate normal distribution with a calculated correlation between ADG and ADFI . Within each contemporary group, four steers with the greatest deviation within each Cartesian quadrant were sampled (n = 16 steers/contemporary group). The resulting design was a 2 X 2 factorial consisting of greater and less ADG and greater and less ADFI.

At the end of the feeding period, selected steers were slaughtered and digesta was collected from the rumen-reticulum, jejunum, cecum, and colon. Samples were buffered in peptone water (pH 7.0) + 15% glycerol and stored at -70°C. Deoxyribonucleic acid (**DNA**) was extracted from the samples. Amplicon library preparations were performed by PCR amplification of the V1 through V3 hypervariable region of the 16S rRNA gene. The PCR amplicon libraries were sequenced using the 2 X 300, v3 600-cycle kit and the Illumina MiSeq sequencing platform (Illumina, Inc., San Diego, CA).

Sequences were processed using the QIIME 1.8.0 software package (Caporaso et al., 2010). Paired reads were joined using fastq-join (Aronesty, 2011) and filtered for quality using the Galaxy server (Blankenberg et al., 2010). Chimeric sequences were checked using ChimeraSlayer (Haas et al., 2011). All cleaned sequences were classified into taxa using Greengenes 16S rRNA Gene Database (DeSantis et al., 2006). Operational taxonomic units (**OTU**) were calculated using the uclust program (0.03 dissimilarity; Edgar, 2010). After calculating richness for each quadrant, singletons were removed from further diversity analyses. Based on rarefaction curves, the number of OTU was normalized via subsampling 25,000 sequences from each sample. A phylogenic tree was built with FastTree (Price et al., 2010) to determine α- and ß-diversity metrics.

The mean abundance of data metrics and each taxon were compared among feed efficiency groups with contemporary group and Cartesian quadrant as fixed effects. Differences were determined at $P < 0.05$ with Benjamini-Hochberg method used for multiple-testing corrections (Benjamini and Hochberg, 1995) Multiple-testing corrections were made for the number of phyla, the number of OTU groups, and other classified taxa groups. Linear contrasts were applied to quadrants to separate whether microbial populations varied by ADG, ADFI or the interactions. Principal coordinate analysis was performed using weighted and unweighted UniFrac analyses (Lozupone and Knight, 2005).

In the study, the rumen content yielded an average of 1,098 ± 382 OTU, of which were classified into 24 phyla, 48 classes, 89 orders, 173 families, and 317 genera. The bacterial diversity was reflected by the diversity index of 6.85 ± 0.36 (Shannon). Although the rumen has a great abundance of microorganisms, their functionality is more specialized, which may result in a lower diversity index than that of the large intestine. Indeed, the most abundant phyla in the rumen were Bacteroidetes and Firmicutes, present at abundances of 53 to 63% and 23 to 33%, respectively. However, over 90% of the Bacteriodetes phylum was composed of the genus *Prevotella*, exemplifying this specialization. Reports have indicated that *Prevotella* is the most

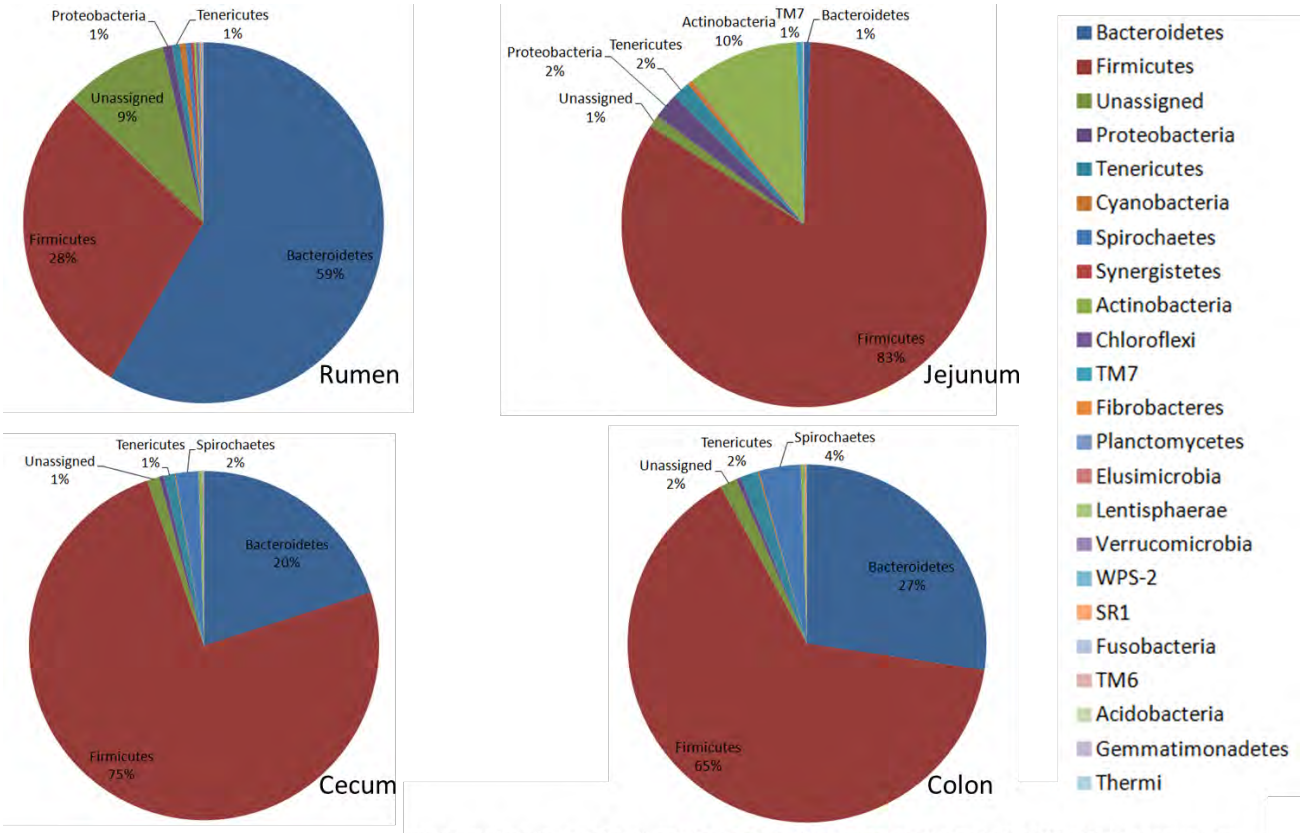
abundant ruminal genus (Stevenson and Weimer, 2007), and these data overwhelming supported those findings. Along with the *Prevotella* abundances (45 to 57%), the bacterial genera in the rumen representing ≥1% of the total sequences included *Dialister* (2.6 to 4.1%), *Succiniclasticum* (2.0 to 4.0%), *Ruminococcus* (1.0 to 2.5%), *Butyrvibrio* (0.5 to 1.1%), and *Mitsuokella* (0.6 to 1.2%).

Compared to the rumen, changes in the bacterial populations of the jejunum were anticipated, as the role of this alimentary tract segment transitions more towards host digestion of nutrients and absorption. The bacterial population of the jejunum was greatly reduced in species abundance and diversity compared with that of the rumen, with an average of 499 ± 159 OTU and a diversity index of 3.91 ± 0.48. These OTU were classified into 21 phyla, 51 classes, 94 orders, 198 families, and 397 genera. The differences in function between the rumen and the jejunum were reflected in the bacterial abundances, as the phylum Firmicutes accounted for up to 90% of the populations in the jejunum, and Bacteroidetes was greatly reduced to 0.4 to 1.1%. Actinobacteria (6 to 13%) made up the greatest abundance of the remaining phyla, followed by Proteobacteria (0.8 to 5.8%), and Tenericutes (0.4 to 4%). Genera and OTU representing ≥1% of the total sequences included *Ruminococcus* (12.2 to 19.6%), *Butyrivibrio* (2.6 to 7.7%), *Lactobacillus* (2.8 to 4.2%), *Bulleidia* (0.8 to 1.9%), *Mogibacterium* (1.1 to 1.7%), *Mitsuokella* (0.05 to 1.27%), and *Propionibacterium* (0.07 to 7%).

The role of postruminal degradation of cellulose and starch as well as the importance of microbial interaction and the maturation of the mucosal immune system highlights the changes in abundance and diversity of bacterial populations observed in the cecum. The cecum averaged 5,572 ± 1,428 OTU with a bacterial diversity index of 7.89 ± 0.47 (Shannon). These data were far greater than that of the rumen and jejunum. The cecal OTU were classified to 18 phyla, 40 classes, 75 orders, 148 families, and 225 genera. Similar to the jejunum, Firmicutes was the most abundant phylum at 68 to 81% of the total sequences. However, Bacteroidetes was greater in abundance compared to the small intestinal segment, at 18 to 26%, followed by the phyla Spirochaetes (1.4 to 3.19%), Tenericutes (0.7 to 1.2%), and Actinobacteria (0.2 to 0.4%). The remaining phyla accounted for less than 0.1% of the sequences. Abundant genera consisted of *Prevotella* (2.1 to 7.3%), *Turicibacter* (4.6 to 6.7%), *Coprococcus* (1.2 to 2.8%), *Ruminococcus* (1.5 to 2.7%), *Dorea* (2.2 to 3.3%), *Blautia* (0.5 to 2.0%), *Clostridium* (1.0 to 1.2%), and *Oscillospira* (1.1 to 1.6%).

Although the colon microbial communities are likely to be similar to those of the cecum, as digesta travels to the more distal regions of the gastro-intestinal tract (**GIT**) functionality as well as environmental conditions shift. Appropriately, the bacterial species abundance and diversity of the colon was greater than the cecum, and expectedly more similar than the jejunum or rumen, averaging 6,025 ± 1,225 OTU and an average diversity index of 8.05 ± 0.20 (Shannon). The OTU were classified to 20 phyla, 46 classes, 83 orders, 152 families, and 231 genera. Most similar to the cecum, but continuing the trend in the lower intestinal tract, the colon bacterial population predominantly consisted of Firmicutes (60-70%). As digesta moves

distally, a trend of greater Bacteroidetes populations was observed, compared to the jejunum and cecum, where this phylum was present in the colon at abundances of 21–33%. Abundances of remaining phyla greater than 0.1% of the sequences consisted of Spirochaetes (2.5–4.5%), Tenericutes (1.2–1.9%), Proteobacteria (0.3–0.5%), Actinobacteria (0.23–0.33%), and Fibrobacteres (0.02–0.29%). The bacterial genera present in greatest abundance within the colon were *Prevotella* (3.0–11.1%), *Ruminococcus* (1.7–2.9%), *Coprococcus* (1.0–2.9%), *Dorea* (1.7–2.2%), *Turicibacter* (1.9–4.4%), *Blautia* (0.3–1.3%), *Oscillospira* (1.1–1.6%), and *Parabacteroides* (0.4–1.4%).



The taxonomic profile for the relative phylum-level abundance of each section classified by representation at ≥0.001% of total sequences. Taxonomic composition of the GIT microbiota was compared based on the relative abundance (reads of a taxon/total reads in a sample).

Within the rumen, although bacterial abundances were consistent with other research (Jami et al., 2014), significantly increased populations of Firmicutes were observed within the $ADG_{Greater} - ADFI_{Less}$ group ($P = 0.0364$), representing the feed efficient group. This association

was of note, for changes in Firmicutes-to-Bacteroidetes ratio is often implicated in obesity research (Ley et al., 2006), and has been correlated with energy harvesting and fat increases in dairy cattle (Jami et al., 2014). Other taxa and OTU abundances were associated with varying degrees of efficiency based on the experimental design, which may play important roles in the fermentative and cellulolytic capacity of the rumen based upon their putative functions. Those abundances associated with the $ADG_{Greater}$-$ADFI_{Greater}$ group included increases in *Prevotella* ($P = 0.0154$), *Lactobacillus* ($P = 0.0419$), and *Dialister* ($P = 0.0062$) populations, whereas *Anaerovibrio* ($P = 0.0291$) was least prevalent. The $ADG_{Greater}$-$ADFI_{Less}$ group included increases in *Butyrivibrio* ($P = 0.0391$) and *Leucobacter* ($P = 0.0215$). The ADG_{Less}-$ADFI_{Less}$ group included increases in *Ruminococcus* ($P = 0.0255$) abundances, but decreases in *Acidaminococcus* ($P = 0.0306$). Finally, the ADG_{Less}-$ADFI_{Greater}$ group saw increases in *Lysobacter* ($P = 0.0462$), *Janibacter* ($P = 0.0161$), and *Succiniclasticum* ($P = 0.0276$) populations. Additionally, the data were analyzed to determine whether microbial populations differed by less vs. greater ADG, less vs. greater ADFI, or their interaction. Within the rumen, the significant changes in microbial abundances were primarily associated with ADG.

Jejunal microbial population analyses significantly associated the genus *Butyrivibrio*, and its family Lachnospiraceae, with the $ADG_{Greater}$–$ADFI_{Less}$ group; the feed efficient group. The *Butyrivibrio* species of greatest abundance that was significant for this association ranged from 1.9 to 6.0% ($P = 0.041$). This may be important functionally, as the hemicellulolytic *Butyrivibrio* can ferment a wide range of sugars, as well as influence the energy pool to enterocytes via butyrate production. The phylum Proteobacteria ($P = 0.030$) was also associated with the $ADG_{Greater}$–$ADFI_{Less}$ group, and has been demonstrated to negatively correlate with Firmicutes populations, as well as positively correlate with feed conversion ratio (Cook et al., 1994; Jami et al., 2014). Several other taxa were significantly associated with variation among feed efficiency groups, such as increases in the AA-fermenting genus *Acidaminococcus* ($P = 0.018$; $ADG_{Greater}$-$ADFI_{Less}$) and the obligately oxalotrophic, ammonium-dependent, aerobic genus *Ammoniphilus* ($P = 0.022$; ADG_{Less}-$ADFI_{Greater}$). All significant taxa and OTU were associated with ADG or the interaction of ADG and ADFI. Interestingly, *Butyrivibrio* was the only assignment that was solely associated with intake.

The evaluation of the cecal bacterial communities revealed no significant differences among the feed efficiency groups at phylum-level abundances. However, among OTU and genus level abundances, *Prevotella* ($P = 0.042$), *Blautia* ($P = 0.042$), *Coprobacillus* ($P = 0.004$), *Dorea* ($P = 0.042$), *Clostridium* ($P = 0.044$), and *Parabacteroides* ($P = 0.027$) were detected with greatest abundance within the $ADG_{Greater}$-$ADFI_{Greater}$ group, while *Ruminococcus* ($P = 0.040$) and *Oscillospira* ($P = 0.041$) were least abundant within the group. The species *Lactobacillus ruminis* ($P = 0.047$) was also least abundant in the ADG_{Less}-$ADFI_{Greater}$ group. The genus *Blautia* is of recent research interest due to its ubiquitous presence among humans and other mammals. These bacteria exist at low abundances, but are thought to contribute to the

metabolic capacity of the host by providing energy from polysaccharides that other gut commensals cannot degrade (Eren et al., 2015).

Similar to the cecum, no significant differences among the feed efficiency groups were observed within the bacterial community abundances of the colon. Differences among the groups did exist at lower levels of classification and at the OTU-level. Among taxa, these organisms included *Anaeroplasma* ($P = 0.0222$), *Paludibacter* ($P = 0.0226$), *Faecalibacterium* ($P = 0.0361$), *Succinivibrio* ($P = 0.0412$), and *Pseudobutyrivibrio* ($P = 0.0479$). *Anaeroplasma* and *Faecalibacterium* were in greatest abundance within the $ADG_{Greater}$–$ADFI_{Greater}$ group, *Paludibacter* was in greatest abundance within the ADG_{Less}– $ADFI_{Less}$ group, and *Succinivibrio* and *Pseudobutyrivibrio* were least abundant within the $ADG_{Greater}$–$ADFI_{Less}$ and ADG_{Less}–$ADFI_{Greater}$ groups, respectively. *Coprococcus* ($P = 0.0323$) and *Clostridium* ($P = 0.0446$) were in greatest abundance within the $ADG_{Greater}$–$ADFI_{Greater}$ group, while *Dorea* ($P = 0.0225$) was least abundant within this group. *Butyrivibrio* ($P = 0.0240$) and *Prevotella* ($P = 0.0435$) were greatest in the ADG_{Less}–$ADFI_{Greater}$ group; the least efficient group, while the abundance of *Oscillospira* ($P = 0.0456$) was greatest within the ADG_{Less}– $ADFI_{Less}$ group. The butyrate producing and strong xylan-degrading activities of *Butyrivibrio* and *Pseudobutyrivibrio* species may lend further insight to their association with feed efficiency in the colon (Morgavi et al., 2013). The bacterial populations within both the cecum and colon were solely associated with intake and/or the interaction of gain and intake, but not gain alone, which may be expected as digesta travels further from the fermentative and digestive sections of the GIT.

Determination of the microbial population associations with feed efficiency, ADG, and ADFI throughout the alimentary tract provides great insight as to the interactions that may occur at both the host and microbial levels based on the putative functions of the organisms involved. As these tissues are distinct in function and environment, so are their microbial populations and effect on the host. The varying microbial phylogenetic diversity and abundance along the tract likely also plays a role, and is a function of, the degree of specialization. However, it is not clear whether changes in the microbiome are contributing to differences in feed efficiency or host factors are driving changes in the microbiome.

Study 2 – Methane production and methanogen levels in steers that differ in residual gain.

Individual feed intake and body weight were measured on 132 fall-born steers for a 70-d period. At the start of the study, steers were 348 ± 1 d of age and weighed 444 ± 0.4 kg. Steers had ad libitum access to a ration that as a percentage of dry matter consisted of 82.75% dry-rolled corn, 12.75 corn silage, 4.5% supplement. The supplement contained 0.95% Rumensin-80. Seven steers with extreme positive residual gain (**RG**), and seven steers with extreme negative RG whose dry matter intake was within 0.32 standard deviations of the means were selected for subsequent measurements.

In vivo methane production was measured over a 6-h period using a headbox respiration chamber. Steers were subsequently slaughtered and rumen and cecum contents were sampled to determine *in vitro* methane production. *In vitro* methane was determined in vials gassed with hydrogen over 2 through 8 h of incubation.

Digesta samples were collected from the rumen, cecum, and rectum at slaughter for the determination of methanogen 16S rRNA. Deoxyribonucleic acid was extracted from the digesta samples. Primer sets that targeted conserved regions of the 16S rRNA gene were used in real-time quantitative PCR using a LightCycler 480 (Roche, Indianapolis, IN) to measure total bacteria, total methanogens, Methanomicrobiales, Methanobacteriales, Methanosarcina, Methanobacterium, Methanobrevibacter Group 1 (*Mbb. ruminantium* + *Mbb. cutcularis*), and Methanobrevibacter Group 2 (*Mbb.. smithii* + *Mbb. wolinii* + *Mbb. thaueri* + *Mbb. gottschalkii* + *Mbb. woesi*). The experimental design for the level of methanogens was a 2 × 3 factorial. The main effects were RG and alimentary tract location.

In vivo enteric methane production did not differ ($P = 0.11$) between the positive RG (112 ± 13 L/d) and the negative RG (74 ± 13 L/d). *In vitro* rumen methane production did not differ between positive RG ($64.26 \times 10^{-5} \pm 10.85 \times 10^{-5}$ mmol·DM g^{-1}·min^{-1}) and negative RG ($61.49 \times 10^{-5} \pm 10.85 \times 10^{-5}$ mmol·DM g^{-1}·min^{-1}; $P = 0.86$). *In vitro* cecum methane production did not differ between positive RG ($4.24 \times 10^{-5} \pm 1.90 \times 10^{-5}$ mmol·DM g^{-1}·min^{-1}) and negative RG ($4.35 \times 10^{-5} \pm 1.90 \times 10^{-5}$ mmol·DM g^{-1}·min^{-1}; $P = 0.97$).

Methanogen 16S rRNA as a percent of the total 16S rRNA bacteria did not differ between RG groups ($P = 0.18$). The methanogen 16S rRNA as a percentage of rumen fluid total bacteria 16S rRNA (5.3 ± 3.1%) did not differ from the methanogen 16S rRNA as a percentage of cecum content total bacteria 16S rRNA (11.8 ± 3.1%; $P = 0.14$). The methanogen 16S rRNA as a percentage of the rectum content total bacteria 16S rRNA (0.7 ± 3.1%) was not different than the rumen content ($P = 0.29$), but was less than the cecum content ($P = 0.01$). Methanomicrobiales 16S rRNA as a percentage of total methanogen 16S rRNA did not differ across sample sites ($P = 0.81$); however, steers with positive RG (10.5 ± 1.6%) was greater compared to steers with negative RG (5.1 ± 1.6%; $P = 0.02$). As a percent of the total methanogen 16S rRNA, 16S rRNA of Methanobacteriales ($P = 0.23$), *Methanobacterium* ($P = 0.60$), and the Methanobrevibacter Group 2 group ($P = 0.41$) did not differ between RG groups. Methanobacteriales and the Methanobrevibacter Group 2 had a greater percentage of the total methanogen 16S rRNA in the rumen compared to the cecum and rectum which did not differ from each other. *Methanobacterium* was a lesser percentage of the total methanogen gene 16S rRNA in the rumen compared to the cecum and rectum which did not differ from each other. Methanobrevibacter Group 1 did not differ between RG group ($P = 0.25$) and tended to differ with collection site. The percentage of 16S rRNA of *Methanosarcina* did not differ with RG group ($P = 0.42$) or collection site.

In our study, total methanogens represent approximately 5% of the total bacterial 16S rRNA in the rumen which is similar to what Frey et al. (2010) observed in the dairy cow and there was not a difference between the RG groups. These findings are consistent with the lack of a difference in rumen *in vitro* methane production. In our study and the study of Popova et al. (2013) in sheep, the cecum had a lower *in vitro* methane production than the rumen. Similar to the rumen, there were no differences in methane production between the RG groups.

The relative contribution of the different methanogens differed across sites in the alimentary tract; however, with the exception of Methanomicrobiales 16S rRNA did not differ between RG groups. This shift in Methanomicrobiales 16S rRNA was not reflected in the Total Methanogen 16S rRNA. The lack of difference in Total Methanogen 16S rRNA is consistent with the lack of difference in methane production. Our findings do not support the hypothesis that differences in RG at an average intake are a consequence of differences in methane production or methanogen populations in the alimentary tract.

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Effects of diet digestibility on feed efficiency and impact of diet type and feeding phase on repeatability of feed efficiency phenotype

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Introduction

Feed efficiency (FE) of a beef animal is critical to producer profitability, but often varies considerably among individuals. Improvements in efficiency of beef production are necessary to sustain the cattle industry. The purpose of this research was to assess the repeatability of FE across growing and finishing phases of feedlot production as well across differing diet types. Additionally, we sought to better understand the contributions of diet digestibility to the FE phenotype of cattle.

Experimental design and methodology

Animal use and methods are extensively described by Russell et al. (2016a). Briefly, this study was conducted over 5 years and utilized 985 crossbred steers (464 ± 32 kg initial BW) fed in 6 replicated groups. Steers were fed at the University of Missouri (MU) for the growing phase and at Iowa State University (ISU) for the finishing phase. Steers were received at MU for a minimum of 21 d prior to initiation of the growing phase portion of the trial. Steers were stratified by BW across growing phase diets including: a whole shell corn-based diet (G-Corn; 528 steers in total; Table 1) or a roughage-based diet (G-Rough; 457 steers; Table 2). Steers were housed in pens with GrowSafe equipped bunks and fed to ad libitum intake. Intermediate BW were recorded every 14 to 28 d and at the conclusion of the growing phase, which ranged in length from 69 to 89 d across the 6 groups. Residual feed intake (RFI) was calculated for steers within growing phase diet as suggested by Basarab et al. (2003) and all steers where shipped to ISU for finishing. At ISU steers were assigned to finishing pens (5 to 6 steers per pen) by growing phase diet and RFI ranking (upper, middle, or lower one-third of the group). Steers received diets nutritionally similar to their growing phase diets after arrival at ISU and were then transitioned to finishing diets that included: a dry rolled corn based diet (F-Corn; Table 3) or a byproduct-based diet (F-Byp). Steers received finishing diets until cattle were visually appraised to have 0.5 in of backfat, and were harvested at Tyson Fresh Meats (Denison, IA). All steers received ractopamine hydrochloride at a rate of 200 mg/hd per d for 27-32 d prior to harvest.

Following completion of the sixth and final group, data from all 985 steers (168 ISU finishing pens total) were collectively assessed. Average growing phase G:F was calculated for each set of steers (5 to 6 head) assigned to a finishing phase pen, and growing phase initial BW was used as a covariate in analysis with the Mixed procedure of SAS to calculate an adjusted growing phase G:F for a pen of cattle. Pens were then classified as highly (HFE; > 0.5 SD from the G:F mean; most efficient cattle), mid (MFE; ± 0.5 SD from the G:F mean), or lowly (LFE; < 0.5 SD from the G:F mean; least efficient cattle) feed efficient. Descriptive statistics about the pens of steers classified in these groupings are shown in Table 4. Data were analyzed using Proc Mixed of SAS, with finishing phase pen as the experimental unit and the model included the fixed effects of growing phase diet, growing phase feed efficiency classification, finishing phase diet and the interactions. Group (1 through 6) was included as a fixed effect as well. Finishing phase starting BW was used as a covariate in the model for finishing phase final BW, DMI, G:F, and HCW.

In groups 4 and 5 a subset of steers were utilized to assess the impact of FE phenotype on diet digestibility (methods described by Russell et al., 2016b). Upon arrival at ISU, following completion of the MU growing phase RFI determination, the 12 greatest and 12 least feed efficient steers from each of the two growing phase diets were selected from group 4 (n = 48, 509 ± 7 kg) and group 5 (n = 48, 467 ± 7 kg). Steers were housed in pens of 6 head, in pens equipped with GrowSafe bunks. Steers received diets nutritionally similar to their growing diets for 15 d, during which time titanium dioxide was included in the diets at an average of 10 g per head daily as an indigestible marker to estimate fecal output. Grab samples of feces were collected prior to feeding on d 14 and 15, and samples of total mixed rations were collected twice during the receiving period. Steers were then transitioned to finishing diets over a period of 18 d and finishing period diet digestibility was assessed by repeating the titanium dioxide feeding protocol immediately prior to addition of ractopamine hydrochloride, with fecal collections occurring on d 28, 29 (group 4) or d 68, 69 (group 5). Feces and diets were analyzed for DM, organic matter, neutral detergent fiber, acid detergent fiber, N, fat, and starch.

Data for the two groups (96 steers in total) were pooled, and steers were ranked by their growing phase G:F to be classified as the 24 greatest (HFE) or 24 least (LFE) feed efficient steers from each growing phase diet. Digestibility data were analyzed using Proc Mixed of SAS, with the receiving period model including the fixed effects of growing phase diet and growing phase FE classification and the interaction. Finishing period data were analyzed with the fixed effects of growing phase diet, growing phase FE classification, finishing phase diet and the interactions. Group (4 or 5) was included in the model as a fixed effect for both phases.

Repeatability of feed efficiency across feeding phases and different diet types

The greatest challenge facing beef producers seeking to measure FE is the ability to measure individual intakes. Measuring intakes in the feedlot requires substantial infrastructure, making intake measurements difficult and expensive (Arthur and Herd, 2008). Thus, measuring FE for a limited period would be beneficial if FE is repeatable over multiple feeding phases or can be predicted using one FE evaluation period. In the present study there were no growing

phase diet × FE classification × finishing phase diet effects on finishing phase growth or carcass traits (Table 5).

Feed efficiency classification impacted marbling score of carcasses, where marbling score was lesser in the HFE steers (417 ± 5.6) than the MFE (433 ± 4.3) and LFE (439 ± 5.1) steers, while marbling score did not differ between MFE and LFE steers. There was no affect of the growing phase diet × finishing phase diet interaction or the growing phase diet × FE classification interaction on finishing phase G:F. However, finishing phase feed efficiency was impacted by growing phase FE classification (Fig. 1), where cattle classified as highly efficient in the growing phase had the best G:F in the finishing period and mid and lowly feed efficient cattle were similarly mid and least feed efficient in the finishing period. Table 6 shows the percent of pens of steers that remained in the same FE classification across both growing and finishing phases, moved one classification (i.e. low to mid, mid to high, etc), or moved two classifications (i.e. low to high or high to low). In general the trends are similar across diet combinations, though it appears cattle classified by FE while grown on roughage displayed more movement across classifications than cattle grown on corn, likely because of the similar nutritional profile between the G-Corn and finishing diets. Assessment of the correlation between adjusted growing phase G:F and finishing phase G:F amongst the differing diet combinations is shown in Table 6. The relationship was positive across all diet combinations and was significant for three of the four combinations, being strongest within cattle grown on corn, likely due to the similar nutritive profile between G-Corn and the finishing diets. The relationship was weakest within cattle grown on roughage and finished on byproduct-based diets but still reflects a positive correlation. The most variability in repeatability of FE across growing and finishing phases appears to be within steers fed fibrous diets and more work is needed to better understand the implication of NDF content and quality on FE determination.

Others have also examined the repeatability of FE over multiple feeding phases. Over three years, Durunna et al. (2011) collected growth and intake data on 490 crossbred steers during two consecutive feeding phases (growing and finishing). Within each year, steers either received the growing phase diet (74% oats, 20% grass hay) in both phases, the finishing phase diet (56.7% barley, 28.3% oats) in both phases or switched from the growing to finishing phase diet across the two periods (Durunna et al., 2011). Steers were classified as low, medium, or highly feed efficient using a 0.5 SD cutoff around the mean for G:F based on first period performance (Durunna et al., 2011). In the feed swap group, 61.6% switched G:F classification; however, similar classification changes were also observed in the all growing phase diet-fed group (G:F: 53.5% change) and the all finishing phase diet-fed group (G:F: 59.1% change; Durunna et al., 2011). Despite a seemingly large movement across classifications, Durunna et al. (2011) reported a far smaller proportion of the total feeding groups that actually moved two classifications (i.e. the low to high, or high to low FE classification; feed swap: 13.3% G:F; growing diet-fed: 11.2% G:F; finishing diet-fed: 11.2% G:F).

An interesting observation from the present study is that there was no interaction between MU growing diets and finishing period G:F, feed efficiency was achieved in different ways between cattle fed the two growing diets. Among those grown on corn HFE and MFE cattle ate

less DM during the finishing period than those classified as LFE, while daily rates of gain were similar among the classification groupings. However, among steers grown on roughage, HFE and MFE steers had greater daily rates of gain than LFE steers while consuming similar amounts of DM across all three groupings. Differences in diet digestibility may help explain differences among individuals in feed efficiency, depending on the nutrient profile of the diet.

Diet digestibility in beef cattle identified as phenotypic extremes for feed efficiency

Table 7 shows descriptive statistics regarding steers utilized in diet digestibility assessments. Receiving phase diets were nutritionally similar to growing phase diets and diet digestibility data are shown in Table 8. Minimal differences between cattle grown on corn and classified as LFE and HFE were observed in digestibility of DM, organic matter, NDF, ADF, CP or starch. However, within steers grown on roughage-based diets, HFE steers excelled at fiber digestion over LFE steers, suggesting ability to digest fibrous diets more completely may have contributed to classification of these steers as highly feed efficient. Diet selectivity and eating behavior was not assessed in these trials and these factors may play important roles in identification of cattle as highly feed efficient on fibrous diets. There were no effects of growing phase FE classification on finishing phase diet digestibility (data not shown).

There was a positive correlation for DM digestibility between feeding phases when steers were grown and finished on similar diets, specifically the roughage-grown byproduct-finished steers and the corn-grown corn-finished steers (Table 9). Although there were no differences in DM digestibility due to FE classification, it does appear that digestibility measured during one feeding phase may help predict digestive capacity during a subsequent phase if similar diet types are fed. Interestingly, fiber digestibility appeared to contribute to FE variation while starch digestibility did not, indicating that there may be more opportunity for improving FE via selection or management for better fiber utilization. Feed efficiency classification effects were most pronounced for growing phase fiber digestibility advantages in the roughage-grown HFE steers. More work is needed to understand the mechanisms by which cattle make most efficient use of fibrous diets.

Summary

Completion of five years of work regarding repeatability of feed efficiency of cattle across growing and finishing phases and different diet types (corn or roughage) has increased our knowledge of feed efficiency. Steers classified as highly feed efficient (HFE) based on growing phase G:F maintained greater G:F in the finishing phase, a relationship that was also congruent for mid (MFE) and low (LFE) feed efficient steers. Thus, growing phase FE appeared to be a reasonable predictor of finishing phase FE. Perhaps the most interesting revelation was that although finishing phase G:F was not directly affected by growing or finishing phase diets, an evaluation of other growth traits revealed differences in how G:F differences resulted from underlying sources of variation. Among steers grown on roughage, finishing phase ADG differed between FE classifications yet DMI was unaffected by FE classification. Dissimilarly, among the corn-grown steers there were no differences detected in finishing phase ADG between FE classifications but DMI differed between classifications. Thus, it appeared that ADG differences

were responsible for finishing phase G:F variation among roughage-grown steers whereas differences in finishing phase G:F among the corn-grown steers resulted from differences in DMI. Though growth performance was affected by growing phase diet and FE classification, carcass differences were limited. There were limited differences among corn-grown steers or corn-finished steers; hence, diet-driven differences were largely isolated to steers fed the high fiber diets.

Examining the relationship between FE across multiple growth phases and diet types is important for determining means by which to select and manage cattle based on FE phenotype.

Ultimately, FE was repeatable across feeding phases but growing phase FE may be a better predictor of subsequent FE when diet types between feeding phases are similar. Though starch digestibility had no relationship with FE, fiber digestibility contributes to FE variation between individuals. Future research should evaluate cattle performance using multiple growing and finishing phase diet combinations but may consider particularly focusing on high fiber diets as roughage-grown steers were the predominant source of variation in the present studies. Understanding the digestive differences between highly and lowly feed efficient steers may be best accomplished by exploring differences in microbial populations/activities.

The ultimate goal of this research is to advance improvement in the beef industry through development of tools and management strategies for producers. Suggested application of our research findings might eventually include testing cattle at weaning to determine their genetic predisposition to be superior fiber digesters, sending those cattle to backgrounding systems to make the most efficient use of low quality, affordable, fibrous feedstuffs while sending the poorer fiber digesters directly to the feedlot to become calf feds. More work is needed before we reach this goal, but ultimately, efficiency of beef cattle production and overall sustainability of the industry can be improved if we understand both the genetic potential and nutritional management required to optimize the cattle feed efficiency.

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Table 1. Composition and analysis of growing phase whole shell corn-based diets (G-Corn) fed to steers (From Russell et al., 2016a)

	Group[1]			
Ingredient, % DM	1, 2, 3	4	5	6
Whole shell corn	78.59	70.92	65.10	64.26
Dried distillers grains	9.72	17.00	24.50	26.07
Soyplus[2]	6.25	6.38	4.51	4.96
Wheat middlings	2.65	2.00	-	-
Porcine blood meal	-	1.30	3.50	2.52
Limestone	1.50	1.40	1.21	1.09
Urea	0.39	0.60	0.47	0.19
Choice white grease	0.20	0.12	0.10	0.19
Salt	0.17	0.04	0.13	0.22
Vitamin premix[3]	0.17	0.16	0.25	0.23
Trace mineral premix[4]	0.17	0.07	0.09	-
Potassium chloride	0.17	-	-	-
Pellet binder	-	-	0.13	0.19
Rumensin 90[5]	0.01	0.01	0.01	0.01
Nutritional analysis[6]				
DM, % as-fed basis	90.7	90.3	88.3	85.1
NDF, % DM	17.8	20.2	21.1	26.4
ADF, % DM	4.4	5.0	4.9	6.5
CP, % DM	17.2	17.9	23.1	20.5

[1] Steers fed in 6 separate, replicated groups.
[2] Soyplus (West Central Cooperative, Ralston, IA).
[3] Vitamin premix fulfills 2,200 IU vitamin A, 275 IU vitamin D, 100 IU vitamin E per kg of diet.
[4] Trace mineral premix fulfills 10 mg Cu, 50 mg Fe, 20 mg Mn, 30 mg Zn, 0.1 mg Co, 0.1 mg Se, 0.5 mg I per kg diet.
[5] Provided Monensin at 150 $mg \cdot steer^{-1} \cdot d^{-1}$, Elanco Animal Health, Indianapolis, IN.
[6] Determined from analysis of total mixed ration samples collected weekly and composited by month.

Table 2. Composition and analysis of growing phase forage and soybean hull-based diets (G-Rough) fed to steers (From Russell et al., 2016a)

	Group[1]			
Ingredient, % DM	1, 3	4	5	6
Soybean hull pellets	40.81	36.57	38.16	36.84
Alfalfa/grass baleage	34.21	-	-	-
Corn Silage	-	36.00	-	-
Rye baleage	-	-	32.49	-
Sudan baleage	-	-	-	36.25
Dried distillers grains	15.13	15.00	22.24	22.70
Soyplus[2]	-	5.50	4.05	1.75
Porcine blood meal	-	0.80	2.02	1.65
Ground corn	8.62	5.00	-	-
Limestone	0.57	0.70	0.61	0.35
Salt	0.25	0.07	0.11	0.18
Vitamin premix[3]	0.20	0.20	0.20	0.18
Trace mineral premix[4]	0.20	0.13	0.07	0.07
MFP[5]	-	0.03	0.05	0.03
Rumensin 90[6]	0.01	0.01	0.01	0.01
Nutritional analysis[7]				
DM, % as-fed basis	79.4	68.9	68.3	66.8
NDF, % DM	50.1	46.9	52.3	57.5
ADF, % DM	32.5	26.5	29.0	31.5
CP, % DM	17.2	16.0	22.3	20.8

[1] Steers fed in 6 separate, replicated groups; forage and soybean hull-based diet was not fed during group 2.
[2] Soyplus (West Central Cooperative, Ralston, IA).
[3] Vitamin premix fulfills 2,200 IU vitamin A, 275 IU vitamin D, 100 IU vitamin E per kg of diet.
[4] Trace mineral premix fulfills 10 mg Cu, 50 mg Fe, 20 mg Mn, 30 mg Zn, 0.1 mg Co, 0.1 mg Se, 0.5 mg I per kg diet.
[5] DL-methionine hydroxy analogue calcium (84 % methionine, Novus International, Saint Charles, MO).
[6] Provided Monensin at 150 $mg \cdot steer^{-1} \cdot d^{-1}$, Elanco Animal Health, Indianapolis, IN.
[7] Determined from analysis of total mixed ration samples collected weekly and composited by month.

Table 3. Composition and analysis of finishing phase diets fed to steers[1] (From Russell et al., 2016a)

	Finishing phase diets[2]	
Ingredient, % DM	F-Corn	F-Byp
Cracked corn	75	30
Dried distillers grains	14.99	39.99
Soybean hull pellets	-	20
Bromegrass hay	8	8
Limestone	1.54	1.54
Salt	0.31	0.31
Vitamin A premix[3]	0.11	0.11
Trace mineral premix[4]	0.035	0.035
Rumensin 90[5]	0.013	0.013
Nutritional analysis[6]		
DM, % as-fed basis	84.5	84.1
NDF, % DM	24.4	42.7
ADF, % DM	8.0	18.7
CP, % DM	11.2	18.4

[1] Steers were fed in 6 separate, replicated groups; ingredient composition of finishing phase diets was consistent across all 6 groups.
[2] Finishing phase diets: F-Corn = cracked corn-based; F-Byp = dried distillers grains and soybean hull-based.
[3] Vitamin A premix contained 4,400,000 IU/kg.
[4] Provided per kilogram of diet (from inorganic sources): 30 mg Zn, 20 mg Mn, 0.5 mg I, 0.1 mg Se, 10 mg Cu, 0.1 mg Co.
[5] Provided Monensin at 200 $mg \cdot steer^{-1} \cdot d^{-1}$, Elanco Animal Health, Indianapolis, IN.
[6] Determined from analysis of total mixed ration samples collected weekly and composited by month.

Table 4. Descriptive statistics of growing phase feed efficiency classifications calculated for finishing phase pens across all groups (From Russell et al., 2016a)

	Growing phase diets[1]					
	G-Corn			G-Rough		
	Growing phase feed efficiency classifications[2]					
	HFE	MFE	LFE	HFE	MFE	LFE
Pens (n)	24	41	25	20	34	24
G:F[3]						
Average	0.258	0.218	0.180	0.228	0.196	0.169
Minimum	0.235	0.203	0.141	0.211	0.185	0.144
Maximum	0.298	0.233	0.202	0.262	0.208	0.183

[1] Growing phase diets: G-Corn = whole shell corn-based; G-Rough = forage and soybean hull-based.

[2] Growing phase feed efficiency classifications: HFE = highly feed efficient (> 0.5 SD from the G:F mean); MFE = mid feed efficiency (± 0.5 SD from the G:F mean); LFE = lowly feed efficient (< 0.5 SD from the G:F mean).

[3] Growing phase G:F for each finishing phase pen calculated using individual BW and DMI data for each steer housed in a finishing phase pen, and utilizing growing phase initial BW as a covariate in the MIXED procedure of SAS 9.3 (SAS Institute Inc., Cary, NC).

Table 5. Effect of growing phase diet and feed efficiency classification on finishing phase growth performance and carcass traits (From Russell et al., 2016a)

	Growing phase diets[1]							
	G-Corn			G-Rough				
	Growing phase feed efficiency classifications[2]							
	LFE	MFE	HFE	LFE	MFE	HFE	SEM	*P*-value[3,4]
Live performance								
Initial BW[5], kg	448	457	459	460	462	475	-	-
Final BW[6, 7], kg	615^{ab}	609^{bc}	605^{c}	605^{c}	612^{ab}	618^{a}	2.6	0.001
ADG, kg/d	1.85^{ab}	1.79^{bc}	1.78^{bc}	1.72^{c}	1.82^{ab}	1.87^{a}	0.029	0.005
DMI[7], kg/d	11.3^{a}	10.7^{bc}	10.6^{c}	11.0^{ab}	11.1^{a}	11.2^{a}	0.12	0.002
Carcass traits								
HCW[7], kg	389^{a}	386^{a}	381^{b}	385^{ab}	387^{a}	390^{a}	1.9	0.003
REA[8], cm^2	86.6^{c}	89.6^{b}	87.9^{bc}	87.9^{bc}	89.1^{b}	91.7^{a}	0.78	0.01

[a, b, c] Least squares means in a row without common superscript differ ($P < 0.05$).

[1] Growing phase diets: G-Corn = whole shell corn-based; G-Rough = forage and soybean hull-based.

[2] Growing phase feed efficiency classifications: HFE = highly feed efficient (> 0.5 SD from the G:F mean); MFE = mid feed efficiency (± 0.5 SD from the G:F mean); LFE = lowly feed efficient (< 0.5 SD from the G:F mean).

[3] Interaction effect of growing phase diet and feed efficiency classification.

[4] Growing phase diet × feed efficiency classification interaction was not significant ($P \geq 0.14$) for G:F, dressing percent, backfat, KPH, yield grade, or marbling score; Three way interaction between growing phase diet, finishing phase diet, and growing phase feed efficiency classification was not significant ($P > 0.2$).

[5] Initial BW pencil shrunk 4 %.

[6] Final BW, pencil shrunk 4 %.

[7] Initial BW applied as a covariate.

[8] Ribeye area.

Table 6. Effect of growing phase and finishing phase diets on feed efficiency classification shifts by steers and the correlation between growing phase and finishing phase G:F.

Item	Pens (n)	Percent of pens changing feed efficiency classifications from growing to finishing			Correlation of G:F between phases[1]
		No change	One classification	Two classifications	r (*P*-value)
G-Corn	90	51.1%	41.1%	7.8%	
F-corn	45	48.9%	40.0%	11.1%	0.47 (0.001)
F-Byp	45	53.3%	42.2%	4.4%	0.40 (0.007)
G-Rough	78	41.0%	42.3%	16.7%	
F-Corn	39	43.6%	43.6%	12.8%	0.37 (0.02)
F-Byp	39	38.5%	41.0%	20.5%	0.29 (0.08)
Overall	168	46.4%	41.7%	11.9%	

[1]Pearson's correlation (r) and associated P-value for the relationship between adjusted growing phase G:F and finishing phase G:F.

Table 7. Descriptive statistics of growing phase growth performance for steers fed corn or roughage-based diets and classified as least or most feed efficient and utilized in diet digestibility assessments (Groups 4 and 5)[1] (From Russell et al., 2016b)

	Diet[2]			
	G-Corn		G-Rough	
	FE Classification[3]			
Item	LFE	HFE	LFE	HFE
Steers, n	24	24	24	24
Initial BW, kg	308.9	279.0	309.1	282.3
Final BW, kg	432.6	415.8	439.7	428.7
ADG, kg/d	1.75	1.90	1.89	1.98
DMI, kg	9.72	7.14	10.28	8.87
G:F	0.181	0.269	0.186	0.228
Minimum	0.102	0.208	0.087	0.178
Maximum	0.198	0.315	0.176	0.302

[1] Pooled values from steers selected as most and least feed efficient from each of two diets fed in two separate groups (48 selected steers/group: 24 steers/diet, 12 steers/FE classification within diet).
[2] Growing phase diets: G-Corn = whole shell corn-based; G-Rough = forage and soybean hull-based.
[3] Growing phase feed efficiency classifications: LFE = least feed efficient, poorest G:F; HFE = most feed efficient, greatest G:F.

Table 8. Receiving phase digestibility as affected by growing phase feed efficiency classification and growing phase diets (From Russell et al., 2016b).

	Growing phase diets[1]					*P*-values[3]		
	G-Corn		G-Rough					
	Growing phase feed efficiency classification[2]							
Item	LFE	HFE	LFE	HFE	SEM	Diet	FE	Diet×FE
Steers, n	24	24	24	24	-	-	-	-
DMI[4], kg	8.9	8.6	10.0	10.0	0.37	<0.001	0.71	0.79
Digestibility, %								
DM	66.9	66.7	66.0	70.3	2.61	0.56	0.51	0.35
OM	68.9	68.4	68.2	72.8	2.58	0.42	0.51	0.31
NDF	58.1[b]	57.1[b]	59.2[b]	73.0[a]	3.03	0.003	0.08	0.01
ADF	46.8	46.6	60.2	69.4	3.84	<0.001	0.34	0.20
CP	59.4	56.9	61.3	64.5	2.81	0.06	0.92	0.30
Starch	87.4	87.9	90.0	91.1	2.47	0.20	0.80	0.89

[a, b] Least squares means in a row without common superscript differ ($P < 0.05$).

[1] Growing phase diets: G-Corn = whole shell corn-based; G-Rough = forage and soybean hull-based.

[2] Growing phase feed efficiency classifications: LFE = least feed efficient, poorest G:F; HFE = most feed efficient, greatest G:F.

[3] *P*-values: Diet = main effect of growing phase diet; FE = main effect of growing phase feed efficiency classification; Diet×FE = interaction effect of growing phase diet and feed efficiency classification.

[4] Titanium dioxide supplementation period DMI, average of final 10 d prior to fecal collection.

Table 9. Dry matter digestibility correlations across growing and finishing phase diets.

		Dry matter digestibility[1]	
Growing phase diet[2]	Finishing phase diet[3]	Corr[4]	*P*-value
Corn	Corn	0.49	0.02
Corn	Byproduct	0.25	0.3
Roughage	Corn	0.21	0.4
Roughage	Byproduct	0.68	<0.001

[1] Dry matter digestibility correlations based on receiving phase and finishing phase diet digestibilities; receiving phase diets nutritionally similar to growing phase diets

[2] Growing phase diets: whole shell corn-based (Corn), forage and soybean hull-based (Roughage)

[3] Finishing phase diets: cracked corn-based (Corn), dried distillers grains and soybean hull-based (Byproduct)

[4] Corr: r, Pearson's correlation coefficient

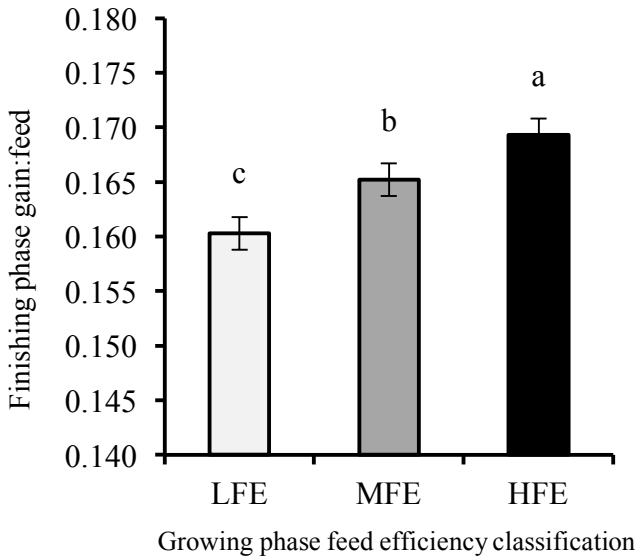

Figure 1. Finishing phase G:F in steers due to growing phase feed efficiency classification: HFE = highly feed efficient (> 0.5 SD from the growing phase G:F mean; n = 44 pens); MFE = mid feed efficiency (± 0.5 SD from the growing phase G:F mean; n = 75 pens); LFE = lowly feed efficient (< 0.5 SD from the growing phase G:F mean; n = 49 pens). Finishing phase initial BW applied as covariate. Values are means ± 0.0015, SEM. Means without common superscript differ ($P \leq 0.05$). From Russell et al. (2016a).

Results of survey of stakeholders regarding knowledge of and attitudes towards feed intake, efficiency and genetic improvement concepts

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Introduction

Individual animal feed efficiency plays a key role in the profitability and sustainability of the US beef industry. During the growing and finishing phase of production, a 10% improvement in feed efficiency has a two-fold greater impact on profit than a 10% increase in rate of gain (Fox et al., 2001). The traits that beef producers routinely record are outputs which determine the value of product sold and not the inputs defining the cost of beef production. The inability to routinely measure feed intake and feed efficiency on large numbers of cattle has precluded the efficient application of selection despite moderate heritabilities (h2 = 0.16-0.46; Archer et al., 1999). Feed costs in calf feeding and yearling finishing systems account for approximately 66% and 77% of costs, respectively (Anderson et al., 2005).Feed costs account for approximately 65% of total beef production costs. Of the metabolizable energy required from conception to consumption of a beef animal, 72% is utilized during the cow-calf segment of production while 28% of calories are utilized in the calf growing and finishing phases of production (Ferrell and Jenkins, 1982). Of the calories consumed in the cow-calf segment, more than half are used for maintenance which presents a large selection target.

A very large potential cost savings to the US beef cattle industry could be realized with selection for feed efficiency. Cattle selected for residual feed intake (RFI) with the same ADG eat less feed thus saving feedlot operators money. Assuming 27 million cattle are fed per year and that 34% of cattle in the feedlot are calves and 66% are yearlings, the beef industry could save over 1 billion dollars annually by reducing daily feed intake by just 0.91 kg. per animal (Weaber, 2012).

The emergence of individual feed intake monitoring systems has increased the availability of data for the genetic evaluation. The deployment of feed efficiency related genetic prediction tools may enable cattle producers to make better selection to improve profitability (Arthur et al., 2004; Hill et al., 2005). The cost and small number of records has slowed deployment of selection tools. At present, only the Am. Angus Assn. publishes a feed efficiency related EPD and only 8% of young sire candidates have the EPD (Am. Angus Assn., 2014). Little research has been conducted to understand the social aspects or barriers to adoption of feed efficiency technology by beef producers on a national scale. One such study (Wulfhorst et al., 2010) focused on the specific willingness of seedstock producers to begin collection of records for computation of RFI and willingness of commercial producers to select bulls based on RFI.

The objective of this study was to assess the awareness, attitudes and knowledge of US commercial cow-calf producers regarding a variety of feed efficiency and genetics concepts. This work was undertaken as a portion of the outreach component of the USDA funded integrated research project (USDA-NIFA-AFRI grant number: 2011-68004-30214) entitled the National Program for the Genetic Improvement of

Feed Efficiency in Beef Cattle. Results from the social survey will be used to refine the project's nationwide producer education program.

Data Collection and Analysis

Social Survey. The survey instrument, sampling frame and data entry were conducted under contract with the USDA National Agricultural Statistics Services (USDA-NASS). The sampling frame for the stratified random sample was derived from USDA-NASS lists and all beef, seed stock, cow/calf, stocker, and feedlot operations from the continental US. The total sample size was 7,500 and was stratified across seven US regions to proportionally represent the number of beef producers in those regions.

The 55 question survey was mailed September 18, 2013 and a second mailing occurred on October 23, 2013. Each mailing included an explanatory letter, the paper survey instrument and a return envelope. Data from returned surveys were entered into a database by USDA-NASS employees and a data set including strata, anonymous responses and weightings was delivered to researchers at Kansas State University.

Descriptive statistics including estimates of weighted frequencies and respective standard errors were generated using the SURVEYFREQ procedure and means were estimated via the SURVEYMEANS procedure (SAS Institute, Inc., Cary, NC). Respondents in each stratum (region) had unequal but known probabilities of inclusion in the sample due to the stratified sample design. Within stratum, each respondent had the same probability of inclusion. Unequal probabilities of inclusion in the sample were accounted for in the weighting of the frequencies. Results presented here are weighted frequencies or means.

Summary of Results and Discussion

A total of 868 (11.6%) respondents returned surveys. Of those, 401 (5.3%) were eliminated from further consideration as these were deemed ineligible for analysis because the respondents indicated that they were not at the time of survey an owner, manager or worker on a beef cattle operation. The remaining responses from 467 surveys were used in this analysis. Response to any given question varied among these 467 due to item nonresponse.

Of the 467 respondents a majority (59.9%) were commercial cow-calf producers while 11.5% were seedstock, 12.0% were seedstock and commercial cow-calf producers, 13.3% were stocker operators and 3.2% were feedlot operators. The scope of the analysis reported here was limited exclusively to the 269 commercial cow-calf respondents of which 93.0% indicated they were owners, 5.1% were managers and 1.8% indicated other specific involvement in beef operation (managing partner, office manager, etc.). On average, the commercial producer respondents, planned to breed 83.1 ± 6.7 head of cows and heifers in 2013, on average used artificial insemination to breed 3.7 ± 1.1 percent of their herd, spent approximately US$1,887 ± 102 to purchase each herd bull on inventory, and had a mean age of 57.4 ± 1.9 yr. with 33.2 ± 1.6 yr. of beef industry experience.

The highest level of education varied among commercial producer respondents with 38.3% 4 year college graduates or beyond, 23.3% with some college coursework, 27.3% high school graduates, 5.0% less than high school diploma and 6.3% not responding. Of the commercial producers responding, 47.1% indicated that 50% or more of their work-time was on a farm or ranch, while 43.3% spent a majority of their occupational work-time off farm. Commercial producers reported that on average 29.9 ± 2.2 % of their family's income was from their beef operation.

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

When questioned about decision making processes used in the business, commercial producers indicated that profitability was the greatest concern (73.8%) and 24.2% identified themselves as an 'early adopter' of new technology. A large majority (77.0%) of producers responded that they tend to let new ideas prove themselves before adoption with 87% considering their current management and selection system to be sustainable. Producers obtain new knowledge by accessing a variety of media and programs/meetings (55.4%), relying on extension educators to teach them about new techniques (40.1%) and rely on seedstock producers and breed associations to provide new information on breeding and selection practices (39.8%).

Feed efficiency concepts. Commercial cow-calf producers struggled to correctly identify definitions of basic feed efficiency measures with 32.6% choosing the correct definition for feed-to-gain ratio and 36.2% correctly defining feed efficiency. Only 16.4% of producers had heard the terms residual or net feed intake (RFI or RFI) and only 14.3% of producers were familiar with residual average daily gain (RADG). A majority (54.8%) of producers identified the genetic improvement of rate of gain as the mechanism used in the beef industry to improve feed efficiency while improved diet formation was identified by 40.6%, feed additives such as ionophores or beta-agonists by 28.4%, growth promoting implants by 35.2% and 24.2% did not know if any of the options were used. Nearly one-half of producers did not know the consequence of selection for increased average daily gain on the cowherd (decreased body fat and increased mature weight), while 13.4% suggested no harmful effects and only 10.3% correctly answered the question.

Producers responded that they were not knowledgeable of methods to select for improved feed efficiency (41.2%) with 28.8% responding slightly knowledgeable, 20.2% somewhat knowledgeable, 7.0% very knowledgeable and 1.5% extremely knowledgeable.

When asked about the largest obstacle to genetic improvement of feed efficiency in beef cattle 11.9% identified a lack of available facilities and equipment to measure individual intakes, 9.7% identified a lack of uniform guidelines, 8.3% suggested there were no obstacles, 8.0% identified a lack of demand from bull buyers for feed efficiency tested bulls, and 7.1% said it was too expensive to collect individual feed intake records.

Most producers (81.8%) responding to the survey had no awareness of the research project that was undertaking the survey with 9.6% having awareness and 8.9% nonresponse.

Genetic concepts. Survey respondents were asked a range of questions to gauge their knowledge and understanding of some basic genetic concepts and attitudes towards new selection tools. Questions were posed to more fully understand producer's utilization of current selection technologies in their operations. Producers were also asked to identify current selection behaviors and the future directions that they may pursue.

Producers use a wide range of information for making selection decisions and plan to use different information for selection decisions in the future as reported in Table 1. Despite much work by industry and extension educators, commercial producers still use data sources that are not corrected for environmental effects.

Commercial cow-calf producers currently lack a basic understanding of new genomic based selection tools and their anticipated benefit to beef cattle selection systems. A majority of producers (62%) responded that they did not know what class of traits should benefit the most from marker assisted selection. Only 13.1% responded correctly that this class includes traits which are difficult and/or expensive to measure and that have significant costs or returns associated with them. More than two-thirds of producers could not identify what was the primary benefit of adding molecular breeding value data to EPD calculations. Only 20.8% cited increase in EPD accuracy as the correct answer. Nearly 70% of cow-calf producers responded that they didn't know how much variation DNA markers explain in a trait.

When asked to summarize which traits were important in their selection objective over the past five years, a large majority (81.4%) of producers identified calving ease/birth weight, followed by reproduction (65.2%), growth traits (64.3%), temperament (63.3%), milk (51.5%), lifetime productivity (36.0%), maintenance efficiency (31.5%), and feed efficiency (30.3%). During the coming five years, producers identified calving ease/birth weight (69.3%), growth traits (66.1%), reproduction (65.8%), temperament (58.5%), milk (47.5%), lifetime productivity (42.4%), feed efficiency (36.7%), and maintenance efficiency (31.1%).

Average daily gain was most frequently identified (41.7%) by commercial producers as the selection criterion that they use to improve feed efficiency. Interestingly, mature weight and cow body condition score were the next most frequently indicated at approximately 27% of respondents. Less than 4% of respondents used maintenance energy EPD, residual average daily gain EPD, or selection indexes that use feed intake predictions.

Producers were asked how much more they would be willing to pay for a bull if a reliable method of evaluation were available to document its genetic merit for feed efficiency. Most frequently (23%) producers indicated that they would not pay any more for a bull with a reliable genetic prediction for feed efficiency, while 13.6% indicated they would increase their purchase price by more than US$500, 11.8% indicated an increase of US$201-$300 and 10.5% would increase their bid by US$101-$200.

Conclusion

Although no direct price signal exists in the beef value chain for feeder cattle of different genetic potentials for feed efficiency, cow-calf and feedlot producers may obtain increased profits through reduced feed cost per unit output through selection for efficiency and growth rate. Results of this social survey suggest that commercial cow-calf beef producers in the US are not well versed in the basic concepts of feed efficiency or of the available methods to improve feed efficiency. Additional educational work must be done to aid producers in understanding the appropriate methods and tools for selection to improve feed efficiency.

Adapted from: Weaber, R.L. et al. Proceedings, 10th World Congress on Genetics Applied to Livestock Production

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Table 1. Frequency of use (SE) for various types of genetic prediction information used by beef producers during past five years and their anticipated future use.[1]

Data type	Use past 5 years[2]	Anticipated future use[2]
Actual measurements	18.4 (3.0)	6.7 (1.8)
Ratios	21.6 (4.0)	13.8 (3.3)
Expected Progeny Differences	29.9 (4.4)	12.4 (3.4)
Genomically Enhanced EPD	5.6 (2.2)	12.6 (3.0)
Productivity of relatives	16.4 (3.5)	14.3 (3.7)
Comments by seller	17.6 (3.8)	11.4 (3.0)
DNA marker results	2.8 (1.5)	15.4 (3.1)
None of above	31.0 (4.9)	42.5 (5.1)

[1]Respondents could select more than one type of information used; column totals will not sum to 100%.
[2]Percentage of respondents indicating use or anticipated use followed by standard error of measurement.

Extension demonstration project outcomes: Industry adoption and translation of project deliverables

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Unfortunately, the amount of feed intake data available to U.S. beef breed associations is spars compared to the amount of data available for growth traits. This makes traditional pedigree-based genetic evaluation for feed intake or efficiency challenging. However, progress in this trait complex could be made as we know that dry matter intake and various "efficiency" traits would respond favorably to selection. Table 1 below depicts the heritability (on the diagonal) and genetic correlations (on the off diagonal) of several feed efficiency traits.

Table 1. Heritabilities and genetic correlations for feed efficiency traits[1].

	ADG	DMI	RFI	G:F
ADG	0.26	0.56	-0.15	0.31
DMI		0.40	0.66	-0.60
RFI			0.52	-0.92
G:F				0.27

[1]Adapted from Rolfe et al. (2011).

Although EPD for traits related to the cost of production are limited, some EPD do currently exist to select for partial efficiency. Examples of those are detailed below.

	Bull A	Bull B
Residual average daily gain	-0.1	0.05
Residual feed intake	-0.3	0.0
Maintenance energy	0	10

Residual average daily gain (Angus)- Calves sired by bull B should gain 0.15 pounds per day more when fed the same amount of feed during the post weaning phase.

Residual feed intake (Gelbvieh)- Calves sired by bull A would consume 0.3 lbs of feed per day less on average than calves sired by bull B to gain the same amount of weight.

Maintenance energy (Red Angus)- Daughters from bull B should require 10 Mcal/month less energy for maintenance. If average hay quality is 0.86 Mcal/lb. this equates to 11 lb. less forage per month.

Even though some EPD do exist for components of efficiency, feed intake phenotypes are expensive to collect and thus for the foreseeable future, wide-spread collection of individual intake data in the seedstock sector will remain sparse at best. Moreover, residual gain and residual feed intake are not phenotypes per se, but rather restricted selection indices. Although these residuals are biologically intriguing, they are

suboptimal at generating response to overall profitability given that they only allow for improvement in either gain or feed intake and not both traits simultaneously.

Selection Methods for Efficiency

In terms of guidelines for the U.S. beef industry to follow relative to genetic selection for improved feed efficiency, Nielsen et al. (2013) recommend an index-based approach. From a total life-cycle perspective, maintenance energy costs are estimated to be about 70% of the total energy intake in the beef production system. Thus a primary goal must be to decrease maintenance energy requirements while not reducing output. This means that profitable selection decisions must contemplate multiple traits simultaneously. Using selection index values will be very beneficial to achieve the overall goal of improved profitability. If constructed correctly, multiple-trait index tools can account for antagonisms that may exist between feed intake and other economically relevant traits, including cow-herd centric traits.

Hazel (1943) first introduced the selection index equations to calculate index coefficients (b) for each of the selection criteria:

$$\mathbf{b = P^{-1}Gv}$$

where **P** is a *n* x *n* matrix of the phenotypic (co)variances among the *n* traits measured and available as selection criteria, **G** is a *n* x *m* matrix of the genetic (co)variances among the *n* selection criteria and *m* objective traits, and **v** is an *m* x 1 vector of economic values for all objective traits.

Rolfe et al. (2011) estimated selection response for three feed efficiency related phenotypes and four different selection indices (Table 2). From these results it is clear that an economic index approach to selection is the most desirable.

Table 2. Expected response (selection intensity*lbs) to selection based on several criterion[1].

Selection Criterion[2]	Direction	DMI Response, lbs.	Gain Response, lbs.
DMI	Down	-125.0	-11.91
GAIN	Up	+57.98	+16.54
G:F	Up	-60.63	+5.29
I_1	Down	-98.33	+4.19
I_2	Down	-84.88	0
I_3	Down	-27.34	+11.91
I_4	Down	0	+16.98

[1] Adapted from Rolfe et al. (2011).

[2] DMI= Dry matter intake; GAIN = Weight gain; G:F = Gain to feed ratio; I_1 = Phenotypic RFI; I_2 = Genetic RFI; I_3= Economic index including DMI and Gain; I_4=Economic index including Gain and RFI.

The improvement of efficiency is inherently a multiple-trait issue and thus the development and utilization of indexes to select for the most profitable animals is critical. An interactive example of such an index is available at www.beefefficiency.org. The interactive tool enables the user to calculate residual average daily gain, residual feed intake, and index three from table 2.

Although Rolfe et al. (2011) illustrated that an economic index based approach was superior to single trait selection when considering both feed intake and gain, a more comprehensive approach is to consider feed intake as a cost in existing economic selection indices such as Angus's $B or Simmental's TI, therefore considering traits such as carcass merit, feed intake, carcass weight, survival, and other traits as dictated by the complete breeding objective. This approach is currently being implemented by several U.S. beef breed associations, in part enabled by the massive number of phenotypes generated through the USDA-NIFA funded project National Program for Genetic Improvement of Feed Efficiency in Beef Cattle that has provided phenotypes and genotypes to these associations at no cost.

The importance of feed intake in a terminal index is well documented. In example, Ochsner et al. (2016) assumed a terminal breeding objective for Beefmaster cattle whereby all calves were born from mature cows, retained through the feedlot phase and sold on a grid-based system. The five objective traits considered for the terminal index included hot carcass weight (HCW), marbling score (MS), ribeye area (REA), 12th-rib fat (FAT) and feed intake (FI), with the latter representing the only expense related phenotype among the objective traits. Relative economic values for the terminal objective traits HCW, MS, ribeye area REA, FAT, and FI were 91.29, 17.01, 8.38, -7.07, and -29.66, respectively. This illustrates that sale weight, in this case hot carcass weight, and feed intake are drivers of profitability. Selection criteria for both indices were selected from the ten EPD currently reported by BBU. The suite of BBU EPD included: birth weight (BWT), WWd, WWm, 365-day yearling weight (YW), scrotal circumference (SC), ultrasound ribeye area (UREA), ultrasound 12th-rib fat (UFAT), ultrasound rump fat (URUMP), ultrasound intramuscular fat percentage (UIMF) and total maternal (TM). Selection criteria considered for the terminal index were YW, UREA, UFAT and UIMF. The accuracy of this index (r_{HI}) was estimated to be 0.50. If additional economically relevant traits could be added to the suite of selection criterion, such as an EPD for FI, this accuracy would increase. In the context of feed intake, this will require additional phenotyping efforts supported by a genomics approach.

A Genomics Approach

Genomic information, in the form of Single Nucleotide Polymorphisms (SNP), has always held the promise to increase the accuracy of Expected Progeny Differences (EPD).

This promise has finally been realized for those breeds that incorporate this information into their EPD calculations. One key advantage to genomic predictors (i.e. Molecular Breeding Values (MBV)) is that this information can be garnered early in the life of the animal thus enabling an increase in the accuracy of EPD particularly on young animals, which have not yet produced progeny. The benefit of the inclusion of genomic predictions into EPD estimates is proportional to the amount of genetic variation explained by the genomic predictor.

Genomic-enhanced EPD were first estimated for carcass traits and then evolved to other production traits for which EPD already existed. This is due to the need for phenotypes to develop (train) the genomic prediction equations. Consequently, genomic tests for "novel" traits such as different measures of efficiency require a significant effort in order to build large resource populations of animals with both phenotypes and genotypes. In this case, strategic genotyping and phenotyping could have an economic advantage over routine collection of very costly phenotypes.

The underlying question commonly asked by producers is "does it work?". It is critical to understand that this is not a valid question, as the true answer is not binary (i.e. yes or no). The important question to ask is "how well does it work?", and the answer to that question is related to how much of the genetic variation the marker test explains. The magnitude of the benefits will depend on the proportion of genetic variation (%GV) explained by a given marker panel, where the %GV is equal to the square of the genetic correlation multiplied by 100.

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. Increased rate of genetic change can occur by increasing the accuracy of EPD, and thus the accuracy of selection, and by decreasing the generation interval. This decrease in the mean generation interval could occur particularly for sires if they are used more frequently at younger ages given the increased confidence in their genetic superiority due to added genomic information.

Figures 1 and 2 illustrate the benefits of including a MBV into EPD (or Estimated Breeding Value (EBV) which is twice the value of an EPD) on accuracy (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 exceed 0.2 accuracy with genomic information alone. This would be comparable to having approximately 7 progeny for a moderately heritable trait like feed intake. It should be noted that although a SNP panel that only explains 10% of the GV would be considered poor for weight traits,

if phenotypes do not exist, a panel of this efficacy would be beneficial.

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

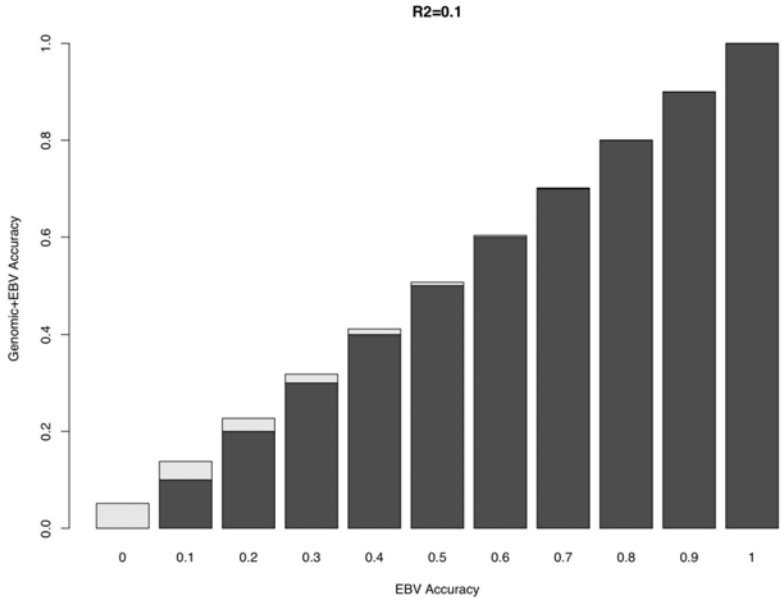
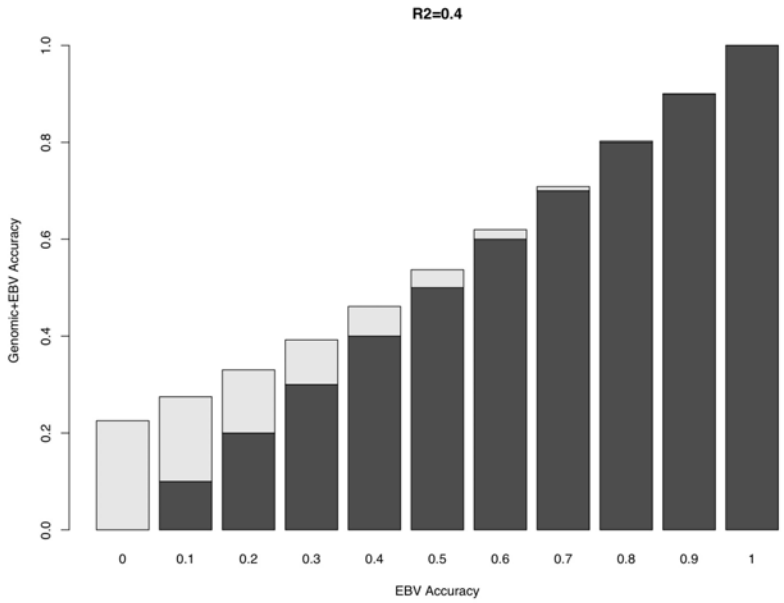


Figure 2. Increase in accuracy from integrating genomic information that explains 40% of the genetic variation into Estimated Breeding Values (EBV).



Current efforts

A USDA-NIFA funded project, National Program for Genetic Improvement of Feed Efficiency in Beef Cattle, to develop genomic predictors for feed intake/efficiency using dense single nucleotide polymorphism (SNP) panels (50,000 and 770,000 SNPs). To do this requires the collection of feed intake records from thousands of animals that are genotyped with either the 50K or 770K (HD) SNP assays across multiple breeds in order to develop genomic predictors that are accurate and robust across cattle populations. Table 3 contains initial genome-wide association results from this project (Saatchi et al., 2014). Four populations of cattle involving over 5,000 animals were used for a genome-wide association study (GWAS) of different feed efficiency related traits. The heritability estimates (h2) represent the proportion of phenotypic variation explained by the SNPs. Although all estimates suggest that these traits are moderately heritable, differences in parameter estimates exist between the resource populations likely due to differences in population size, structure (e.g., the number of contemporary groups, degree of relatedness among animals, etc.), and data collection methods.

Table 3. Genomic heritability estimates for ADG, MBW, RFI and DMI[1]

Population[2]	N	SNP Density	ADG h^2	MBW h^2	RFI h^2	DMI h^2
HH	847	HD	0.27	0.50	0.45	0.41
USMARC	1,160	50K	0.30	0.47	0.49	0.35
SM x AN	1,444	HD	0.23	0.38	0.32	0.27
AN	1,580	HD	0.19	0.49	0.21	0.35

[1] ADG = Average daily gain, MBW = mid-test metabolic body weight, RFI = Residual feed intake, DMI = dry matter intake.

[2] HH=Hereford cattle fed at Olsen Ranches, USMARC=F_1[2] composites from the Meat Animal Research Center Cycle VII, SM x AN=Legacy Simmental x Angus animals fed at the University of Illinois, AN=Angus cattle fed at Circle A and the University of Missouri.

Saatchi et al. (2014) also identified regions of the genome that appear to harbor large effect quantitative trait loci (QTL). Given the complex nature of these traits (the fact they are controlled by numerous genes), a large effect QTL was considered as a locus explaining greater than 1% of the additive genetic variation. A total of 5, 5, 17, and 10 of these large effect QTL were identified for ADG, DMI, MBW and RFI, respectively. Some of the QTL identified had substantially larger effects than might have been expected. For instance, a QTL in Angus explained over 10 and 14% of the additive genetic variation in DMI and MBW, respectively. No QTL identified for RFI explained greater than 2.5% of the additive genetic variation. These QTL regions were generally breed specific, further illustrating why genomic predictors are not easily transferable across breeds.

In 2009, the concept of an integrated project focused on the development and translation of genomic selection tools in beef cattle was initiated as a collaboration between the National Beef Cattle Evaluation Consortium, the University of Nebraska-Lincoln, the U.S. Meat Animal Research Center, and the seven largest U.S. beef breed associations. This project, called the Weight Trait Project (WTP) due to the initial focus on weight traits, has served as the industry demonstration project for the before mentioned USDA-NIFA project. The WTP has engaged 24 seedstock producers from seven states representing the following U.S. beef breeds: Angus, Hereford, Red Angus, Charolais, Gelbvieh, Limousin, and Simmental. Through this demonstration project, these producers were able to nominate herd bulls that were used via AI to breed cows either at the U.S. Meat Animal Research Center or the Rex Ranch. The corresponding progeny were then feed in individual feed intake facilities and genotyped with the BovineSNP50v2 beadchip. All sires were genotyped with the HD assay (770K). All corresponding phenotypes have been provided to the respective beef breed associations. Over 770 calves were produced with complete feed intake data representing 63 sires.

Summary

Results from this project illustrate that by using either the 50K or 770K SNP assay, the genomic heritability estimates of traits related to feed efficiency are in general agreement with heritability estimates from the scientific literature using phenotypes and pedigree information. The fact that these traits are moderately heritable and that the SNP assays can explain large proportions of the phenotypic variation suggest that genetic progress in these traits can be made by using genomic selection. However, this study further illustrates the breed specific nature of genomic predictors and thus caution should be used if attempting to use a genomic predictor in a population that is distantly related to the training population (e.g., across breeds). The continued collection of feed intake phenotypes will be required to refine and retrain genomic predictions overtime. To this end, strategic phenotyping and the use of multiple-trait GWAS models are needed to ensure that genotyped populations represent the larger target population and that information can be borrowed from more densely recorded traits such as the plethora of weight phenotypes (e.g. post weaning gain) currently available.

In terms of delivering tools and information to the beef industry for use in National Cattle Evaluation, this project has provided both phenotypes and genotypes to beef breed associations, initial predication equations to three beef breed associations, and online resources for the calculation of an economic-based efficiency index. For those breeds that relatively recently began including feed intake into current indices, many of the phenotypes were provided by this project. Next steps will need to include expanding the number of breeds for which prediction equations are developed, and exploring the utility of a newly developed assay with putative functional content (GGPF250).

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Bolt and an Alternative Approach to Genomic EPDs

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Introduction

Misztal et al. (2009) and Aguilar et al. (2010) introduced approaches for single-step analyses that combined genotyped and non-genotyped animals in the same analysis on the basis of pedigree and genomic relationship matrices and their inverses. Fernando et al. (2014) and Garrick et al. (2014) presented an alternative computing algorithm for the same model that gives identical genomic enhanced EPDs but has different computational properties. That single-step approach, called the Hybrid Model, provides solutions for the marker effects and the imputation errors for non-genotyped animals, rather than directly providing the EBVs. It has computational advantages over that of Misztal et al. (2009) in that it does not require any large matrix inverse, and it has the ability to implement marker selection methods such as Bayes C (or other forms of the Bayesian alphabet). Implementing a marker selection approach resulted in a substantial increase in the accuracy of the predictions from the same amount of genotype data. Our aim in this paper was to present an alternative formulation of the mixed model equations (MME) from those presented in Fernando, et al. (2014) and Garrick, et al. (2014). Putatively called the Super Hybrid Model (SHM; Fernando and Garrick, unpublished), the new MME are even easier to assemble and solve then those of the Hybrid Model.

Additionally, we present here results from implementing these models in the Biometric Open Language Tools software package (Bolt) available from ThetaSolutions LLC. Designed specifically to work with commodity class General Purpose Graphics Processing Units (GPU), we have solved and sampled very large, complex multiple trait SHM that include maternal effects. In addition to the original Hybrid Model, and the SHM, we have implemented the original single-step approach (SSGBLUP) of Misztal et al. (2009) in Bolt. Breeding companies and organizations in several countries are currently converting their routine evaluations to use Bolt, including the Pan American Cattle Evaluation (PACE) of Hereford cattle and the multibreed International Genetic Solutions (IGS) evaluation of Angus, Red Angus, Gelbvieh, Limousin, Maine Anjou, Shorthorn, and Simmental pure- and crossbred cattle from US and Canada. Here we discuss implementation of Bolt for IGS for their twelve participating beef breed associations.

The Super Hybrid Model

The basic form of the SHM includes the usual fixed effects; marker effects, α; breeding value effects for animals that are not genotyped, u_n; and residual effects, e. The model equation is

$$y = Xb + Z_n u_n + Z_g M_g \alpha + e$$

where X is an incidence matrix of fixed effects, b, on observations in y; $Z = [Z_n \quad Z_g]$, is an incidence matrix of animals with observations in y; g and n subscripts refer to animals who were genotyped and animals who were not genotyped respectively; M is the matrix of marker values

and α are the random additive marker effects; u_n are the random breeding values for animals who were not genotyped and e are the residual effects on y.

In large problems the only substantial amount of work is the formation of the diagonal block for the marker effects. However, Bolt has optimized routines that have achieved over 7TFlops on inexpensive enthusiast class hardware when performing this computation making it highly tractable. Additionally, the computation of the diagonal blocks is performed only once, in parallel, during assembly of the MME.

We have developed optimized asynchronous parallel methods for high performance sampling of the dependent variables (Golden et al., 2014). Using Gibbs sampling results in high quality estimates of the prediction error variances including the variance of functions of the EPD such as economic indexes. Sampling also permits the implementation of marker selection models which results in substantial increases in accuracy over SSGBLUP which always fits all markers.

Other features of the SHM formulation of the MME include no large inverse matrices as are required in SSGBLUP or solutions involving the forward/backward substitution solve (or other solve) at each round of sampling as was required for efficient implementation of Fernando et al. (2014).

Expanding the SHM to include extra polygenic effects is trivial and extending it to maternal effects and multiple traits is straight forward. Including an extra polygenic effect is important when the markers do not describe all the additive genetic variance of the traits. This has been shown to be the case with current marker information (Saatchi and Garrick, 2016). Failure to do so results in widely-used sires with high accuracy EPD having slightly different genomic prediction estimates compared to those from traditional pedigree analyses.

The Bolt Software

Bolt is a collection of over one hundred software tools implemented as a set of commands used to manipulate data and the matrices involved in statistical problem assembly and solution. Combining Bolt with an environment such as the Born Again Shell (bash) or other computer language like environments (e.g., Python) provides a full featured language the professional analyst can use for many classes of statistical analysis of very large data sets.

Bolt is supported in the Linux environment and is designed to use low-cost computer workstation hardware with at least one general purpose CUDA class graphics processing unit (GPU). GPU computing has become a standard method in scientific computing for achieving very high performance computations at a relatively low cost (Owens, et al., 2008). Originally developed to process data for video editing and the computer gaming industry, GPU were adapted to provide general purpose computing for numerically intensive problems. Two widely used programming environments available for GPU computing include OpenCL and CUDA. The CUDA environment is available only for use with GPU designed by the NVidia Corporation while OpenCL can be used on other manufacturers' GPU (e.g., Advanced Micro Devices, Inc.) as well as Nvidia's GPU. However, the CUDA programming environment developed by

NVidia, is more fully featured and exceeds most performance benchmarks compared to other manufacturers' GPU. Particularly, the sparse matrix libraries and basic linear algebra libraries in the CUDA environment are highly optimized. CUDA is freely available and is well supported. NVidia sells both enterprise and enthusiast class GPU. We have found that lower cost enthusiast class GPU actually perform faster than the enterprise class GPU and are a fraction of the cost. Although Bolt supports both types of processors, we recommend its use with low cost consumer class workstations using enthusiast class GPU in the CUDA environment and Linux.

Bolt is designed not only to use GPU but to maximize the parallel execution capability of multiple core CPU, often achieving full so-called embarrassingly parallel execution. Additionally, Bolt is designed to take advantage of systems with multiple-GPU installed. Bolt's design makes it easy for professional analysts to make decisions about applying CPU cores and GPU to a single analysis or splitting the CPU cores and GPU among different problems. The complexity of CPU and GPU control is largely abstracted from the analyst so that the best analytical methods to apply to a problem can be focused on.

The IGS International Genetic Evaluation

Lead by a consortium of beef breed associations, the International Genetic Solutions organization has worked with Theta Solutions, LLC to implement a multi-breed genetic evaluation including data from twelve different beef breed associations from North America.

The first prototype analysis included thirteen traits' representing threshold and continuous observations from 6,987,238 pedigree observations including 45,176 observations on animals with genotypes, and 5,663,965 animals with performance observations. Traits were run in meaningful multiple trait combinations. For example, EPDs for birth weight, weaning weight, milk, and total maternal were solved together. The model included extra polygenic effects for birth additive direct, weaning additive direct and weaning additive maternal effects.

The analysis was performed on a computer built on an ASRock X99 Extreme11 motherboard with an Intel Xeon E5-2643 V3 (6 core at 3.4GhHz) processor. It had 64G of ECC DDR4 memory and four Titan X GPU. No overclocking of the CPU or GPU was performed. Our previous work (Golden, et al., 2015) has shown that substantial benefit from overclocking can be obtained. However, the E5-2643 cannot be overclocked.

The timings given here are for the so-called MSRP (Saatchi and Garrick, 2016) subset of genetic markers. The strategy implemented for the IGS analysis is to use a Bayes C0 analysis for an informative subset of markers identified from a Bayes C analysis (with pi=.95) applied to higher denity (e.g. 70k markers) periodically performed to refresh and validate the subset list. Our as yet unpublished studies have shown that this results in equivalent accuracies of the Bayes C analysis predictions' and are substantially more accurate than Bayes C0 of larger marker sets (e.g., BovSNP50). Another advantage is these analyses using relevant subsets of markers complete relatively quickly, allowing for new analyses to be performed when new genotype data are received. This way, IGS can turn around results to their members and customers as frequently as daily. The wall-clock time to assemble the SHM for this analysis was 50 minutes

and 25 seconds. Once assembled the time to solve the equations to obtain the EPDs using a PCG solver was 9 minutes and 39 seconds.

A Bayes C0 sampling strategy with four parallel chains of ten thousand samples each after being seeded with the PCG solver solutions was used to obtain prediction error variances. The wall clock time to obtain the prediction error variances was 5 hours and 44 minutes.

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EPDs and Risk

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Introduction

About 30 years ago there was concern in both the beef and dairy industries that too much emphasis was being given to accuracy of genetic evaluation. This article will discuss attempts to reduce emphasis on accuracy and, thus increase emphasis on the predictor of genetic value itself which is commonly known as estimated breeding value (EBV). Accuracy is a key component of more useful measures of risk such as standard error of prediction which can be used to create confidence ranges in units of measurement for true breeding value based on the EBV and the standard error of prediction. The concept of standard error of prediction can be extended to comparison of pairs of EBV. The influence of genomic relationships and Bayesian analyses on accuracies and standard errors of prediction will also be briefly introduced.

Accuracy

Reports of genetic evaluations, in addition to EBV (or EPD = EBV/2 or PTA = EBV/2), provide an item named 'accuracy'. Accuracy is an indicator of risk of possible change in the EBV. Accuracy is defined as the correlation between the EBV and true BV of an animal. High accuracy suggests little possible change and low accuracy suggests considerable possible change when later genetic evaluations are based on many, many more records. Accuracy of an EBV is the same as the accuracy of a corresponding EPD. A more useful measure of risk is the standard error of prediction (SEP) which depends on squared accuracy and the genetic standard deviation of the trait. [The square of the genetic standard deviation is the genetic variance of the trait. Genetic variance (symbol is Vg for this discussion) is the part of the total (phenotypic) variance for a trait that is due to effects of genes of animals.] SEP is in units of how a trait is measured (e.g., pounds) and thus is a quantitative measure of possible change. Accuracy is 'unit-less' and can range from 0.0 to 1.0. SEP can range downward from the genetic standard deviation for accuracy of 0.0 to 0.0 for accuracy of 1.0. As would be expected, the standard error of prediction for an EPD is one-half the standard error of prediction for an EBV.

Reliability

High accuracy may receive too much emphasis relative to the EBV of an animal. To reduce emphasis on traditional accuracy other measures of 'accuracy' have been proposed and reported with EBV. The dairy industry uses a method named 'reliability' which was implemented in about 1989 by Paul VanRaden and others at the Animal Improvement Programs Laboratory of the USDA which for many years did the genetic evaluations for all U. S. dairy breeds. Reliability is simply the square of traditional accuracy and represents the fraction of genetic variance accounted for by the EBV. Squared accuracy (reliability) approaches perfection (1.00) more slowly than traditional accuracy. It too is unit-less. (See Table 1.) For example with accuracy of 0.90, reliability is 0.81. Smaller reliability relative to traditional accuracy reduces the temptation to over emphasize 'accuracy' and thus will increase emphasis on the EBV.

BIF-Accuracy

The beef industry chose a different approach. Richard Willham proposed an expression which was implemented by some beef breeds about 1985. It also is unit-less and approaches 1.00 even more slowly than reliability. It has been named 'BIF-accuracy'. It has been somewhat confusing because of the name and the equation used which is based on traditional accuracy squared and the standardized standard error of prediction as well as a square root:

$$\text{BIF-accuracy} = 1.0 - \text{SQRT}[1.0 - \text{acc}^2].$$

As accuracy increases toward 1.0, BIF-accuracy increases at a rate dependent on SQRT[1.0 – acc^2]. The rate of increase toward 1.0 is much less than the rate for accuracy or the rate for reliability. [See Table 1.] The standard error of prediction (SEP) is SQRT[(1.0 – acc^2)(Vg)]. SQRT[1.0 – acc^2] is standardized SEP (that is, it corresponds to genetic variance, Vg = 1.0). Thus BIF-accuracy basically tracks the approach of SEP to zero.

Progeny accuracy

An approach, never proposed or implemented, to reduce emphasis on accuracy would have been to report traditional accuracy for a future progeny of a sire. Accuracy for a future progeny with no records is one-half the accuracy of the EBV of its sire. The reason for the one-half is that the sire is related by one-half to his progeny. Even if proposed it probably would not have been adopted because 'accuracies' less than 0.50 would, no doubt, have created doubt about validity of corresponding EBV or EPD.

Standard error of prediction

The standard error of prediction (SEP) provides a more direct measure of risk (possible change) or chance that true breeding value is so much greater or so much smaller than the EBV than does any of the 'accuracies'. SEP was introduced in discussion of BIF-accuracy as SQRT[(1.0 – acc^2)(Vg)] where Vg is the genetic variance of the trait. Prediction error is the difference between EBV and true BV:

$$\text{PE} = (\text{EBV} - \text{true BV}).$$

Variance of prediction error, V(PE), which is also often referred to as prediction error variance, PEV is:

$$\text{PEV} = \text{V(PE)} = \text{V(EBV} - \text{true BV)} = (1.0 - \text{acc}^2)(\text{Vg}).$$

A numerical value for PEV rather than SEP (the square root of PEV) comes directly from the statistical method used to obtain EBV and fortunately without having to know any true BV. Prediction error variance (PEV) is in units of measurement squared (for example, lb x lb). The square root of PEV is SEP which is in units of measurement (that is, lb) so that SEP as an indicator of risk is on the actual scale of measurement. The SEP decreases as accuracy increases. [See Table 1.] A property of Henderson's mixed model equations used to obtain EBV is that the PEV's are the diagonal terms of the inverse of the coefficient matrix of those equations. That inverse can be used to solve for EBV but, unfortunately, inverses needed for most breed evaluations are impossible to obtain with current and foreseeable computing power. Iterative

methods are used to solve for EBV. In theory the same iterative methods can be used to obtain individual PEV, but in practice are not feasible. [But see **Bayes.**] Time required would be time for solving for EBV multiplied by the number of animals in the pedigree. Usually practical values of accuracy can be approximated. From approximate accuracy, PEV can be computed. With inverse solutions to the genetic evaluation equations, PEV can be determined directly and then used to obtain traditional accuracy.

The standard error of prediction is a direct measure of possible change. Possible change is risk in units of the trait and thus has dollar value. Risk can be 'positive' or 'negative'. That is, the chance true BV may exceed EBV by a certain amount is the same as the chance true BV is less than EBV by the same amount. The up-side risk (possible gain) is the same as down-side risk (possible loss). Monetary values of up-side and down-side risk are not necessarily equivalent.

Confidence ranges

Confidence ranges are often used to determine probabilities of possible change assuming a bell-shaped distribution of true BV around the EBV. One-half of true BV would be expected to be greater than the EBV and one-half would be expected to be less than the EBV. The interval from EBV – (1)SEP to EBV + (1)SEP corresponds to 68% of possible BV for an animal centered on the EBV for the animal. The range can be shrunk or expanded corresponding to the probability of true BV being in the interval. For example, the interval from EBV – (2)SEP to EBV + (2)SEP would be expected to contain 95% of true BV. Units of SEP other than (1) or (2) would correspond to other confidence ranges.

With a 68% confidence range, 32% would be outside the range: 16% above the positive end of the range and 16% below the negative end of the range. With the 95% range, 2.5% would be expected to be greater than the upper end of the CR and 2.5% would be expected to be less than the lower end of the CR. Ranges for many combinations of EBV and SEP will overlap considerably. The more important of EBV or SEP is the EBV which centers the range. Comparison of ranges provides a more direct measure of risk than does accuracy.

Comparison of pairs of EBV

Selection decisions are essentially based on comparison of the EBV of a pair of animals. The ideas of confidence ranges and possible change can be applied to differences in pairs of EBV. The explanation becomes more complicated but the statistical principles are the same. Now there are two prediction errors:

$$PE_1 = EBV_1 - BV_1 \text{ and } PE_2 = EBV_2 - BV_2.$$

To form confidence ranges, variance of $PE_1 - PE_2$ is needed instead of V(PE). In expanded form $V(PE_1 - PE_2) = V(PE_1) + V(PE_2) - (2)COV(PE_1,PE_2)$. What is new is the covariance between the pair of prediction errors. A covariance is a measure of how two things vary together. EBV of a pair of relatives would be expected to be correlated (positive covariance) because some of the same information would be used in both EBV. Except for close relatives in the same management unit, the covariance is likely to be small relative to $V(PE_1)$ and $V(PE_2)$. [That is my expectation until proved to be different for other than close relatives.] Obtaining a prediction error covariance requires the inverse of the coefficient matrix of the genetic evaluation

equations as do the variances of prediction errors. The potential number of prediction error covariance's is much larger than number of prediction error variances: n(n – 1)/2 where n is the number of animals in the pedigree. Approximations of prediction error covariance's are probably more difficult to obtain than approximations of V(PE). If iteration were used to obtain V(PE) for an animal, a by-product would be the PE covariance's between its EBV and the EBV of all other animals in the pedigree.

If the PE covariance can be safely ignored, the standard error of the difference between a pair of EBV can be calculated easily although accuracies for two EBV must be known or approximated. Then $V(PE_1 - PE_2) = V(PE_1) + V(PE_2) = (1.0 - acc_1^2)Vg + (1.0 - acc_2^2)Vg = (2.0 - acc_1^2 - acc_2^2)Vg$. The square root of $V(PE_1 - PE_2)$ is the standard error of the predicted difference (SEPD) between EBV. [SEPD is not the standard error of an EPD.] Computation of SEPD would not be needed for most pairs of animals. The animals of most interest are potential herd sires. For pairs of interest, SEPD can be obtained using a simple table which would apply to all traits. The table values would be multiplied by the genetic standard deviation for a specific trait. The number of rows and columns of the table would correspond to ascending or descending levels of accuracy; for example, from 0.05 to 0.95 by increments of 0.05. [See Table 2.] Entries in the table would be $SQRT[(2.0 - acc_i^2 - acc_j^2)]$ for the intersection of the i^{th} row and j^{th} column. [Table values corresponding to accuracies between, for example, 0.75 and 0.85 could be obtained by interpolation although interpolation may be of little practical importance.] As an example of the use of the table if accuracy for bull 1 was 0.55 and accuracy for bull 2 was 0.95, the table entry is 1.05 [$SQRT(2.0 - 0.55^2 - 0.95^2) = 1.05$]. The second step in obtaining SEPD is to multiply the 1.05 by the genetic standard deviation of the trait, SQRT[Vg].

If SQRT[625] = 25 is the genetic standard deviation for the trait, $SEPD(EBV_1 - EBV_2) = 1.05 \times 25 = 26.25$. Confidence ranges and possible changes will now correspond to $BV_1 - BV_2$ given $EBV_1 - EBV_2$. The confidence ranges will be centered at $EBV_1 - EBV_2$. Interpretation will be as for SEP, but for $BV_1 - BV_2$ rather than for $BV_1 - 0.0$ or $BV_2 - 0.0$. Still to be determined is whether $COV(PE_i, PE_j)$ can be safely ignored. A relatively small covariance would not change SEPD of much importance. Such covariance's, will be positive and thus would make SEPD calculated not including the covariance smaller than it should be, but how much smaller would be important needs to be investigated. A large covariance (correlation) between PE of EBV of a sire and PE of EBV of his son would be expected especially if one had no progeny with records. A sire and his son would seem unlikely to be compared. Paternal half sibs would be more likely to be candidates for selection. If they had no records or progeny with records their EBV would be equal as would SEP so that SEPD would not be important.

Some of the following speculation, if confirmed, would make some of the preceding discussion irrelevant.

G-BLUP

With G-BLUP (using the genomic relationship matrix, G, rather than the identity by descent relationship matrix, A), all genotyped sires will have the same or nearly the same accuracy and the same SEP and SEPD because the same information is available for all sires (same SNPs). Exceptions are for genotyped sires having many progeny with records. Confidence ranges would differ only by the center value, EBV or $EBV_1 - EBV_2$. Different 'chips' might yield different accuracy. It would seem that covariance's between PE are more likely to be non-

zero with G-BLUP than A-BLUP. Would covariance's be the same for all pairs of genotyped animals? If so, iteration for only one column of the inverse of the coefficient matrix would be needed to obtain prediction error variances and covariance's between all pairs of prediction errors.

Bayes

Bayesian methods may make 'direct' calculation of SEP more feasible. Bayesian 'solutions' are obtained by iteration similar to iteration to obtain traditional solutions. The usual method, Gibb's sampling, produces MCMC chains of 'solutions' for an individual which correspond to a distribution around the true BV. The final 'solution' is usually taken to be the average or median of the chain of solutions after 'burn-in' and thinning. Chains could be obtained holding VC constant, that is, Gauss-Seidel iteration but with sampling for solutions but not variance components. The chains for an individual can be used to calculate something comparable to variance of prediction error from which something comparable to accuracy could be calculated as before. The covariance between pairs of predictors could also be obtained from pairs of chains which would incorporate the covariance between pairs of prediction errors.

Summary

Traditionally accuracy has been defined as the correlation between EBV and true BV and has been used as an indicator of risk of possible change.

Reliability (squared accuracy, acc^2) and BIF accuracy ($1 - SQRT[1 - acc^2]$) both go towards a maximum of 1.0 more slowly with more information than accuracy and were developed to reduce emphasis on 'high' accuracy vs. EBV.

The standard error of prediction is a more quantitative measure of risk than accuracy. It goes toward 0.00 as accuracy increases: $SEP = SQRT[(1.0 - acc^2)(Vg)]$ where Vg is genetic variance of the trait. The SEP can be used to obtain ranges such as EBV – 2(SEP) to EBV + 2(SEP) which would include true BV with confidence of 95%. Of the other 5%, 2.5% would be above the upper end of the range and 2.5% below the lower end of the range.

The concept of SEP can be extended to differences in pairs of EBV. SEPD would be the standard error of the difference between a pair of EBV. Confidence ranges would be centered on $EBV_1 - EBV_2$. If the covariance between pairs of prediction errors, $Covariance(PE_1, PE_2)$, is small relative to $V(PE_1)$ and V(PE2), SEPD can be approximated well by $SQRT[(2.0 - acc_1^2 - acc_2^2)Vg]$. A table of SEPD corresponding to pairs of accuracies can then be used to obtain SEPD for any trait and pair of EBV.

Using the genomic relationship matrix (G-BLUP) rather than the identity by descent relationship matrix is likely to result in nearly equal accuracy for many genotyped animals. Then SEP and SEPD would also be equal. Confidence ranges would also be equal but with different centers depending on EBV.

Variances and covariance's of MC-MC chains from Gibb's sampling could be used to obtain equivalents of variances and covariance's of prediction errors and from those equivalents

accuracies can be obtained without the inverse of the coefficient matrix and without approximations of accuracy.

Table 1. Comparison of accuracy, reliability, BIF-accuracy and standard error of prediction (genetic standard deviation of 25).

Accuracy	Reliability	BIF-accuracy	SEP
0.10	0.01	0.005	24.75
0.20	0.04	0.020	24.00
0.30	0.09	0.046	22.75
0.40	0.16	0.083	21.00
0.50	0.25	0.134	18.75
0.60	0.36	0.200	16.00
0.70	0.49	0.286	12.75
0.80	0.64	0.400	9.00
0.90	0.81	0.564	4.75
1.00	1.00	1.000	0.00

Table 2. Table values corresponding to accuracies for two EBV or two EPD which when multiplied by the genetic standard deviation of the trait result in the standard error of prediction of difference between the two EBV or two EPD.

	Accuracy for first EBV								
Acc-2	0.05	0.25	0.35	0.45	0.55	0.65	0.75	0.85	0.95
0.05	1.41	1.41	1.41	1.49	1.38	1.35	1.30	1.22	1.09
0.25	1.41	1.41	1.41	1.40	1.38	1.35	1.30	1.21	1.09
0.35	1.41	1.41	1.40	1.39	1.38	1.34	1.29	1.21	1.08
0.45	1.40	1.40	1.39	1.38	1.37	1.33	1.28	1.20	1.07
0.55	1.38	1.38	1.38	1.37	1.35	1.32	1.26	1.18	1.05
0.65	1.35	1.35	1.34	1.33	1.32	1.28	1.23	1.14	1.00
0.75	1.30	1.30	1.29	1.28	1.26	1.23	1.17	1.08	0.93
0.85	1.22	1.21	1.21	1.20	1.18	1.14	1.08	0.98	0.81
0.95	1.09	1.09	1.08	1.07	1.05	1.00	0.93	0.81	0.61

Selection Enhanced Estimates of Marker Effects on Means and Variances of Beef Tenderness[1]

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Introduction

Historic surveys of retail beef have identified beef tenderness as a critical issue to consumer acceptability of beef and suggested continued investigation of pre-harvest and post-harvest interventions to improve beef tenderness (Morgan et al., 1991). Koohmaraie (1996) identified the protease μ-calpain (***CAPN1***) and its inhibitor calpastatin (***CAST***) as major factors affecting post-mortem tenderization in meat. Genetic markers in *CAPN1* (Page et al., 2002; White et al., 2005) and *CAST* (Casas et al., 2006; Morris et al., 2006) are commercially available to beef producers. However, early studies evaluating these markers had low frequency of rare homozygote animals and occasionally ignored those animals from analysis (White et al., 2005; Morris et al., 2006) – removing the opportunity to evaluate mode of inheritance (additive or dominance) for a genetic marker. Therefore, selection was used in 2 populations (Angus and MARC III – ¼ Angus, ¼ Hereford, ¼ Red Poll, and ¼ Pinzgauer composite) to equalize the allele frequency of *CAPN1* haplotypes and *CAST* genotypes to enhance estimates for slice shear force (**SSF**) of: 1) effect size, 2) mode of inheritance, and 3) interaction between *CAPN1* and *CAST* (Tait et al., 2014a; Tait et al., 2014b). Furthermore, these studies evaluated the potential for genotype specific residual variances and found these models to fit significantly better than single residual variance models for *CAST* genotypes.

Genetic Markers

The *CAPN1* haplotypes evaluated in this study were based on two previously identified SNP: CAPN1_316 (BTA 29; rs17872000) (Page et al., 2002) and CAPN1_4751 (BTA 29; rs17872050) (White et al., 2005). The CAPN1_316 marker segregates C and G alleles, whereas CAPN1_4751 segregates C and T alleles. The CAPN1_316 and CAPN1_4751 SNPs were used to define haplotypes within the *CAPN1* gene. Haplotypes of interest in these studies were: CAPN1_316 allele C with CAPN1_4751 allele C (**CAPN1-CC**), CAPN1_316 allele G with

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CAPN1_4751 allele C (**CAPN1-GC**), and CAPN1_316 allele G with CAPN1_4751 allele T (**CAPN1-GT**). Additionally, a SNP in *CAST* (BTA7; rs109221039) (Casas et al., 2006) segregating C (**CAST-C**) and T (**CAST-T**) alleles was selected to increase the frequency of CAST-C in these populations.

Populations, Selection, and Tenderness Phenotype

Angus and MARC III composite populations from a previous calving ease selection experiment (Bennett, 2008) were chosen for selection of *CAPN1* and *CAST* markers based on initial marker allele frequencies. The Angus population was selected for the 2 *CAPN1* haplotypes expected to be most divergent for tenderness (White et al., 2005) (CAPN1-CC and CAPN1-GT) and MARC III was selected to equalize the 3 most prominent *CAPN1* haplotypes (CAPN1-CC, CAPN1-GC, and CAPN1-GT). Both populations were selected to increase the CAST-C allele. Selection occurred for 3 years (Angus) or 4 years (MARC III), and then 3 years of progeny were evaluated (Figure 1). Haplotype and allele frequencies during the evaluation phase for Angus were: CAPN1-CC = 0.530, CAPN1-GT = 0.363, and CAST-C = 0.348. Haplotype and allele frequencies during the evaluation phase for MARC III were: CAPN1-CC = 0.267, CAPN1-GC = 0.326, CAPN1-GT = 0.385, and CAST-C = 0.397.

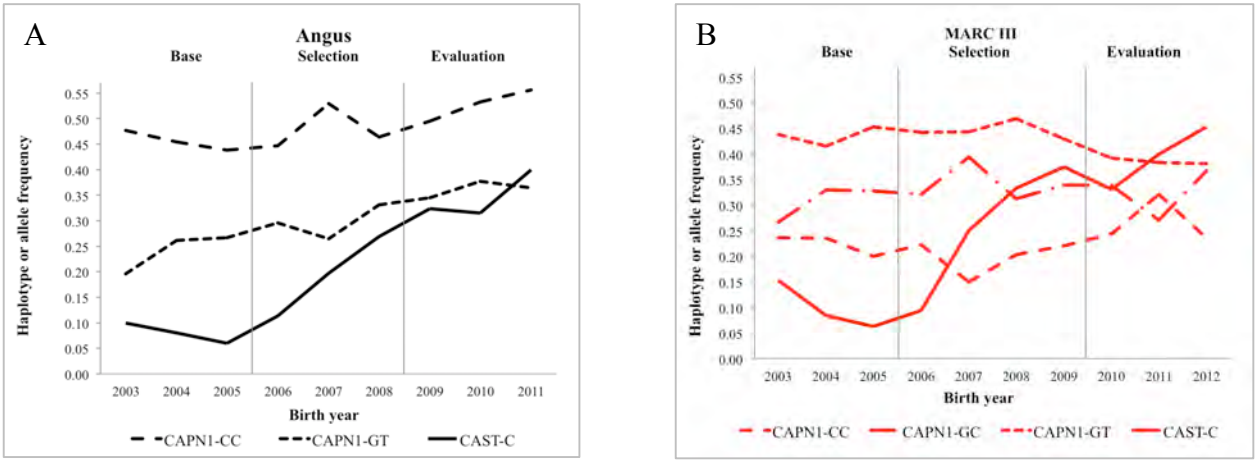

Figure 1. Haplotype or allele frequency by birth year in Angus (A) and MARC III composite (B) populations selected to equalize *CAPN1* and *CAST* genetic markers using marker assisted selection. Adapted from: A – Tait et al. (2014a) and B – Tait et al. (2014b)

Only steers were evaluated for carcass traits (Angus n = 199; MARC III n = 254). All steers within a population were harvested on a single day within each year at a commercial abattoir (Angus average age = 433 d; MARC III average age = 452 d). Carcasses were weighed hot, electrically-stimulated, and chilled using the facility's proprietary system. At 36 h postmortem, carcasses were ribbed between 12th and 13th ribs and camera-measured carcass data were collected. A LM steak from the 13th rib region was returned to the U.S. Meat Animal Research Center to evaluate SSF at 14 d postmortem (Shackelford et al., 1999).

Statistical Analysis

Haplotypes and genotyping errors were identified with GenoProb software (Thallman, 2008). GenoProb genotypes were used for the analysis. A single trait animal model utilized MTDFREML software (Boldman et al., 1995) to estimate the heritability and genetic marker effects within each population independently. Fixed effects modeled were: year of birth (3 yr for each population), age of dam (2, 3, 4, or ≥ 5 yr), covariate age (days) of steer, *CAPN1* diplotype (Angus = 3 classes; MARC III = 6 classes), and *CAST* genotype (3 classes).

Genotype specific residual variance models. Genotype specific residual variance models were analyzed using SAS version 9.3 (SAS Inst., Cary, NC) software, providing the additive genetic variance matrix from the MTDFREML heritability analysis and defining heterogeneous residual variances based on *CAPN1* or *CAST* genotypes in the MIXED procedure. A likelihood ratio test was performed to test whether the genotype specific residual variance model fit better than the single residual variance model.

Results and Discussion

Estimates of *CAST* genetic effects on SSF were significant in both Angus ($P < 0.001$) and MARC III ($P < 0.01$) steers (Table 1). Furthermore, the additive mode of inheritance for *CAST* genetic effect was significant in both Angus ($P < 0.001$) and MARC III ($P = 0.05$) steers, whereas the dominance mode of inheritance was not significant in Angus ($P = 0.43$) nor MARC III ($P < 0.22$) steers (Table 1). The *CAST* genotype additive effects were similar in direction and scale between Angus (-1.257 ± 0.261 kg / CAST-T allele) and MARC III (-0.902 ± 0.464 kg / CAST-T allele) steers (Table 2).

Estimates of *CAPN1* genetic effects on SSF were significant in Angus ($P < 0.001$) but not significant in MARC III ($P = 0.12$) steers (Table 1). The lack of significance in MARC III steers is likely a function of more *CAPN1* diplotypes being evaluated. The CAPN1-GT haplotype effect contrasted to CAPN1-CC haplotype was larger in MARC III steers (1.153 ± 0.483 kg) than in Angus steers (1.049 ± 0.246 kg), but was also less precisely estimated in MARC III steers (Table 2). Furthermore, in MARC III steers, CAPN1-GC was not significantly different ($P = 0.45$) from the average of the CAPN1-GT and CAPN1-CC effects on SSF (Tait et al., 2014b). Therefore CAPN1-GC can be assumed to have ½ the additive effect of CAPN1-GT when contrasted to CAPN1-CC. In both Angus and MARC III populations, no interaction was found between *CAPN1* and *CAST* genotypes ($P \geq 0.40$; Table 1).

Table 1. Significance of *CAPN1* and *CAST* genetic effects, modes of inheritance, and fit of genotype specific residual variance models for 14-day slice shear force in Angus and MARC III cattle populations; Adapted from Tait et al. (2014a) and Tait et al. (2014b)

Type of effect	Angus	MARC III
CAPN1, *P*-Value	< 0.001	0.12
CAST, *P*-Value	< 0.001	< 0.01
CAPN1 × *CAST* interaction, *P*-Value	0.55	0.40
CAPN1 Additive effect, *P*-Value	< 0.001	NA[1]
CAPN1 Dominance effect, *P*-Value	0.19	NA[1]
CAST Additive effect, *P*-Value	< 0.001	0.05
CAST Dominance effect, *P*-Value	0.43	0.22
CAPN1 Genotype specific residual variance model, *P*-Value	0.05	0.03
CAST Genotype specific residual variance model, *P*-Value	2.5×10^{-4}	5.0×10^{-4}

[1]NA = Not available because 3 *CAPN1* haplotypes were selected and evaluated in MARC III population.

Table 2. Estimated genotypic effects (± SE) and variance components for 14-day slice shear force under single residual variance or *CAST* genotype specific residual variance models in Angus and MARC III cattle populations; Adapted from Tait et al. (2014a) and Tait et al. (2014b)

Type of residual variance model	Angus	MARC III
Single		
CAPN1-GT – CAPN1-CC effect, kg	1.049 ± 0.246	1.153 ± 0.483
CAST-T additive effect, kg	-1.257 ± 0.261	-0.902 ± 0.464
σ_g, kg	1.23	1.88
σ_e, kg	1.79	3.58
h^2	0.32	0.22
***CAST* genotype specific**		
CAPN1-GT – CAPN1-CC effect, kg	1.080 ± 0.224	1.081 ± 0.465
CAPN1-GC – ((CAPN1-CC + CAPN1-GT)/2) effect, kg	NA[1]	0.312 ± 0.417
CAST-T additive effect, kg	-1.240 ± 0.341	-0.940 ± 0.553
σ_g, kg	1.23	1.88
$\sigma_{e\text{-}CC}$, kg	2.82	4.86
$\sigma_{e\text{-}CT}$, kg	1.99	3.98
$\sigma_{e\text{-}TT}$, kg	1.22	2.54
h^2_{CC}	0.16	0.13
h^2_{CT}	0.27	0.18
h^2_{TT}	0.50	0.35

NA[1] = Not available because CAPN1-GC haplotype was not evaluated within Angus population

Genotype specific residual variance models were more strongly supported for the *CAST* genotype specific residual variance models than the *CAPN1* genotype specific residual variance models in both Angus ($P = 2.5 \times 10^{-4}$ vs. $P = 0.05$, respectively) and MARC III ($P = 5.0 \times 10^{-4}$ vs. $P = 0.03$, respectively) populations (Table 1). In both populations, the most tender *CAST* genotype (CAST-T homozygote) also had the smallest genotype specific residual variance (Table 2). Furthermore, there was a progressive trend amongst *CAST* genotype specific residual variances where the more tough the expected mean, the larger the genotype specific residual variance (and hence phenotypic variance) (Figure 2). In comparison, *CAPN1* genotype specific residual variance models were not as strongly supported in Angus ($P = 0.05$) and MARC III ($P = 0.03$) populations (Table 1) and the genotype with the smallest genotype specific residual variance was a different heterozygous genotype in each population (Tait et al., 2014a; Tait et al., 2014b).

The economic value in the multi-trait selection objective for *CAPN1* and *CAST* genetic markers should be driven by the risk of an animal with a particular genotype producing beef that is "tough" (above some SSF threshold). Single residual variance models will have a different proportion of animals above some tough designation threshold than *CAST* genotype specific residual variance models and this could have important ramifications for selection emphasis on *CAST* markers depending on which distribution is assumed for the *CAST* genotypes.

The observation of *CAST* genotype specific residual variance models fitting significantly better than single residual variance models in replicated populations provides novel, powerful information about the *CAST* genetic effects on beef tenderness. Additionally, the progressive nature of these residual variances where the most tender genotype has the smallest residual variance and the toughest genotype has the largest residual variance provides a unique opportunity for application or utilization of this marker. This knowledge may someday be extended to national cattle evaluation programs by modeling tenderness to have a different heritability based on genotype at a single genetic marker.

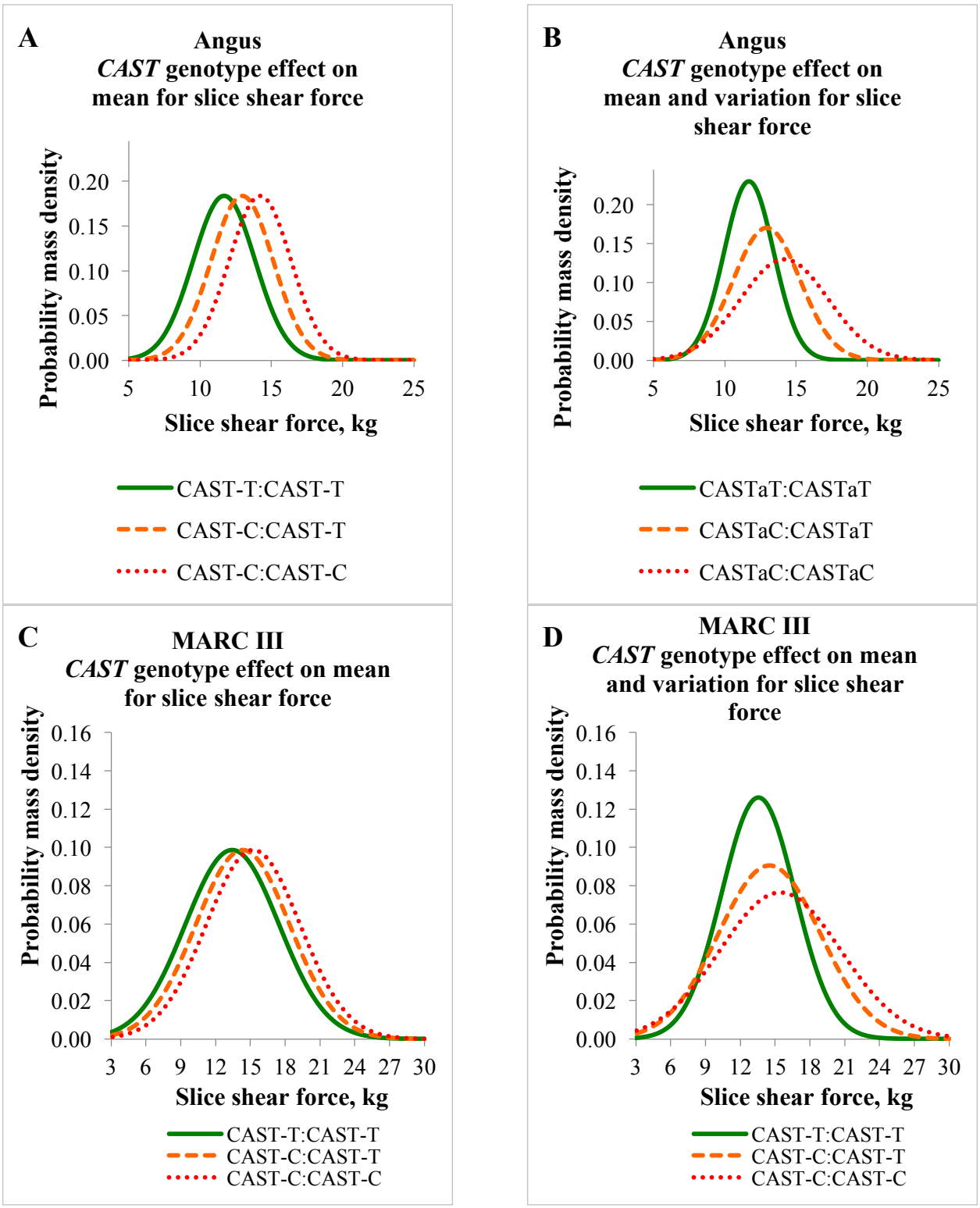

Figure 2. Additive effects of *CAST* genotype on LM slice shear force in Angus (A & B) and MARC III (C & D) populations under single residual variance model (A & C) or *CAST* genotype specific residual variance model (B & D). Adapted from: A & B – Tait et al. (2014a) and C & D – Tait et al. (2014b)

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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, 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 26 breeds are presented in this report. Mean EPDs for growth traits are shown in Table 1 (26 breeds), for other production traits in Table 2 (20 breeds), and for carcass and composition traits in Table 3 (21 breeds). Several breeds also have EPDs and indices 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 and Thallman in these proceedings).

This list is likely incomplete; evaluations for some breeds are not widely reported. We are aware of recent EPD evaluations for the Blonde d'Aquitaine, North American Piedmontese, American Pinzgauer, and American Waygu breeds but their EPDs do not appear to have been updated in the last year. 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 2014 average EPDs from 2016 evaluations for growth traits

Breed	Birth Weight (lb)	Weaning Weight (lb)	Yearling Weight (lb)	Maternal Milk (lb)	Total Maternal (lb)
Angus	1.3	51	91	23	
Black Hereford	2.8	45.6	78.4	21.9	44.6
Hereford	3.3	48.2	78.2	20.3	44.4
Murray Grey	3.8	24	37	4	16
Red Angus	-1.3	57	88	20	
Red Poll	1.7	15	24	6	
Shorthorn	2.4	55	66	18	46
South Devon	2.3	43.6	81.7	25.1	46.9
Beefmaster	0.6	23	45	9	21
Braford	1.1	12	18	3	9
Brahman	1.8	16	25.6	5.6	
Brangus	1.2	24.4	46.5	9.5	21.7
Red Brangus	1.7	12.1	19.4	5.5	11.6
Santa Gertrudis	0.2	3.8	5.2	0.5	
Senepol	1.1	12	14.9	4.4	9.8
Simbrah	3.7	60.0	81.3	21.9	51.8
American Akaushi	-0.1	24.0	44.4	26.3	38.3
Braunvieh	2.7	44.4	68.0	34.6	56.8
Charolais	0.5	26.7	48.7	8.7	22
Chianina	2.3	43.3	63.1	15.3	37.0
Gelbvieh	0.5	65.6	96.8	26.8	59.7
Limousin	1.3	62.7	92.3	26.8	58.2
Maine-Anjou	1.6	47.2	62.6	19.1	42.8
Salers	1.8	41.0	78.3	19.9	40.4
Simmental	1.9	63.4	92.5	21.6	53.3
Tarentaise	1.3	17.5	30.8	0.7	9.4

Table 2. Birth year 2014 average EPDs from 2016 evaluations for other production traits

Breed	Calving Ease Direct (%)	Calving Ease Maternal (%)	Scrotal Circ. (cm)	Docil. Score	Mature Weight (lb)	Heifer Pregnancy (%)	Stayability (%)
Angus	5	8	0.84	14	31	10.6	
Hereford	1.1	1.3	0.8		87		
Murray Grey	-0.6	-0.1	0.2		55		
Red Angus	5	4				10	11
Shorthorn	5.0	1.0					
South Devon			0.1				
Beefmaster			0.4				
Brahman				0.0			
Brangus	3.8	4.1	0.45				
Simbrah	2.5	6.0		8.7			
American Akaushi	3.2	5.5					
Braunvieh	5.8	0.7	0.02				
Charolais	3.3	3.9	0.75				
Chianina	5.1	-3.2					
Gelbvieh	10.2	6.4				3.7	6.2
Limousin	7.9	6.2	0.66	19.6			16.7
Maine Anjou	7.6	2.4					
Salers	0.2	0.3	0.3	8.7			23.6
Simmental	8.9	9.4		10.7			20.5
Tarentaise	-0.1	0.7					

Table 3. Birth year 2014 average EPDs from 2016 evaluations for carcass and composition traits

Breed	Carcass Wt (lb)	Retail Product (%)	Yield Grade	Carcass			Rump fat (in)	WBSF (lb)
				Marbling Score	Ribeye Area (in^2)	Fat Thickness (in)		
Angus	33.0			0.59	0.53	0.017		
Hereford	61			0.09	0.31	0.003		
Murray Grey	32	0.4		0.0[a]	0.11[a]	0.00[a]	0.00[a]	
Red Angus	20		-0.01	0.45	0.13	-0.007		
Shorthorn	12.0			0.05	-0.05	-0.03		
South Devon	28.3	0.8		0.4	0.23	0.01		
Beefmaster				-0.10[a]	-0.16[a]	-0.01[a]		
Braford	7			0.01	0.06	0.012		
Brahman	1.4	-0.01		0.00	0.01	0.00		0.02
Brangus				0.02[a]	0.34[a]	-0.041[a]		
Santa Gertrudis	3.3			-0.01	0.04	0.002		
Simbrah	23.5		-0.23	-0.07	0.45	-0.060		-0.05
American Akaushi				0.75[a]	0.11[a]	0.057[a]		
Braunvieh				0.56	0.35	-0.090		
Charolais	16.8			0.04	0.32	0.005		
Chianina	10.9	0.53		0.10	0.32	-0.06		
Gelbvieh	27.6		-0.18	0.09	0.45			
Limousin	26.3		-0.19	-0.01	0.48	-0.040		
Maine-Anjou	9.0	0.37		0.05	0.21	-0.041		
Salers	20.5	0		0.2	0.02	0.00		
Simmental	27.6		-0.33	0.14	0.79	-0.056		-0.33

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

Table 4. Birth year 2014 average EPDs from 2016 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 ($)
	0.21	0.4	0.5	-8.36	43.73	42.62	31.51	106.09

Hereford	Baldy Maternal Index ($)	Brahman Influence Index ($)	Certified Hereford Beef Index ($)	Calving Ease Index ($)	Udder Score	Teat Score
	17.9	15.7	23.1	15.3	0.98	1.04

Red Angus	Mature Cow Maintenance (Mcal/mo)
	0

Gelbvieh	30-Month Pregnancy	DMI (lb/d)	ADG (lb/d)	RFI (lb/d)	$ Cow ($)	Efficiency Profit Index ($)	Feeder Profit Index ($)
	1.1	0.016	0.005	-0.010	61.11	101.81	69.51

Limousin	Mainstream Terminal Index ($)	Gestation Length (d)
	50.04	-2.1

Simmental	All Purpose Index ($)	Terminal Index ($)	Simbrah	All Purpose Index ($)	Terminal Index ($)
	121	67.7		71.3	50.5

Shorthorn	$ Calving Ease	$ Feedlot	$ British Maternal Index
	17.9	52.68	111

Murray Grey	600-d wt (lb)	Gestational Length (d)	Days to Calving (d)
	53	-0.2	-0.9

ACROSS-BREED EPD TABLES FOR THE YEAR 2016 ADJUSTED TO BREED DIFFERENCES FOR BIRTH YEAR OF 2014

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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 1-8 for birth weight, weaning weight, yearling weight, maternal milk, marbling score, ribeye area, fat thickness, and carcass weight, 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 2016 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 change over time as breeds put selection 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 1-8 contains estimates of the differences between the averages of calves from sires of each breed born in year 2014. 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 (born in 2014) of two different breeds 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 2016 update of estimates of sire breed means from data of the Germplasm Evaluation (GPE) project at USMARC adjusted to a year 2014 basis using EPD from the most recent national cattle evaluations. The 2014 basis year is chosen because yearling records for weight and carcass traits should have been accounted for in EPDs for progeny born in 2014 in the Spring 2016 EPD national genetic evaluations. Factors to adjust Spring 2016 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 5-8 summarize the factors for marbling score (MAR), ribeye area (REA), fat thickness (FAT), and carcass weight (CWT).

The across-breed table adjustments apply **only** to EPD for most recent (spring, 2016)

national cattle evaluations. Serious errors can occur if the table adjustments are used with earlier or later 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 2015 (Kuehn and Thallman, 2015):

New samplings of sires in the USMARC GPE program continued to increase progeny records for all of the breeds. The GPE program has entered a new phase in which more progeny are produced from breeds with higher numbers of registrations. Breeds with large increases in progeny numbers as a percentage of total progeny included South Devon and Tarentaise (especially for yearling weight, carcass traits, and maternal milk) and Santa Gertrudis and Chiangus (especially for maternal milk). However, all of the breeds continue to produce progeny in the project and sires continue to be sampled on a continuous basis for each of the 18 breeds in the across-breed EPD program. These additional progeny improve the accuracy of breed differences estimated at USMARC (column 3 in Tables 1-8) particularly for breeds with less data in previous GPE cycles (e.g., South Devon, Tarentaise, Santa Gertrudis, Chiangus).

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), Kuehn et al. (2007-2011), and Kuehn and Thallman (2012-2015). 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 and different selection histories, 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 by any treatment combination where applicable, 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, FAT, and CWT), breed (fit as genetic groups), sex (heifer, steer) and slaughter date by any treatment combination where applicable 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 (vs. ultrasound) 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 1-8. 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. In addition, the regression coefficients by sire breed may reflect differences in

genetic trends for different breeds. 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, FAT, and CWT, 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):

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

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 2016 EPD for breed i for animals born in the base year (YY, which is two years before the update; e.g., YY = 2014 for the 2016 update),

$\text{EPD(i)}_{\text{USMARC}}$ is the weighted (by total relationship of descendants with records at USMARC) average of 2016 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 2016: 1.17, 0.81, 0.96, and 1.08 BWT, WWT, YWT, and MILK, respectively;

1.00 was applied to MAR, REA, FAT, and CWT 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 1.73 lb, 14.91 lb, 24.39 lb, -0.05 marbling score units (i.e. 4.00 = Sl^{00}, 5.00 = Sm^{00}), 0.26 in^2, 0.035 in, and 31.25 lb in for BWT, WWT, YWT, MAR, REA, FAT, and CWT 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 8.64 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 2014 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, 7, and 8 summarize data from the carcass traits (MAR, REA, FAT, and CWT). 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 2014 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 2014) 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 2011 through 2015 at USMARC (Column 4) to make these differences more interpretable to producers on scales they are accustomed to.

Figures 1-4 illustrate the relative genetic trends of most of the breeds involved (if they submitted trends) adjusted to a constant base using the adjustment factors in column 6 of Tables 1-8. These figures demonstrate the effect of selection over time on breed differences; breeders within each breed apply variable levels of selection toward each trait resulting in reranking of breeds for each trait over time. These figures and Column 5 of Tables 1-8 can be used to identify breeds with potential for complementarity in mating programs.

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 yearling weight for a Gelbvieh bull is +98.0 (which is above the birth year 2014 average of 96.8 for Gelbvieh) and for a Simmental bull is +89.0 (which is below the birth year 2014 average of 92.5 for Simmental). The across-breed adjustment factors in the last column of Table 3 are -29.3 for Gelbvieh and -12.1 for Simmental. Then the adjusted EPD for the Gelbvieh bull is 98.0 + (-29.3) = 68.7 and for the Simmental bull is 89.0 + (-12.1) = 76.9. The expected yearling weight difference when both are mated to another breed of cow, e.g., Hereford, would be 68.7 – 76.9 = -8.2 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 deviated.

Birth Weight

The range in estimated breed of sire differences relative to Angus for BWT (Table 1, column 5) ranged from -0.1 lb for Red Angus to 7.2 lb for Charolais and 10.8 lb for Brahman. Red Angus had 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 small and less than 1.0 lb for all breeds relative to last year's update (Kuehn and Thallman, 2015).

Weaning Weight

All of the 17 breed differences (Table 2, column 5) were within 6 lb of the values reported by Kuehn and Thallman. (2015). Otherwise, changes in breed effects for all 18 breeds seem to be stabilizing since continuous sampling started in 2007, with most minor year-to-year changes coming from selection progress in Angus (increases in the mean EPD each year).

Yearling Weight

Breed of sire effects for yearling weight were also similar to Kuehn and Thallman (2015) in general. Angus continued to have the greatest rate of genetic change for yearling weight (+3 lb since last year), causing most breed of sire differences relative to Angus to decrease at least slightly.

Maternal Milk

Changes to the maternal milk breed of sire differences (Table 4, column 5) were generally small. All changes were less than 4 lb difference from those reported in 2015. However, the breed solution estimates (Table 4, column 3) are expected to change the most in future updates as GPE heifers from each of the 18 breeds being continuously sampled are

developed and bred. Females from newly sampled South Devon or Tarentaise sires have continued to add progeny in this update; difference from Angus changed very little in these breeds. We would expect their solutions to change the most in future reports.

Marbling, Ribeye Area, Fat Thickness and Carcass Weight

Most changes to breed of sire differences were minor for each of these carcass traits. Salers had a decreased breed average in 2015, likely due to a processing error—this error seems to have been corrected this year. The breed mean for marbling in Limousin seemed to increase (+0.06) relative to the average of the bulls in GPE (-0.9) resulting in a change in their breed difference since 2015. Generally changes for other carcass traits were minor.

Accuracies and Variance Components

Table 9 summarizes the average Beef Improvement Federation (BIF) accuracy for bulls with progeny at USMARC weighted appropriately by average relationship to animals with phenotypic records. 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 10 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 0.55, 0.17, 0.43, and 0.15, respectively. Heritability estimates for MAR, REA, FAT, and CWT were 0.53, 0.47, 0.42, and 0.52 respectively.

Regression Coefficients

Table 11 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 1.17 for BWT, 0.81 for WWT, and 0.96 for YWT were used to adjust breed of sire solutions to the base year of 2014. 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 at USMARC, especially steers and market heifers, 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 11. 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 1.08 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, FAT, and CWT are shown in Table 12. 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 higher, though they have decreased from the previous year. The MAR regressions were the most variable, possibly because the primary source of marbling variation in many of the breeds is ultrasound-estimated intramuscular fat which generally exhibits a lower level of variation. While REA, FAT, and CWT are both close to the theoretical estimate of 1.00, we continued to use the theoretical estimate of 1.00 to derive breed of sire differences and EPD adjustment factors. Pooled regression estimates for these three traits may be used in future updates.

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 were last reported in Kuehn et al. (2007; available online at http://www.beefimprovement.org/content/uploads/2013/07/BIF-Proceedings5.pdf). 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.

Table 1. Breed of sire solutions from USMARC, mean breed and USMARC EPD used to adjust for genetic trend to the year 2014 base and factors to adjust within breed EPD to an Angus equivalent – BIRTH WEIGHT (lb)

	Number		Ave. Base EPD		Breed Soln	BY 2014	BY 2014	Factor to
			Breed	USMARC	at USMARC	Sire Breed	Sire Breed	adjust EPD
	AI	Direct	2014	Bulls	(vs Ang)	Average	Difference[a]	To Angus
Breed	Sires	Progeny	(1)	(2)	(3)	(4)	(5)	(6)
Angus	196	2278	1.3	1.6	0.0	86.3	0.0	0.0
Hereford	183	2565	3.3	2.4	3.6	90.6	4.3	2.3
Red Angus	69	815	-1.3	-1.6	-0.8	86.2	-0.1	2.5
Shorthorn	59	603	2.4	2.7	6.8	92.1	5.8	4.7
South Devon	29	240	2.3	2.0	4.3	90.6	4.3	3.3
Beefmaster	58	565	0.6	1.3	5.1	90.3	4.0	4.7
Brahman	60	716	1.8	0.7	11.1	97.1	10.8	10.3
Brangus	59	564	1.2	0.9	3.2	89.6	3.2	3.3
Santa Gertrudis	29	334	0.2	0.6	5.5	90.9	4.6	5.7
Braunvieh	36	492	2.7	4.2	5.4	89.7	3.3	1.9
Charolais	124	1277	0.5	0.2	7.8	93.5	7.2	8.0
Chiangus	30	357	2.3	2.1	4.3	90.5	4.2	3.2
Gelbvieh	90	1159	0.5	2.1	3.9	88.3	2.0	2.8
Limousin	86	1242	1.3	1.5	2.6	88.6	2.3	2.3
Maine Anjou	51	583	1.6	2.2	5.7	90.9	4.5	4.2
Salers	58	517	1.8	2.4	3.1	88.6	2.3	1.8
Simmental	110	1320	1.9	3.1	5.5	90.1	3.8	3.2
Tarentaise	17	291	1.3	2.1	4.6	89.7	3.4	3.4

Calculations:
(4) = (3) / b + [(1) – (2)] + (Recent Raw Angus Mean: 86.6 lb) with b = 1.17
(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 2014 base and factors to adjust within breed EPD to an Angus equivalent – WEANING WEIGHT (lb)

	Number		Ave. Base EPD		Breed Soln	BY 2014	BY 2014	Factor to
			Breed	USMARC	at USMARC	Sire Breed	Sire Breed	adjust EPD
	AI	Direct	2014	Bulls	(vs Ang)	Average	Difference[a]	To Angus
Breed	Sires	Progeny	(1)	(2)	(3)	(4)	(5)	(6)
Angus	196	2106	51.0	28.2	0.0	570.7	0.0	0.0
Hereford	181	2373	48.2	29.6	-5.2	560.1	-10.6	-7.8
Red Angus	69	781	57.0	52.5	-5.7	545.4	-25.4	-31.4
Shorthorn	59	569	55.0	56.5	-6.8	538.1	-32.6	-36.6
South Devon	29	219	43.6	28.4	-9.1	552.0	-18.8	-11.4
Beefmaster	58	532	23.0	23.9	11.0	560.6	-10.1	17.9
Brahman	58	621	16.0	7.5	19.8	580.8	10.1	45.1
Brangus	59	534	24.4	21.3	4.1	556.1	-14.6	12.0
Santa Gertrudis	29	315	3.8	6.5	11.8	559.8	-10.9	36.3
Braunvieh	36	457	44.4	45.5	-6.7	538.6	-32.1	-25.5
Charolais	123	1163	26.7	15.2	17.5	581.0	10.3	34.6
Chiangus	30	320	43.3	46.5	-7.1	536.0	-34.7	-27.0
Gelbvieh	90	1087	65.6	59.1	6.8	562.8	-8.0	-22.6
Limousin	86	1142	62.7	45.6	-0.7	564.2	-6.5	-18.2
Maine Anjou	51	541	47.2	46.0	-10.3	536.5	-34.3	-30.5
Salers	58	491	41.0	34.8	-0.6	553.4	-17.3	-7.3
Simmental	109	1209	63.4	57.1	15.8	573.7	3.0	-9.4
Tarentaise	17	282	17.5	-0.5	-2.9	562.4	-8.4	25.1

Calculations:
(4) = (3) / b + [(1) – (2)] + (Raw Angus Mean: 548.0 lb) with b = 0.81
(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 2014 base and factors to adjust within breed EPD to an Angus equivalent – YEARLING WEIGHT (lb)

	Number		Ave. Base EPD		Breed Soln	BY 2014	BY 2014	Factor to
	AI	Direct	Breed 2014	USMARC Bulls	at USMARC (vs Ang)	Sire Breed Average	Sire Breed Difference[a]	adjust EPD To Angus
Breed	Sires	Progeny	(1)	(2)	(3)	(4)	(5)	(6)
Angus	162	1834	91.0	50.3	0.0	1057.4	0.0	0.0
Hereford	158	2170	78.2	48.9	-28.8	1016.1	-41.4	-28.6
Red Angus	57	706	88.0	74.9	-9.7	1019.8	-37.6	-34.6
Shorthorn	59	515	66.0	64.3	-3.2	1015.1	-42.3	-17.3
South Devon	28	193	81.7	56.6	-20.0	1021.0	-36.4	-27.1
Beefmaster	56	425	45.0	45.4	-4.2	1011.9	-45.5	0.5
Brahman	56	564	25.6	13.2	-29.3	998.6	-58.8	6.6
Brangus	57	433	46.3	39.1	-7.0	1016.7	-40.7	4.0
Santa Gertrudis	24	291	5.2	9.9	2.4	1014.6	-42.8	43.0
Braunvieh	33	441	68.0	70.9	-28.2	984.4	-73.0	-50.0
Charolais	111	1061	48.7	29.9	19.2	1055.5	-1.9	40.4
Chiangus	26	287	63.1	66.0	-23.9	989.0	-68.4	-40.5
Gelbvieh	82	1020	96.8	77.9	-1.7	1033.9	-23.5	-29.3
Limousin	76	1052	92.3	60.9	-29.5	1017.4	-40.0	-41.3
Maine Anjou	51	506	62.6	61.8	-26.1	990.3	-67.1	-38.7
Salers	52	466	78.3	67.0	-8.7	1019.0	-38.4	-25.7
Simmental	88	1052	92.5	83.5	20.2	1046.8	-10.6	-12.1
Tarentaise	17	254	30.8	2.7	-40.3	1002.8	-54.6	5.6

Calculations:
(4) = (3) / b + [(1) – (2)] + (Raw Angus Mean: 1016.7 lb) with b = 0.96
(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 2014 base and factors to adjust within breed EPD to an Angus equivalent – MILK (lb)

Breed	AI Sires	Number Direct Gpr	Direct Progeny	Ave. Base EPD Breed 2014 (1)	Ave. Base EPD USMARC Bulls (2)	Breed Soln at USMARC (vs Ang) (3)	BY 2014 Sire Breed Average (4)	BY 2014 Sire Breed Difference[a] (5)	Factor to adjust EPD To Angus (6)
Angus	143	3162	751	23.0	15.3	0.0	555.7	0.0	0.0
Hereford	137	3812	932	20.3	10.9	-23.4	535.7	-20.0	-17.3
Red Angus	48	1029	275	20.0	16.0	4.3	555.9	0.3	3.3
Shorthorn	49	528	189	18.0	20.3	9.9	554.8	-0.9	4.1
South Devon	24	378	90	25.1	20.2	9.5	561.7	6.0	3.9
Beefmaster	46	443	138	9.0	9.2	-0.2	547.6	-8.1	5.9
Brahman	56	865	252	5.6	7.1	16.9	562.1	6.4	23.8
Brangus	46	414	125	9.5	6.4	-2.8	548.5	-7.2	6.3
Santa Gertrudis	21	279	112	0.5	-1.6	0.1	550.2	-5.5	17.0
Braunvieh	30	729	187	34.6	34.2	19.5	566.5	10.8	-0.8
Charolais	97	1775	452	8.7	5.9	-1.3	549.6	-6.1	8.2
Chiangus	24	268	112	15.3	14.6	-2.6	546.3	-9.4	-1.7
Gelbvieh	74	1688	408	26.8	29.7	18.0	561.8	6.1	2.3
Limousin	64	1933	438	26.8	25.2	-4.1	545.7	-9.9	-13.7
Maine Anjou	43	740	201	19.1	19.3	-2.4	545.5	-10.1	-6.2
Salers	47	626	201	19.9	19.2	10.5	557.6	2.8	5.9
Simmental	78	1901	454	21.6	25.6	16.0	558.7	3.0	4.4
Tarentaise	14	374	100	0.7	4.0	14.0	557.6	1.9	24.2

Calculations:

(4) = (3) / b + [(1) – (2)] + (Raw Angus Mean: 548.0 lb) with b = 1.08

(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 2014 base and factors to adjust within breed EPD to an Angus equivalent – MARBLING (marbling score units[a])

	Number		Ave. Base EPD		Breed Soln	BY 2014	BY 2014	Factor to
			Breed	USMARC	at USMARC	Sire Breed	Sire Breed	adjust EPD
	AI	Direct	2014	Bulls	(vs Ang)	Average	Difference[b]	To Angus
Breed	Sires	Progeny	(1)	(2)	(3)	(4)	(5)	(6)
Angus	145	831	0.59	0.23	0.00	5.88	0.00	0.00
Hereford	154	1015	0.09	0.02	-0.52	5.07	-0.81	-0.31
Red Angus	53	268	0.45	0.48	-0.02	5.47	-0.41	-0.27
Shorthorn	57	267	0.05	0.03	-0.34	5.20	-0.68	-0.14
South Devon	23	70	0.40	-0.06	-0.37	5.61	-0.27	-0.08
Brahman	55	235	0.00	-0.01	-1.02	4.51	-1.37	-0.78
Santa Gertrudis	24	139	-0.01	-0.02	-0.79	4.73	-1.14	-0.54
Braunvieh	32	206	0.56	0.50	-0.43	5.14	-0.73	-0.70
Charolais	66	329	0.04	-0.02	-0.58	5.00	-0.88	-0.33
Chiangus	26	133	0.10	0.14	-0.43	5.05	-0.83	-0.34
Gelbvieh	81	452	0.09	-0.24	-0.74	5.10	-0.77	-0.27
Limousin	69	424	-0.01	-0.26	-0.92	4.85	-1.03	-0.43
Maine Anjou	51	253	0.05	0.03	-0.77	4.77	-1.11	-0.57
Salers	48	230	0.20	-0.37	-0.69	5.40	-0.48	-0.09
Simmental	86	490	0.14	-0.01	-0.58	5.09	-0.79	-0.34

Calculations:

(4) = (3) / b + [(1) – (2)] + (Raw Angus Mean: 5.52) 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 2014 base and factors to adjust within breed EPD to an Angus equivalent – RIBEYE AREA (in^2)

	Number		Ave. Base EPD		Breed Soln	BY 2014	BY 2014	Factor to
			Breed	USMARC	at USMARC	Sire Breed	Sire Breed	adjust EPD
	AI	Direct	2014	Bulls	(vs Ang)	Average	Difference[a]	To Angus
Breed	Sires	Progeny	(1)	(2)	(3)	(4)	(5)	(6)
Angus	145	832	0.53	0.11	0.00	13.57	0.00	0.00
Hereford	154	1015	0.31	-0.02	-0.20	13.28	-0.29	-0.07
Red Angus	53	268	0.13	-0.07	-0.17	13.19	-0.39	0.01
Shorthorn	57	267	-0.06	-0.09	0.17	13.35	-0.22	0.37
South Devon	23	70	0.23	0.21	0.39	13.56	-0.01	0.29
Brahman	55	240	0.01	0.05	-0.10	13.01	-0.57	-0.05
Santa Gertrudis	24	140	0.04	0.02	-0.17	13.00	-0.58	-0.09
Braunvieh	32	206	0.35	0.33	1.01	14.17	0.60	0.78
Charolais	66	332	0.32	0.16	1.07	14.38	0.80	1.01
Chiangus	26	134	0.32	0.18	0.41	13.70	0.13	0.34
Gelbvieh	81	454	0.45	0.37	1.01	14.24	0.67	0.75
Limousin	69	425	0.48	0.39	1.30	14.54	0.96	1.01
Maine Anjou	51	253	0.21	0.20	1.07	14.22	0.65	0.97
Salers	48	231	0.02	0.02	0.85	14.00	0.43	0.94
Simmental	86	491	0.79	0.56	0.95	14.33	0.75	0.49

Calculations:

(4) = (3) / b + [(1) – (2)] + (Raw Angus Mean: 13.15 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 2014 base and factors to adjust within breed EPD to an Angus equivalent – FAT THICKNESS (in)

	Number		Ave. Base EPD		Breed Soln	BY 2014	BY 2014	Factor to
			Breed	USMARC	at USMARC	Sire Breed	Sire Breed	adjust EPD
	AI	Direct	2014	Bulls	(vs Ang)	Average	Difference[a]	To Angus
Breed	Sires	Progeny	(1)	(2)	(3)	(4)	(5)	(6)
Angus	145	832	0.017	0.003	0.000	0.677	0.000	0.000
Hereford	154	1014	0.003	-0.003	-0.062	0.607	-0.070	-0.056
Red Angus	52	266	-0.007	-0.010	-0.029	0.637	-0.040	-0.016
Shorthorn	57	267	-0.033	-0.029	-0.136	0.522	-0.155	-0.105
South Devon	23	70	0.010	0.008	-0.127	0.537	-0.140	-0.133
Brahman	55	240	0.000	-0.002	-0.149	0.515	-0.162	-0.145
Santa Gertrudis	24	140	0.002	0.003	-0.080	0.582	-0.095	-0.080
Braunvieh	32	205	-0.090	-0.091	-0.186	0.478	-0.199	-0.092
Charolais	66	331	0.005	0.006	-0.205	0.457	-0.220	-0.208
Chiangus	26	133	-0.060	-0.024	-0.120	0.507	-0.170	-0.093
Limousin	69	424	-0.040	-0.069	-0.203	0.488	-0.189	-0.132
Maine Anjou	51	253	-0.041	-0.032	-0.221	0.433	-0.245	-0.187
Salers	48	231	0.000	-0.007	-0.205	0.464	-0.213	-0.196
Simmental	86	491	-0.056	-0.053	-0.185	0.475	-0.202	-0.129

Calculations:

(4) = (3) / b + [(1) – (2)] + (Raw Angus Mean: 0. 663 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. Breed of sire solutions from USMARC, mean breed and USMARC EPD used to adjust for genetic trend to the year 2014 base and factors to adjust within breed EPD to an Angus equivalent – CARCASS WEIGHT (lb)

	Number		Ave. Base EPD		Breed Soln	BY 2014	BY 2014	Factor to
			Breed	USMARC	at USMARC	Sire Breed	Sire Breed	adjust EPD
	AI	Direct	2014	Bulls	(vs Ang)	Average	Difference[a]	To Angus
Breed	Sires	Progeny	(1)	(2)	(3)	(4)	(5)	(6)
Angus	145	832	33.0	14.3	0.0	913.7	0.0	0.0
Hereford	154	1015	61.0	42.9	-30.5	882.7	-31.0	-59.0
Red Angus	53	268	20.0	12.4	-11.0	891.7	-22.0	-9.0
Shorthorn	57	267	11.6	11.1	-10.4	885.2	-28.5	-7.1
South Devon	23	70	28.3	15.3	-23.9	884.2	-29.5	-24.8
Brahman	55	241	1.4	0.4	-41.7	854.4	-59.4	-27.8
Santa Gertrudis	24	140	3.3	5.7	-6.4	886.2	-27.5	2.2
Charolais	66	332	16.8	10.7	9.3	910.5	-3.2	13.0
Chiangus	26	134	10.9	11.4	-21.1	873.5	-40.2	-18.1
Gelbvieh	81	454	27.6	18.4	-10.9	893.4	-20.4	-15.0
Limousin	69	425	26.3	6.6	-19.7	895.1	-18.7	-12.0
Maine Anjou	51	253	9.0	10.2	-20.0	873.8	-39.9	-15.9
Salers	48	232	20.5	15.5	-22.3	877.8	-36.0	-23.5
Simmental	86	491	27.6	22.3	12.3	912.8	-1.0	4.4

Calculations:
(4) = (3) / b + [(1) – (2)] + (Raw Angus Mean: 895.1 lb) with b = 1.00
(5) = (4) – (4, Angus)
(6) = (5) – (5, Angus) – [(1) – (1, Angus)]

Table 9. 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), fat thickness (FAT), and carcass weight (CWT) for bulls used at USMARC

Breed	BWT	WWT	YWT	MILK	MAR	REA	FAT	CWT
Angus	0.82	0.80	0.75	0.75	0.55	0.55	0.53	0.53
Hereford	0.68	0.65	0.64	0.61	0.32	0.44	0.35	0.56
Red Angus	0.92	0.92	0.92	0.89	0.72	0.70	0.70	0.60
Shorthorn	0.82	0.81	0.80	0.80	0.46	0.45	0.46	0.57
South Devon	0.46	0.49	0.44	0.50	0.07	0.09	0.10	0.33
Beefmaster	0.88	0.90	0.80	0.68				
Brahman	0.53	0.51	0.45	0.34	0.11	0.14	0.10	0.28
Brangus	0.89	0.83	0.73	0.73				0.70
Santa Gertrudis	0.73	0.69	0.58	0.56	0.42	0.49	0.51	0.46
Braunvieh	0.63	0.56	0.32	0.50	0.11	0.18	0.09	0.18
Charolais	0.82	0.76	0.69	0.70	0.47	0.50	0.44	0.45
Chiangus	0.82	0.79	0.79	0.75	0.25	0.22	0.34	0.57
Gelbvieh	0.85	0.84	0.84	0.82	0.63	0.58		0.56
Limousin	0.94	0.93	0.93	0.92	0.66	0.65	0.66	0.61
Maine Anjou	0.79	0.78	0.77	0.77	0.26	0.25	0.29	0.55
Salers	0.82	0.82	0.76	0.79	0.28	0.31	0.36	0.61
Simmental	0.94	0.94	0.94	0.93	0.72	0.71	0.71	0.60
Tarentaise	0.92	0.91	0.90	0.88				

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

Table 10. 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), fat thickness (FAT; in^2), and carcass weight (CWT; lb) from mixed model analyses of USMARC data

Analysis	BWT	WWT[a]	YWT
Animal within breed (18 breeds)	69.19	489.50	3552.36
Maternal genetic within breed (18 breeds)		445.59	
Maternal permanent environment		706.81	
Residual	57.23	1306.33	4634.15

Carcass Direct	MAR	REA	FAT	CWT
Animal within breed (13-16 breeds)	0.288	0.670	0.0105	2382.21
Residual	0.258	0.764	0.0144	2170.34

[a]Direct maternal covariance for weaning weight was -44.17 lb^2

Table 11. 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

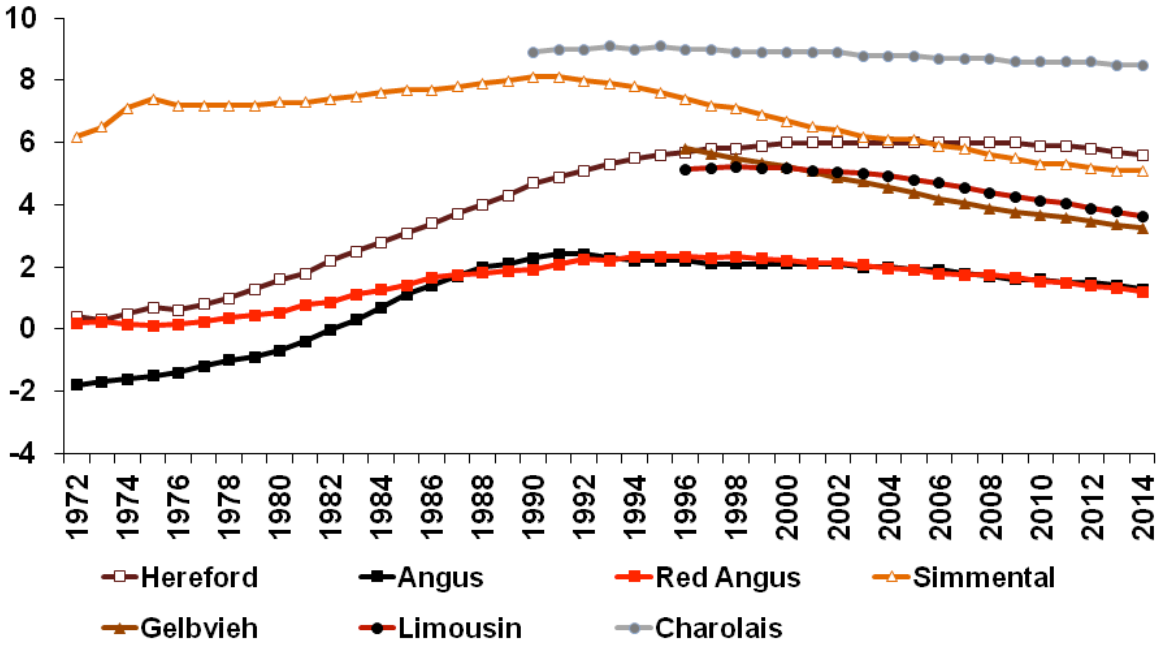
	BWT	WWT	YWT	MILK
Pooled	1.17 ± 0.03	0.81 ± 0.03	0.96 ± 0.04	1.08 ± 0.06
Sire breed				
Angus	1.13 ± 0.09	0.88 ± 0.06	1.12 ± 0.07	1.06 ± 0.15
Hereford	1.18 ± 0.07	0.70 ± 0.05	0.98 ± 0.06	1.07 ± 0.14
Red Angus	1.00 ± 0.13	0.70 ± 0.13	0.62 ± 0.15	1.18 ± 0.25
Shorthorn	0.74 ± 0.18	0.51 ± 0.14	0.40 ± 0.17	0.63 ± 0.41
South Devon	-0.01 ± 0.39	0.97 ± 0.26	0.56 ± 0.30	1.22 ± 0.95
Beefmaster	1.91 ± 0.27	0.76 ± 0.20	0.77 ± 0.32	8.24 ± 1.68
Brahman	1.88 ± 0.21	1.13 ± 0.17	1.31 ± 0.21	0.66 ± 0.60
Brangus	1.49 ± 0.22	0.80 ± 0.19	0.88 ± 0.17	0.82 ± 0.55
Santa Gertrudis	3.16 ± 0.64	1.20 ± 0.23	1.16 ± 0.28	0.25 ± 1.00
Braunvieh	0.79 ± 0.27	0.66 ± 0.28	0.32 ± 0.25	1.67 ± 0.62
Charolais	1.09 ± 0.12	0.93 ± 0.10	0.87 ± 0.11	0.96 ± 0.21
Chiangus	1.30 ± 0.25	0.28 ± 0.22	0.47 ± 0.26	0.34 ± 0.42
Gelbvieh	1.11 ± 0.13	0.87 ± 0.10	1.16 ± 0.12	0.86 ± 0.23
Limousin	1.08 ± 0.12	0.79 ± 0.07	0.86 ± 0.08	1.35 ± 0.21
Maine Anjou	1.47 ± 0.16	0.90 ± 0.18	0.80 ± 0.23	1.86 ± 0.38
Salers	1.31 ± 0.22	0.82 ± 0.24	0.64 ± 0.23	1.67 ± 0.35
Simmental	1.15 ± 0.13	1.40 ± 0.12	1.31 ± 0.12	0.86 ± 0.28
Tarentaise	1.21 ± 0.49	1.01 ± 0.21	1.39 ± 0.32	1.25 ± 0.80

Table 12. Pooled and within-breed regression coefficients marbling (MAR; score/score), ribeye area (REA; in^2/in^2), fat thickness (FAT; in/in), and carcass weight (CWT; lb) of F_1 progeny on sire expected progeny difference and by sire breed

	MAR	REA	FAT	CWT
Pooled	0.53 ± 0.04	0.81 ± 0.05	0.91 ± 0.08	0.97 ± 0.06
Sire breed				
Angus	0.78 ± 0.07	0.70 ± 0.12	0.98 ± 0.13	0.94 ± 0.10
Hereford	0.73 ± 0.13	0.62 ± 0.12	1.01 ± 0.16	1.05 ± 0.11
Red Angus	1.07 ± 0.15	1.12 ± 0.19	1.03 ± 0.34	1.08 ± 0.22
Shorthorn	1.30 ± 0.25	0.75 ± 0.38	1.34 ± 0.47	0.50 ± 0.28
South Devon	-0.05 ± 0.19	2.06 ± 2.36	3.10 ± 2.38	-1.02 ± 0.86
Brahman	1.70 ± 0.89	1.16 ± 0.33	0.97 ± 0.55	0.51 ± 0.23
Santa Gertrudis	1.01 ± 0.64	0.77 ± 0.47	1.70 ± 0.82	1.21 ± 0.46
Braunvieh	-0.02 ± 0.50	0.58 ± 0.28	-1.93 ± 3.37	0.36 ± 0.39
Charolais	1.03 ± 0.18	0.86 ± 0.16	1.32 ± 0.34	0.88 ± 0.26
Chiangus	0.70 ± 0.19	0.37 ± 0.45	0.67 ± 0.37	0.62 ± 0.42
Gelbvieh	1.15 ± 0.17	1.29 ± 0.16		1.49 ± 0.18
Limousin	1.08 ± 0.25	0.82 ± 0.13	1.07 ± 0.28	0.85 ± 0.13
Maine Anjou	-0.43 ± 0.48	-0.61 ± 0.49	-0.54 ± 0.50	1.36 ± 0.31
Salers	0.04 ± 0.06	1.35 ± 0.52	0.79 ± 0.51	0.74 ± 0.43
Simmental	0.94 ± 0.15	0.70 ± 0.14	0.19 ± 0.28	1.55 ± 0.20

Figure 1. Relative genetic trends for birth weight (lb) of the seven most highly used beef breeds (1a) and all breeds that submitted 2016 trends (1b) adjusted for birth year 2014 using the 2016 across-breed EPD adjustment factors.

1a.



1b.

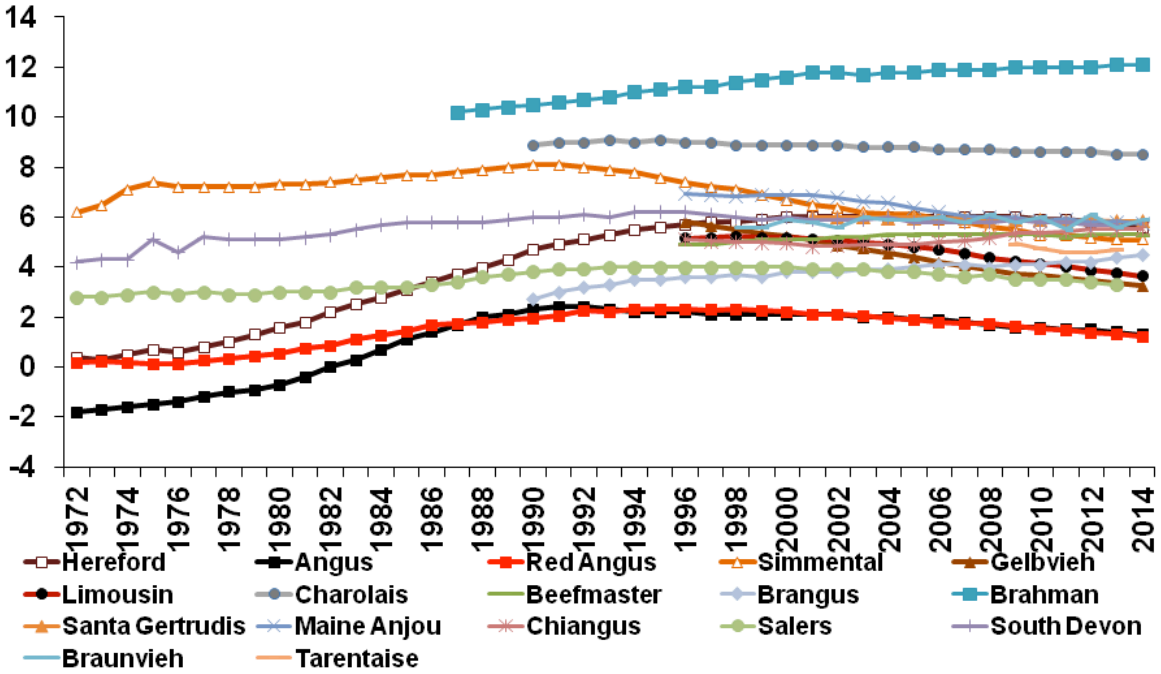
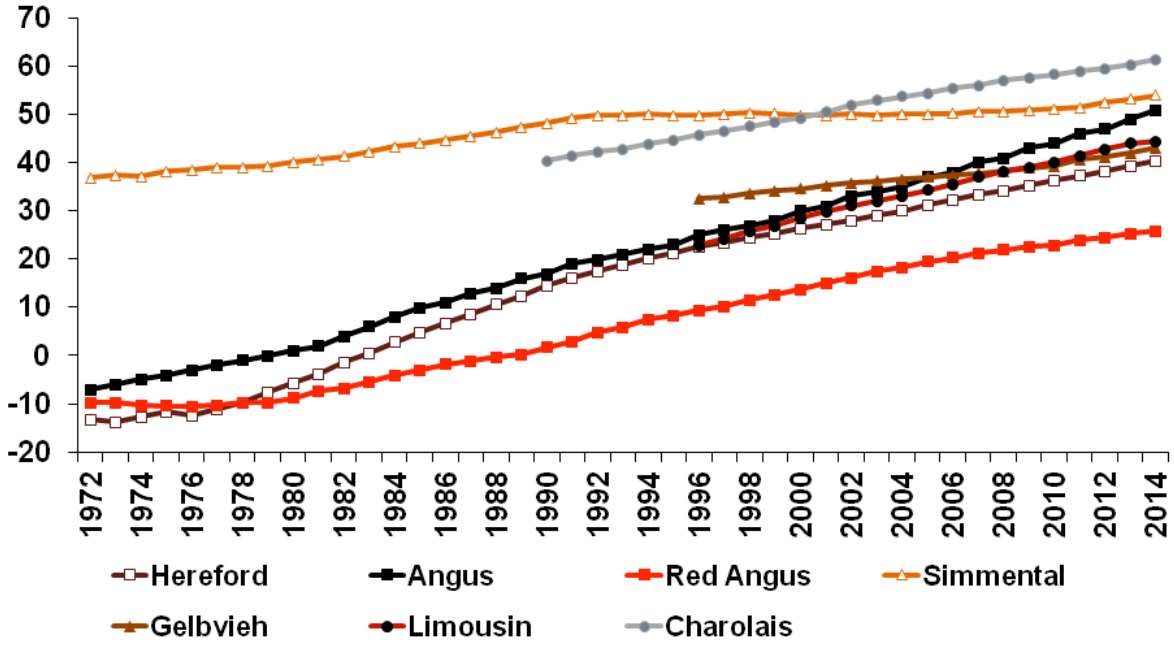


Figure 2. Relative genetic trends for weaning weight (lb) of the seven most highly used beef breeds (2a) and all breeds that submitted 2016 trends (2b) adjusted for birth year 2014 using the 2016 across-breed EPD adjustment factors.

2a.



2b.

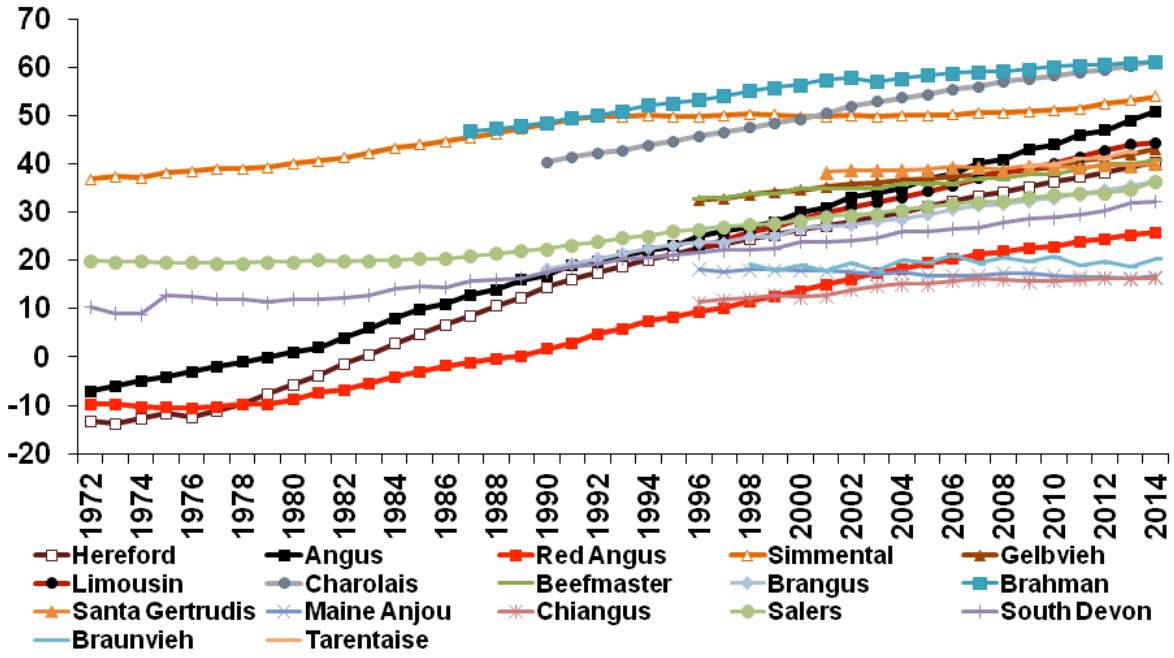
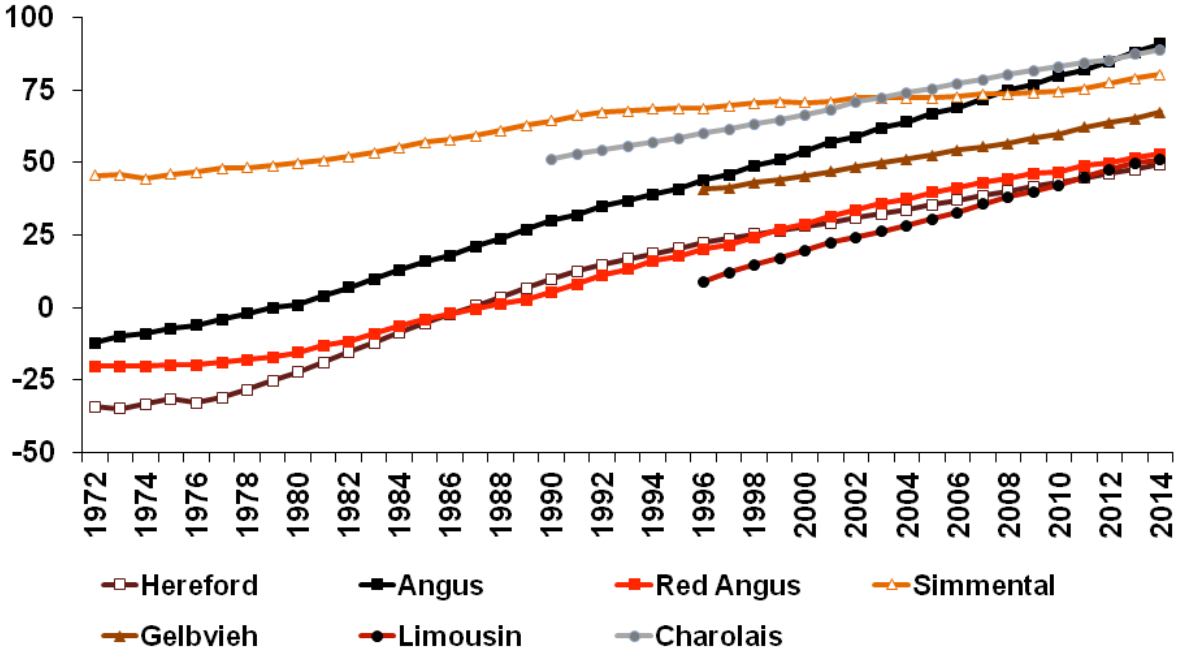


Figure 3. Relative genetic trends for yearling weight (lb) of the seven most highly used beef breeds (3a) and all breeds that submitted 2016 trends (3b) adjusted for birth year 2014 using the 2016 across-breed EPD adjustment factors.

3a.



3b.

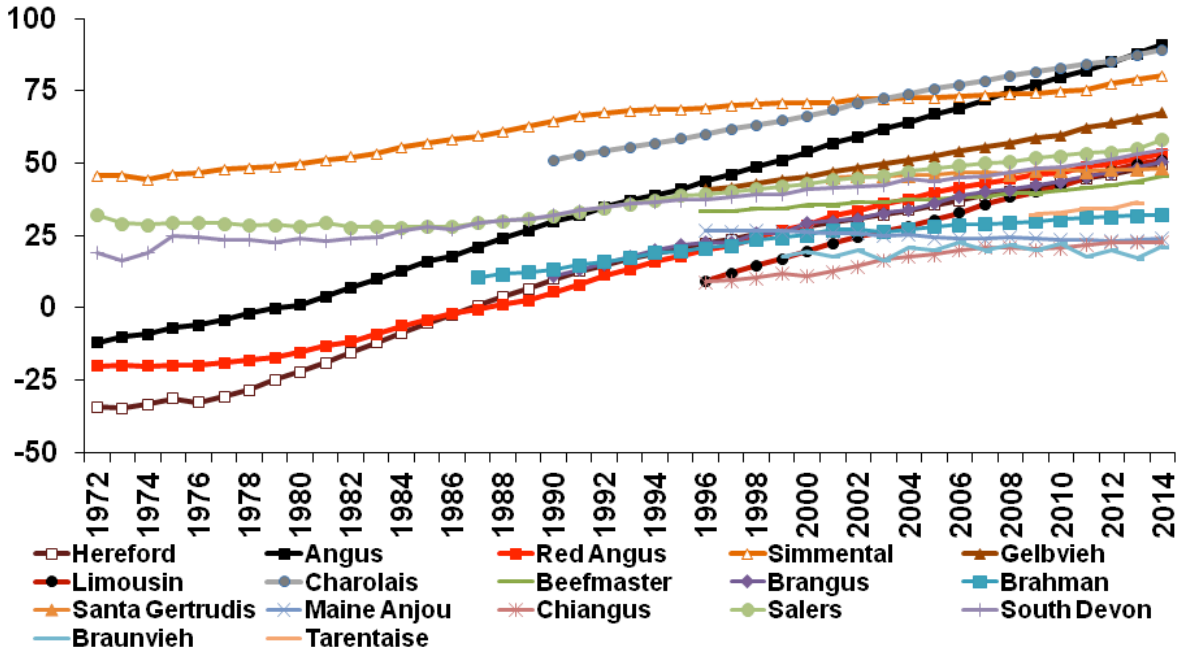
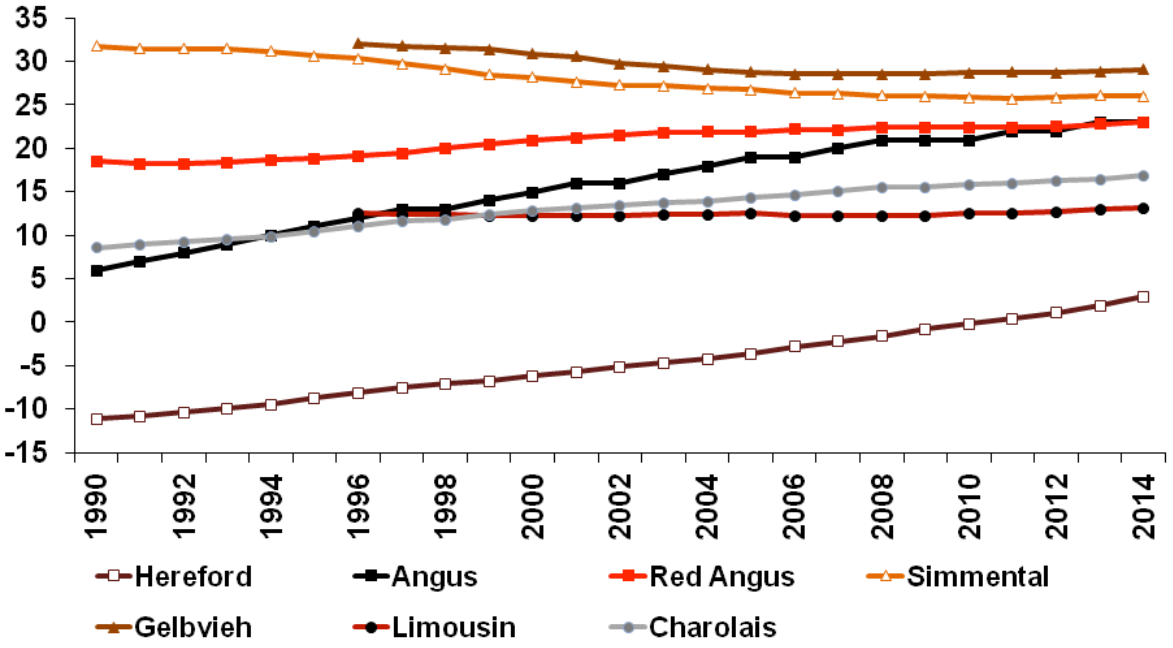
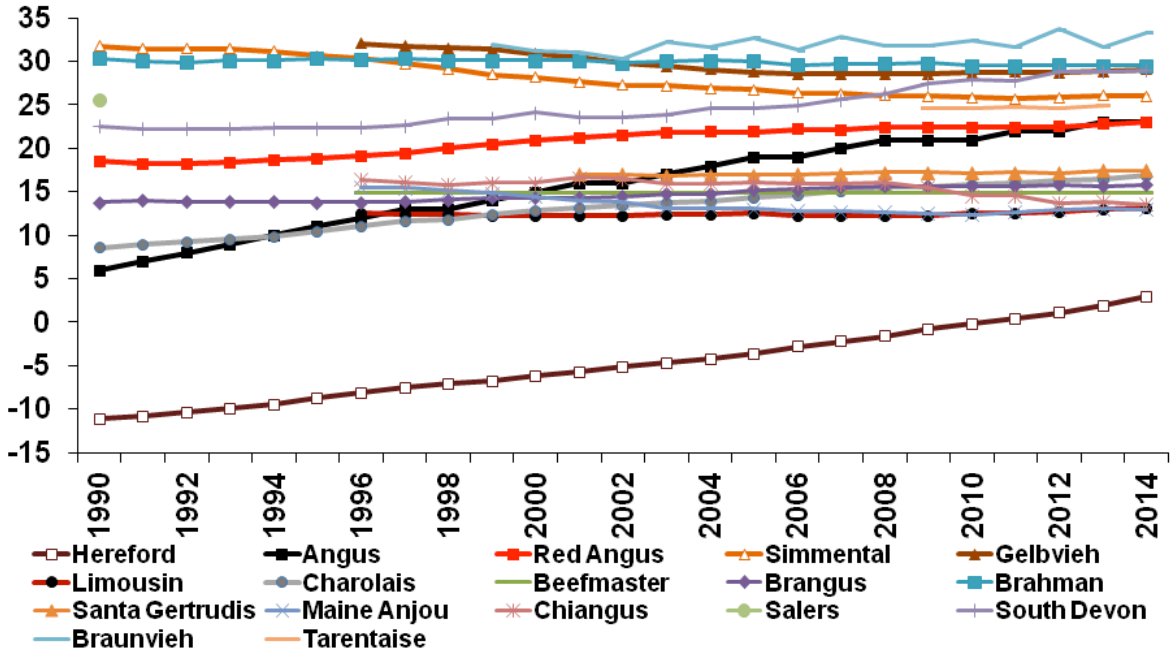


Figure 4. Relative genetic trends for maternal milk (lb) of the seven most highly used beef breeds (4a) and all breeds that submitted 2016 trends (4b) adjusted for birth year 2014 using the 2016 across-breed EPD adjustment factors.

4a.



4b.



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Breeding Objectives Indicate Value of Genomics for Beef Cattle

M. D. MacNeil, Delta G

Introduction

A well-defined breeding objective provides commercial producers a mechanism for extracting value from the investment in genomics by seedstock producers. Advantages of genomic prediction include increased accuracy of expected progeny differences (EPDs) for traits that have been components of routine genetic evaluations. Perhaps more importantly, genomic prediction makes it possible to include traits that are too costly or too difficult to measure, and traits that are measured too late in life or are sex-limited such that candidates for selection cannot have EBV with high accuracy at the time when selection decisions are made. Genomically enhanced EPDs may also allow for a marked reduction in generation interval, thus accelerating the annual rate of genetic improvement. Here, the value of genomic prediction, on a trait by trait basis, is extended to explore the contribution of genomic prediction to selection for a multi-trait breeding objective indicative of economic merit. A simple two-trait objective indicative of feed efficiency is illustrated first, followed by objectives for terminal and maternal strains of Angus.

Materials and Methods

The conceptual model employed to incorporate of genomic information into multiple-trait economic breeding objectives is shown in Figure 1.

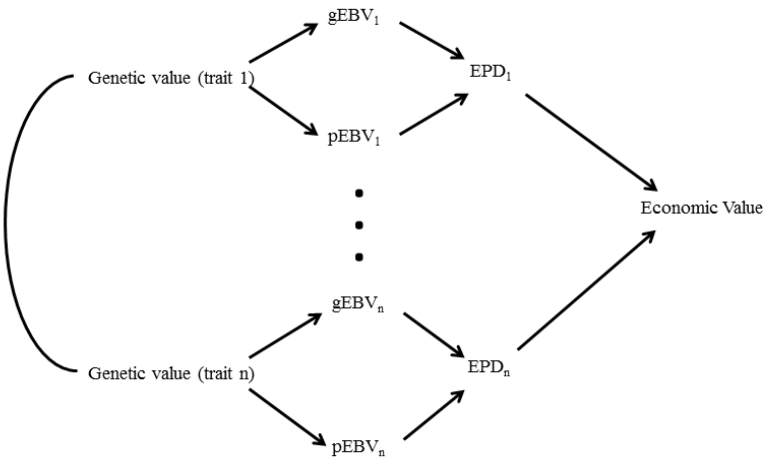

Figure 1. Conceptual model employed to incorporate of genomic information into multiple-trait economic breeding objectives.

True genetic values for each of n, possibly correlated traits, are the cause of differences in both genomic and phenotypic estimated breeding values gEBV and pEBV, respectively. The separate EBVs are then merged (blended) as a function of their respective accuracies to produce an EPD for each of the n traits. Finally, for each animal the sum of products of economic weights and EBV is calculated to predict its economic value. Formally, a breeding objective (O) reflects

the functional relationship between breeding values (BV) of biological traits and profit (e.g., O = a1BV1 + a2BV2 + a3BV3 …; where ai is economic value of the ith economically relevant traits. Implementing a breeding objective depends on a genetic evaluation system such that: $\hat{O}$ = a1EPD1 + a2EPD2 + a3EPD3 … By definition economic values are the change in profit that is expected from a single unit change in the associated trait, holding all other traits constant.

Here, three distinct objectives are evaluated: 1) feed efficiency, a linear transformation of the ratio of postweaning average daily gain to feed intake; 2) a terminal objective based on work for the Circle A Angus Sire Alliance; and 3) a maternal objective also for Angus. A series of differing accuracies of the EBV components of the feed efficiency objective were evaluated. Shown here are results calculated for accuracies of the EBV quartet [pEBV1, gEBV1, pEBV2, gEBV2] of [0.50, 0.00, 0.61, 0.00], [0.50, 0.40, 0.61, 0.40], [0.50, 0.60, 0.61, 0.60], [0.60, 0.40, 0.70, 0.40], and [0.60, 0.60, 0.70, 0.60].

For the terminal sire objective, economic weights were calculated by simulation based data from Angus calves born during a 4-month spring calving season and weaned at an average age of 192 days. After weaning, the calves were fed a diet of moderate energy density for an average of 106 d before transport to a feedlot for finishing. Daily feed intake of individual animals was measured in contemporary groups of 96 steers using a Calan Broadbent Feeding System. A stepwise series of five diets that increased in energy density were used throughout the finishing period. Harvest date was determined to target a contemporary group to average 1.3 cm fat depth at the 12-13 rib and/or to avoid discounts for under- and over-weight carcasses. The afternoon before harvest, steers were weighed and then transported overnight to the packing plant for harvest and collection of carcass data. Carcass data included: harvest date, hot carcass weight, marbling score, fat depth, LM area, and percentage kidney, pelvic and heart fat. The terminal breeding objective is described by statistics presented in Table 1.

Table 1. Estimates of mean (μ), phenotypic standard deviation (σ), heritability (h^2), economic weights ($\partial P/\partial t$), and accuracies for traits (t) included in an Angus terminal sire breeding objective.

Trait	μ	σ	h^2	$\partial P/\partial t$	relative value, %	accuracy[a]	
						$_g$EBV	$_p$EBV
Birth weight, lb.	77.9	11.0	0.41	-0.85	8.8	0.68	0.76
Weaning weight, lb.	427.	86.9	0.23	0.41	25.4	0.56	0.66
ADG, lb./d	2.90	0.40	0.36	47.40	16.9	0.66	0.60
DFI, kg/d	20.2	2.20	0.41	-10.02	21.1	0.74	0.56
Marbling score[b]	5.8	1.00	0.26	13.54	10.3	0.67	0.59
Yield grade	3.4	0.70	0.22	-35.28	17.4	0.65	0.57

[a] $_g$EBV = genomic EBV; $_p$EBV = phenotypic EBV
[b] 4.0 = Slight^{00}; 5.0 = Small^{00}; etc.

The maternal objective considered Angus as a specialized dam line used in a 2-breed rotation crossbreeding system wherein income was derived from calves sold at weaning. Here the simulation described progression of the cows through their life cycle as a function of age-specific mortality and reproduction. As with the terminal objective, spring-born calves were weaned at 192 days of age. The maternal breeding objective is described by statistics presented in Table 2.

Table 2. Estimates of mean (μ), phenotypic standard deviation (σ), heritability (h^2), economic weights (∂P/∂t), and accuracies for traits (t) included in a breeding objective for an Angus specialized dam line.

Trait	μ	σ	h^2	∂P/∂t	relative value, %	accuracy[a]	
						$_g$EBV	$_p$EBV
Stayability, %	55.1	16.2	0.21	8.00	50.6	0.58	0.37
Heifer pregnancy, %	91.0	22.6	0.14	1.61	11.6	0.45	0.31
Calving ease (d), %	85.5	28.6	0.12	1.90	16.0	0.62	0.65
Calving ease (m), %	-		0.13	1.90	16.7	0.32	0.46
Weaning weight (d), lb.	564.7	109.1	0.30	0.086	4.4	0.56	0.66
Weaning weight (m), lb.	-		0.14	-0.023	0.8	0.36	0.51

[a] $_g$EBV = genomic EBV; $_p$EBV = phenotypic EBV

For each breeding objective two scenarios were simulated: 1) where the accuracies of both the phenotypic and genomic EBV were as presented in Tables 1 and 2; and 2) where the accuracies of the genomic EBV were = 0.0. Accuracy estimates for the phenotype-based EPD were from a 2015 Angus national cattle evaluation for 2014 bulls that were not genotyped. Thus, the accuracies of the EBV were approximate those available for choosing among yearling bulls.

Finally, the "Breeder's equation": $R = h\sigma_a i$, wherein, R = response to selection, h = square root of heritability or accuracy, σ_a= genetic standard deviation, and i = selection intensity was used to assess selection response as a function of changes in accuracy due to the addition of genomic information to traditional phenotype-based predictions of genetic merit.

Results and Discussion

The five scenarios analyzed for the feed efficiency objective reflect meaningful circumstances. In scenarios 1-3, accuracies of the pEBV equal the square roots of the corresponding heritability estimates. Thus, the EBV are assumed to be based only on individual performance records. In scenarios 4 and 5, the accuracies of the pEBV were increased to reflect the addition of records from sibs. Accuracies of the gEBV were selected to reflect no genomic information (scenario 1), modest accuracy gEBV (scenarios 2 and 4), and higher accuracy gEBV (scenarios 3 and 5). Higher accuracy pEBV were not considered as it is thought to be unlikely that greater levels of accuracy could be attained prior to the time selection decisions are typically made. Adding genomic information improved accuracy of the feed efficiency EPD when only the individual phenotypes were available. However, as the accuracy of phenotypic information contributing to the feed efficiency EPD increased, the value of genomic information became negligible.

For individual traits in the terminal objective, selection response is increased through the use of genomic predictors by 9% to 41% with the least effect on birth weight and the greatest effect on dry matter intake. In general, these effects were greater on postweaning traits that are less frequently recorded and(or) monitored with indicator traits. For individual traits in the maternal objective, selection response is increased through the use of genomic predictors by 12% to 76% with by far the greatest effects on stayability and heifer pregnancy, traits that are unobserved on bull candidates for selection at the time when the selection decisions are typically reached

Use of breeding objectives allows consequences of incorporating genomic information to be translated into economic terms. Assume the classical pyramid paradigm for flows of genetic and economic signals in the beef industry. Conceptually, the industry is divided into two segments. One, a seedstock or stud breeding sector wherein data recording and subsequent genetic evaluation facilitate genetic improvement that results in enhanced profitability for the commercial producers that form the second segment. These commercial producers benefit from the selection decisions that have been made by stud breeders and reward them for the enhanced genetic merit of the stock that they sell for use in commercial production. Here, assume that in the seedstock segment 5% of bulls and 30% of heifers are retained for breeding. The value of incorporating genomic information into EBVs that are components of multiple-trait breeding objectives for Angus cattle is illustrated in Figure 2. Other things being equal, these results indicate selection response for economic merit would be increased 1.25- and 1.56-fold by including genomic information in the EBV in the two objectives, respectively. In economic terms, adding genomic information to the prediction of EBV yields $11.55 for the terminal index and $50.85 for the maternal objective. If an individual terminal sire were to produce say 60 commercial progeny, then the expected net increase would total $346.50 and a maternal sire producing 15 replacement females add $326.00 to the bottom line of the cow-calf producer.

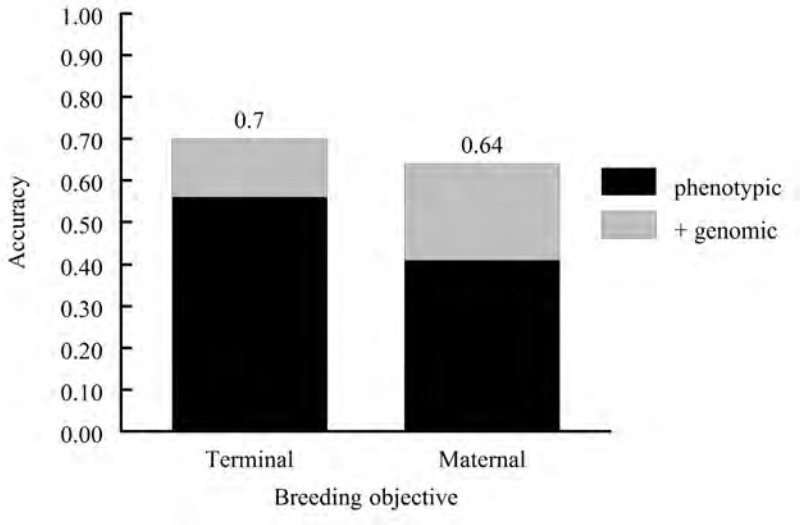

Figure 2. Effect of adding genomic information to traditional phenotype-based EBV on the accuracy of breeding objectives for selection of beef cattle as specialized sire (terminal) and dam (maternal) lines.

Implications

Genomically enhanced EBVs are more accurate predictors of merit than traditional EBV. These increases in accuracy can yield economic returns in commercial production that are more than sufficient to offset the cost of genotyping by the seedstock producers.

Using Genomic Tools in Commercial Beef Cattle: Taking Heifer Selection to the Next Level

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Introduction

The use of genomic technology is revolutionizing beef cattle evaluation and selection. High density genotyping and integration into national cattle evaluations are further bending the genetic improvement curve. While up until now these advancements in technology have been primarily used in the seedstock industry, opportunities now exist for use in commercial beef herds. A fundamental decision facing commercial producers is selection of replacement females and as the U.S. beef herd rebuilds, it is important to select heifers with the highest genetic potential as brood cows.

Utilizing available genomic testing and the multiple-trait, economic based indexes that accompany these tests offer producers an opportunity to select heifers for optimum lifetime improvement at a very young age and affordable price. This approach may be used in conjunction with, or as a replacement for traditional selection methods based on visual appraisal, first born, heaviest at weaning or dams performance. As a result it allows for a more balanced and desired response across traits instead of the potential consequences of selection based predominantly on visual appraisal. It follows that understanding anticipated multi-trait response to selection and associated sources of value return are important for adoption of this technology by commercial cow-calf producers.

Development of GeneMax Advantage

In 2014 in collaboration with Angus Genetics Inc. and Certified Angus Beef, Zoetis released GeneMax Advantage to the beef industry. Advantage is a genomic test that is applicable to beef females that are ≥ 75% Black Angus composition. Advantage was originally developed using over 39,000 Angus seedstock animals tested with HD50K molecular breeding values (MBV) that were a part of National Cattle Evaluation for registered Angus cattle conducted by the American Angus Association. This platform was used as the foundation for Advantage because it contains the most reliable genomic predictions for maternal, growth and carcass traits available for Angus cattle.

Table 1 shows the most recently estimated correlations between MBV and the respective phenotypic data from the latest Angus validation (American Angus Association and Angus Genetics Inc, 2016). These correlations range from .37 to .80, with the higher correlation indicating a stronger relationship between the molecular predictions and the phenotypic data. Explained variation, the proportion of additive genetic variability explained by the molecular predictions and calculated as the square of the correlation, ranges from .14 to .64 with an average of .44 across all evaluated traits. Approximate progeny equivalents (not shown) from these correlations range from 6 for carcass weight up to 23 for yearling weight.

Table 1. Correlations between molecular breeding values and phenotypic data in the most recent Angus validation[1].

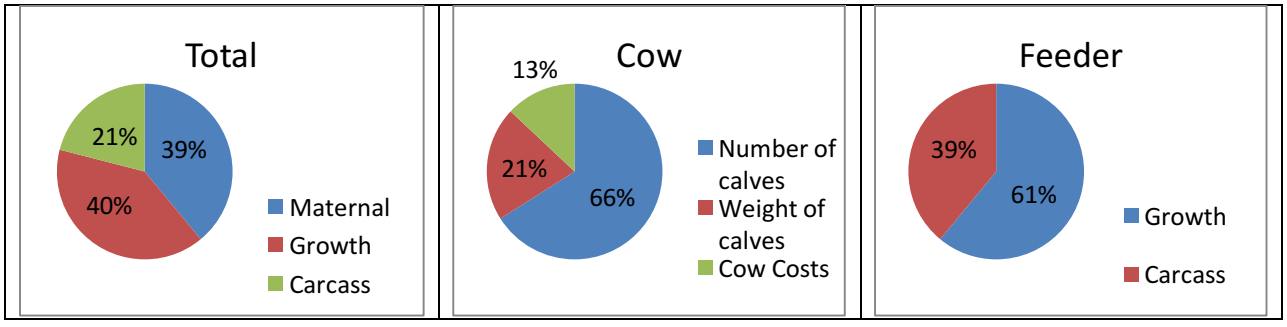
Trait	Correlation		Trait	Correlation		Trait	Correlation
CED	.67		SC	.80		CWT	.60
BW	.69		DOC	.68		MARB	.65
WWT	.56		HP	.62		REA	.68
YWT	.68		MILK	.37		FAT	.65
DMI	.73		MWT	.74			
YHT	.75		MHT	.71			

[1]Based on validations including >108,000 head.
Source: American Angus Association and Angus Genetics Inc. 2016.

The foundation of Advantage are MBV for commercial heifers based upon a strategically developed assay and imputation to the Zoetis custom HD Illumina platform used for the registered Angus population. These MBV are predicted for thirteen traits and then consolidated into three bio-economic indexes that can be used for heifer selection, mating and marketing decisions. Advantage indexes were derived using simple selection index methodology and economic assumptions used by AGI in the economic ($) indexes available to both breeders and commercial cow-calf users of Angus genetics. Relative economic values for each trait were modeled by considering both costs and returns for each stage of production using deterministic modeling and all inputs in the economic modeling (costs and returns) are based on three-year rolling averages (American Angus Association, 2016; Beal, 1998; Beal, 1998b; CattleFax, 2014; Fox et al., 1988; McCorkle and Bevers, 2009; NRC, 2000).

The indexes offered with Advantage are Total - encompassing traits from conception to carcass, Cow - which includes traits associated with maternal and reproductive performance, and Feeder - which includes traits associated with post-weaning gain, efficiency and carcass attributes valued on a quality grade based grid. In addition to the three indexes, outlier reporting is also provided for four traits: marbling, tenderness, docility and cow cost. Relative trait weightings for the trait groupings are shown in Figure 1. Maternal traits included in the Total index include heifer pregnancy rate, calving ease maternal and mature size. Growth and intake traits include weaning and yearling weight and dry matter intake. Carcass related traits include carcass weight, ribeye area, fat, and marbling. As shown in Figure 1, the Total index is reasonably balanced across trait areas, whereas the Cow Advantage index places emphasis on maternal traits that impact number of calves, weaned calf weight and costs associated with milk and cow size. The Feeder Advantage index places roughly 60% emphasis on growth and feed intake and 40% on carcass traits.

Figure 1. Relative contribution of trait categories for Advantage Total, Cow and Feeder indexes.

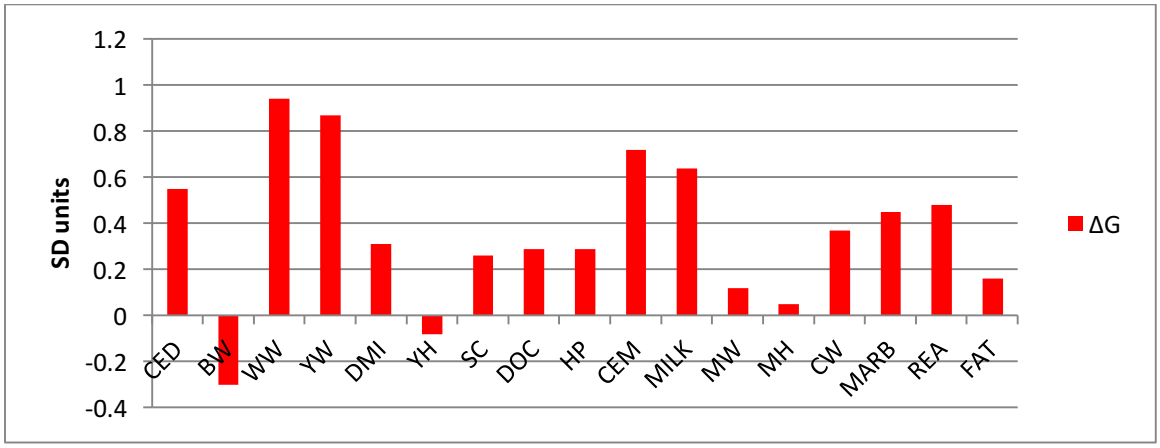


Annually, relative economic weights are re-estimated using updated economic costs and returns. Now that sufficient genotypes are available on commercial heifers, MBV are used from this population in the model to estimate relative economic values. These values are more indicative of the commercial population in which results will be utilized and tend to show less genetic variability than parameters from the registered genotyped animals. Once final index values are calculated on their underlying economic scale, they are transformed to a normally distributed 1 to 100 point score with 50 representing the mean of the tested commercial Angus heifer population.

Potential Genetic Improvement

Using genetic parameters estimated from 37,519 animals with genotypes prior to March, 2016, potential genetic improvement has been estimated for individual traits and overall economic value. Assumptions are that two-thirds of heifers of a given heifer-calf crop are genomically tested, that 45% of tested heifers are then selected as replacements based on the Total Advantage index, and for the purpose of estimating potential genetic improvement, that males (service sires) are HD-50K tested and selected using the same index and represent bulls from the top 25% of the seedstock population. Using these assumptions annual economic improvement of $7.26 is theoretically possible. Figure 2 shows potential genetic improvement from continual selection for Total Advantage index over a 5 year period. Using an index that is weighted according to economic value of the respective traits results in a small but balanced response in generally the desired direction for all traits considered.

Figure 2. Potential standardized cumulative genetic change over a five year period of continual selection based on Total Advantage index.



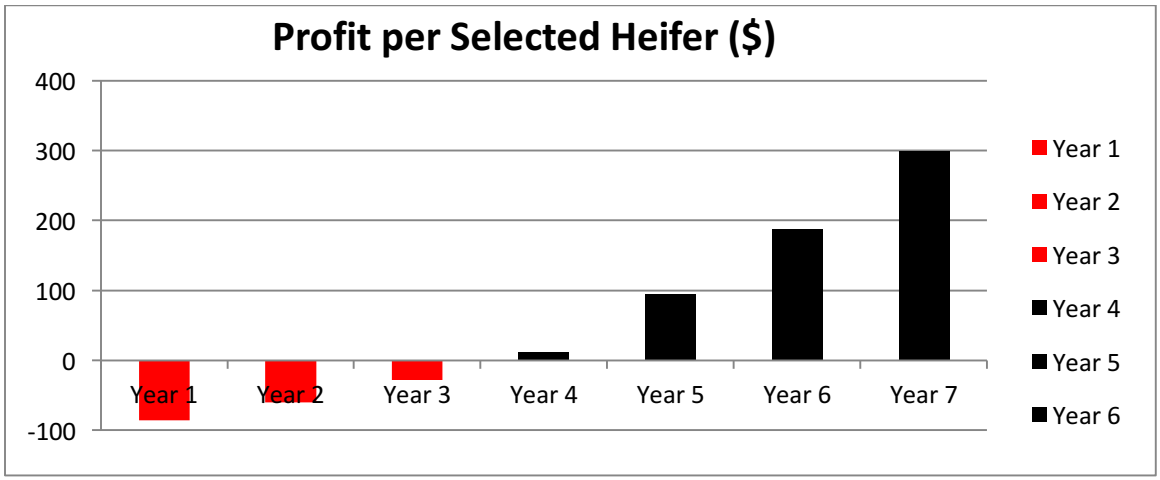
Value of Genomic Testing

As with any investment in a new practice or technology, producers have to consider the potential return on their investment. Cost has to be weighed against potential returns to assess whether or not to utilize the new technology. Major considerations for a cow-calf producer include deciding whether a genetic investment will impact the number of live calves per exposed female, increase the number and weight of weaned calves or reduce replacement rates by decreasing involuntary culling of cows. If improvements in output can be attained while either maintaining or reducing feed requirements, the net result should be beneficial.

Using similar assumptions to predicting possible rate of genetic gain, the value return to commercial cow-calf users of GeneMax Advantage technology for replacement heifer selection was estimated. Along with testing and selection rates described above, it was assumed that selected heifers produce 6 calves lifetime and testing cost is $39/head. Revenue is generated from selected females and their descendants (retained daughters' and their marketed progeny, as well as marketed steer and heifer progeny) and is discounted at a rate of 6% back to year one in which testing costs were incurred. The inclusion of descendants is important because a key component of genetic improvement is the transmission of favorable genes to an animal's offspring. Selection intensity in each generation of descendants was assumed to be equivalent to that of the original selected heifers.

In the first year, only testing costs are incurred from both selected and culled heifers and no revenue is generated. Beginning in year 2 and continuing through year 7, revenue is generated through the selected heifers' offspring (6), grand-offspring from daughters (up to 10) and great-grand-offspring from grand-daughters (up to 3). Figure 3 depicts annual cumulative returns to the original investment of genomically tested candidate heifers.

Figure 3. Discounted lifetime returns generated from the initial genomic testing investment.



In the scenario considered, break even occurs between years 3 and 4 in the original tested heifer's lifetime. Revenues increase considerably from years 4 through 7, where descendants also significantly contribute to total value and demonstrate the added value of this technology to future generations. Under assumptions considered here, there is a potential of approximately $300 additional lifetime profit per female from a more informed heifer selection decision.

To put this into perspective, a $39 test cost is approximately $15 more than what would be spent on a typical vaccination and deworming program on a replacement heifer up until her first calving and represents about 43% of what would be spent on her health protocol through six calving crops. Preventative health management is an integral part of minimizing risk and optimizing cow lifetime productivity and genomic testing provides an additional tool to identify replacement heifers with the highest potential lifetime productivity.

Other Potential Uses of the Genomic Results

Another practical feature of this technology is Sire Match where registered HD-50K and i50K tested bull batteries are specifically matched to daughters that originated from multi-sire pastures and or AI sires. This can then also be used to either manage inbreeding and associated

impacts on reproductive, fitness and survival traits as well as for corrective mating to optimally match the heifers and potential breeding sires' strengths and weaknesses.

In addition to using results to select and mate replacement heifers, there are other potential uses of genomic testing of commercial heifers. For example, where more heifers are tested than needed, excess heifers can be marketed to other producers as value added replacements. In the case of custom heifer growers, genomic tests and their accompanying index rankings may be used to price heifers accordingly. The Show Me Select program in Missouri is an example of where genomic information is being used to market replacement heifers at a premium compared to non-tested heifers (Decker, 2016).

Likewise when combined with bull battery GE-EPD information, the steer/herd mates and or progeny of tested and selected heifers and cows now possess more documented genetic merit for post-weaning feedlot gain, feed efficiency and carcass performance, and increasingly may be sold as value added feeder calves through programs such as Reputation Feeder Cattle and Top Dollar Angus (http://reputationfeedercattle.com; http://www.topdollarangus.com). These programs are conduits through which commercial cow-calf adopters of genomic technology can derive greater immediate returns from their investment in testing and begin to change traditional paradigms associated with feeder cattle price discovery.

Summary

Genomic testing is now becoming more widely available to the commercial beef industry to help make more informed decisions associated with the replacement heifer enterprise. While tests are available to more accurately identify heifers with highest genetic merit for maternal, feedlot performance and carcass characteristics at a very young age, it is important to understand the amount of genetic variation explained in the tested population and the sources of value return from the investment in testing. These sources of return include more informed selection and culling decisions, lifetime complimentary mating decisions (and associated bull/semen buying), as well as the more immediate impact of feeder cattle price discovery.

The technology presented here offers producers valuable information based on arguably the most accurate genomic predictions available to the beef industry for the target population of seventy-five percent and higher Black Angus replacement heifer candidates. Depending upon the producers' goals, different economic selection indexes more correctly identify replacement heifers to fit their production system and generate higher lifetime net returns. If these indexes are used on an ongoing basis along with intense sire selection, significant genetic improvement and expressed productivity can be achieved. Genetic improvement is a long-term investment and utilization of tools such as genomic selection can help mitigate risks and increase the opportunity for better performance and financial returns to commercial beef producers.

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Genomics: Return on Investment - Fact or Fiction?

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Introduction

For nearly a decade, genomic technology has been incorporated into selection decisions made in the livestock industry. Genomic technology can be used in livestock production (cattle) in several ways: 1) accelerating genetic progress by increasing selection pressure through the use of genomically-tested seedstock, 2) selecting for difficult to measure traits (feed intake, etc.) 3) selecting replacement heifers at both the commercial and seedstock level, 4) marketing and selling pedigreed livestock at premium prices, 5) determining parentage in multiple sire pastures and for sire/dam verification for increased accuracy in genetic predictions, 6) monitoring genetic mutations to avoid economic losses from affected progeny, 7) developing and deploying mating plans to achieve genetic gain while controlling inbreeding and 8) combining genomics, EPDs and reproduction technologies (IVF-MOET, Embryo Transfer, single cell analysis on embryos) to rapidly accelerate genetic change and reduce generation interval. The rate of adoption of genomic technology has varied between livestock species, as well as between breeds and segments within the species. Initially, adoption was primarily hindered due to cost, efficacy of the tests and scope of the traits available for genomic selection.

Today, for most species and many breeds within those species, moderately efficacious tests are utilized across a wide variety of traits, however the debate still exists on how to determine when the technology is economically beneficial for the end-user producer. This paper will discuss the application of genomic technology and potential return on investment (ROI) for the various phases of the U.S. beef cattle industry: seedstock, commercial/cow-calf, and feed yard. While many of the published ROI examples are from dairy, it is expected that similar thoughts can be applied to beef and several research groups are working toward that end.

How does genomic analysis pay?

The potential streams for return on investment for genomic technology can be sorted into two categories, increases in profit due to genetic improvement and increases in profit unrelated to genetic improvement.

In order to recognize a return on investment due to genetic improvement, more rapid genetic progress must be made through manipulating the variables impacting the rate of genetic change (accuracy of selection, selection intensity, generation interval, and genetic variation (Figure 1)) and/or realizing cost savings due to decreased expenses associated with retaining breeding animals or gains in efficiency due to performance. Items unrelated to genetic improvement, but that may provide a return for investing in genetic technology are making better mating decisions and marketing animals.

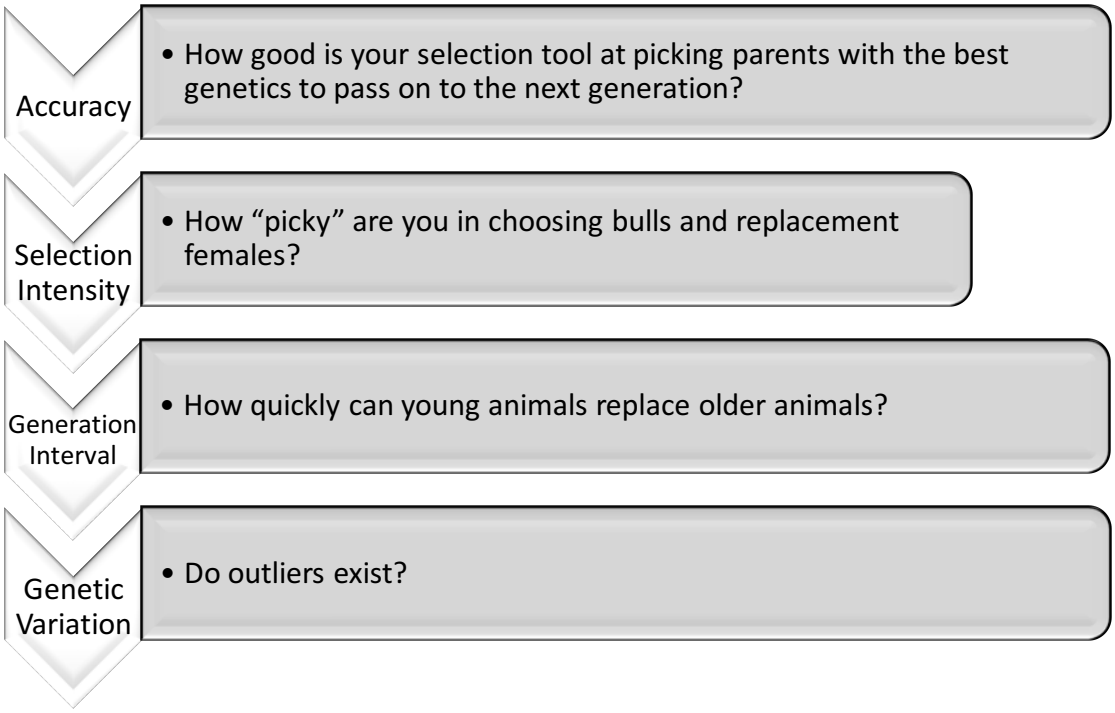


Figure 1: Variables Impacting Rate of Genetic Change

Seedstock

Early on, the return on investment for genomic testing was recognized in the dairy industry.

In their model of the German dairy industry, König et al. (2009) showed the economic advantage in various genomic breeding programs compared to the conventional progeny-test breeding program that was typical at the time. Genomic breeding programs considered costs of genotyping, selection intensity, degree of use of young sires with genotypes only compared to young bulls with some daughter records, and different accuracies for genomic indexes for bulls and cows. In all scenarios considered, genomic breeding programs offered 1.36 to 2.59 times the economic advantage over a traditional program. This assumed that the accuracy of genomic EBVs was at least .7, which would be equivalent to about .29 for BIF accuracy. This is less than the accuracy attained by genomic-enhanced EPDs currently offered by most beef breed associations.

Similarly, in a small, Dutch dairy population, Thomasen et al., (2014) showed that all genomic selection scenarios (one a hybrid system using both progeny-tested bulls and young genomically-tested bulls and the other a system using only young, genomically-tested bulls) were superior to the conventional progeny-test system from a profit standpoint.

In beef cattle in Australia, Van Eenennaam et al. (2011) estimated that use of genomic testing increased selection response between 29 and 158% depending on marketing method and the type of index (maternal or terminal). For commercial bulls and stud bulls, this improvement was valued between AU$89-$565/hd and $5,332-$27,910/hd, respectively, above traditional

performance testing. On a per test basis (because the entire bull calf crop was tested, but not all went on to be AI sires or even commercial bulls) the value of the DNA test was $204-$1,119 per test purchased.

Increasing revenue due to an improvement in the rate of genetic change caused by improved accuracy of selection criteria is certainly partially responsible for economic advantages obtained through genomic testing. However, some studies in dairy cattle have suggested the majority of the economic advantage is derived from cost savings associated with keeping, testing, and maintaining fewer bulls for shorter periods of time (Thomasen et al., 2014, Pryce and Hayes, 2012).

This cost savings was illustrated nicely in New Zealand, where prior to implementation of genomic selection, one farming cooperative progeny tested nearly 300 bulls per year. After adopting the use of genomic testing in young bulls, the number dropped to 160. It was estimated that at that time, the cost to progeny test a bull was $NZ30,000-$40,000 (Spellman, 2012). Thus, progeny testing fewer bulls resulted in a savings of $4.2 million. Additionally, the increased use of young sires was estimated to increase genetic gain by 40-50%.

Similarly, Schaeffer (2006) estimated progeny testing bulls would cost the Canadian AI industry CAD$25 million/year (500 bulls at $50,000 per bull). If this cost were attributed only to the 20 bulls returned to service, the cost of progeny testing was $1.25 million/bull at that time. After accounting for generation interval, accuracy of selection, and selection intensity the cost to the industry of changing the population by one genetic standard deviation was $116 million. The cost for implementing a genomic selection scenario was estimated to be $1.95 million in total, but that investment reduced the cost of proving bulls by 92% and the cost of a one genetic standard deviation change was reduced to $4.17 million. This a is reduction in cost to the industry of over $111 million/yr at a time when the cost of genotyping was $500/hd.

Commercial/Cow-calf sector

Work in the dairy industry has shown that the major factors impacting return on genomic selection at the commercial level are: the cost of the test, the accuracy of the test, the proportion of females that will be retained, and the information already available to make selection decisions (Spellman et al., 2012; Pryce and Hayes, 2012; Weigel et al., 2012), preliminary work in the U.S. cow/calf sector indicates the factors impacting return on investment for testing would be similar.

Weigel et al. (2012) examined breeding strategies that used genomic testing in commercial dairy females compared to breeding strategies that did not. After accounting for the cost of testing in the selected females and their unselected contemporaries, they analyzed the difference in the lifetime net merit breeding value (LNM$). In all cases, the strategies that used genetic testing resulted in higher LNM$. However, the greatest advantages where seen when testing was done in the youngest animals (heifer calves) with very little other information (no known pedigree) and when selection intensity was very high (many animals were culled). For example, LNM$ averaged $28 more for selected females than their unselected contemporaries when the top 90% were retained, when only the top 20% of females were retained, the difference

grew to $259. When sire was known, the differences between keeping the top 90% vs the top 20% shrunk to $14 and $121, respectively.

Decker (2015) used the University of Missouri herd as an example for the value of genomic testing in commercial beef cattle. These high-percentage Angus commercial heifers were tested with GeneMax™ Advantage test from Zoetis. The average Total Advantage score for all tested heifers was 77.8 (Figure 2). If the top 60% of the heifers were kept, (the bottom 40% culled) the average increased to 86.2 (Figure 3), at $1.50/per 1-point increase in score, this meant that the selected heifers were expected to be $63/hd more profitable over their lifetime (assuming 5 calves) than the whole group (Figure 4).

Figure 2. Average, minimum and maximum GeneMax Total Advantage scores for all tested heifers.

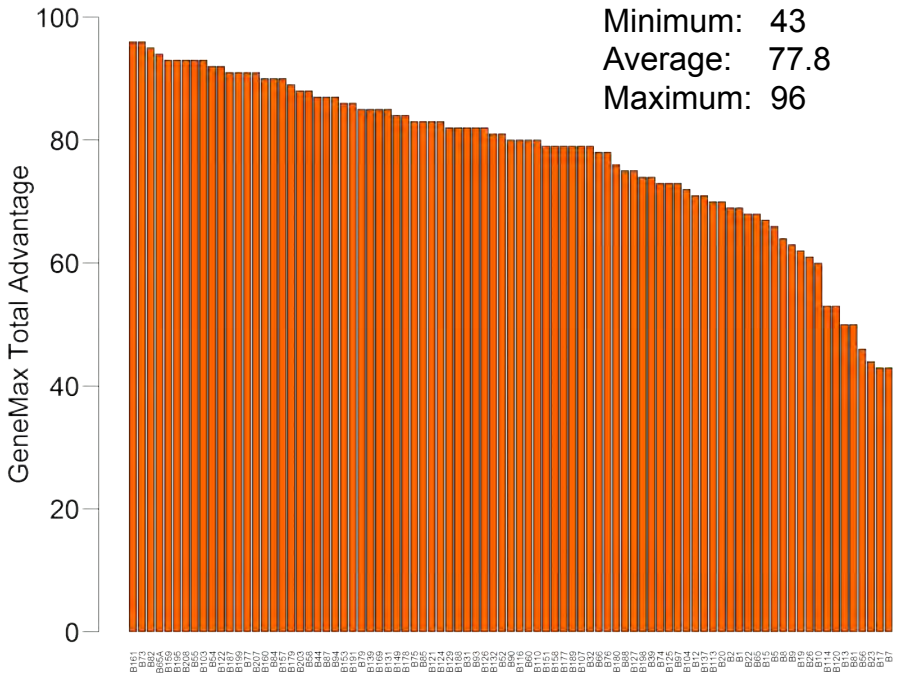


Figure 3. Average, minimum and maximum GeneMax Total Advantage scores for top 60% of heifers

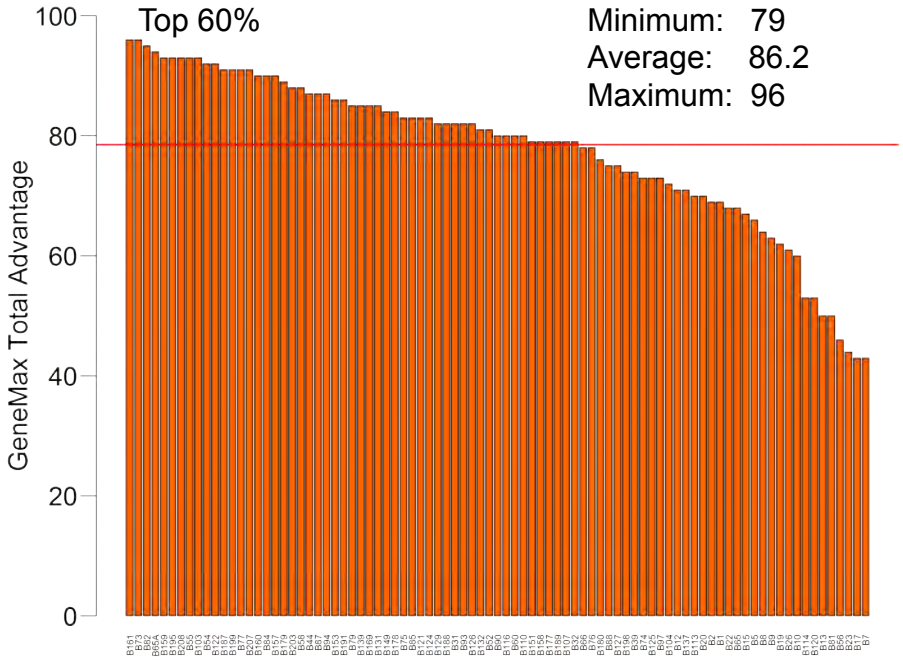
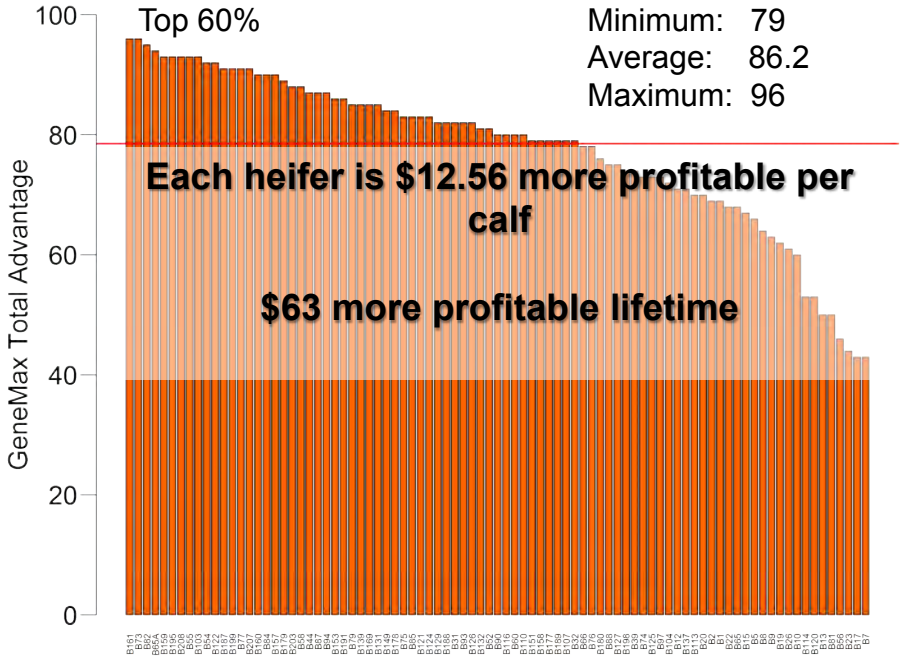


Figure 4. Annual and lifetime profit difference between the tested group and top 60%.



Several published documents do caution that genomic testing at the commercial level may not pay in all instances. Van Eenennaam and Drake (2012) estimated that in Australia, the breakeven cost for DNA testing all potential replacement candidates (when no other information was available) was AU$13 for the domestic market and $24 if targeting the export market. If other sources of information were available, such as the heifer's own 400 day weight, this breakeven cost dropped to $8. It's important to note that this analysis only evaluated the benefit of the technology for retaining animals in the herd, but using the technology to make mating decisions was not considered, which is a loss in the value of the technology.

Pryce (2014) also explored the economic returns expected when genomic-tested females were retained as replacement heifers in the Australian dairy industry. In a 100 cow dairy, when the cost of the genomic analysis was $AU 60 and the majority of heifers were needed as replacements, there were situations when testing did not make economic sense (Table 1). However, when the cost of the test was lowered to $40, all levels of selection intensity favored use of genomic technology (Table 2). Again, this analysis focused on the value of genomics for selection purposes, but not the value of using results for more strategic mating.

Table 1. Net Profit after Genotyping Costs at $60/hd

		Heifers retained			
		15	20	25	30
Heifers available	20	-5.07			
	25	13.87	-13.11		
	30	21.10	6.45	-18.98	
	40	18.82	21.10	1129	-5.07
	50	4.96	20.81	21.10	13.87

Table 2. Net Profit after Genotyping Costs at $40/hd

		Heifers retained			
		15	20	25	30
Heifers available	20	21.60			
	25	47.20	11.89		
	30	61.10	36.45	5.02	
	40	72.16	61.10	43.29	21.60
	50	71.62	70.81	61.10	47.20

Feeder Cattle

Early promise for genomic technology suggested that perhaps it could be used to manage feedlot cattle by sorting them into similar groups based on genomic results. However, Thompson et al. (2014) showed that increases in profit due to marker assisted management were extremely small (less than $3 per head). On the other hand, using genomic results to select cattle for placement in the feed yard holds more promise with expected increases in profit by up to $38/hd, with average daily gain and marbling being the traits that contribute to the greatest increase in profit. In fact, there are programs that have been deployed in the industry in the last 3

years that have recognized the benefit of genetically differentiating feeder cattle (for example Top Dollar Angus and Reputation Feeder Cattle).

Compared to traditional methods of marketing feeder cattle (marketing whole groups live, dressed, or on a grid), using genomic technology to sort them into marketing groups does improve the opportunity for profit (Thompson et al., 2015). However, profit realized (from $1-$8.51/hd depending on how cattle were marketed previously compared to after using genomic results) is not enough to cover the cost of genomic testing at this time.

So, for use in feeder and fed cattle, it appears that genomic technology holds the most promise for use in selecting them for placement (Thompson et al., 2014; Thompson et al. 2015). With commercially-available tests, targeted panels that focus on the key profit-driving traits (currently, marbling and gain) are the most promising for a return on investment. However, if there was a value proposition for palatability traits such as tenderness, genomics would be a key driver in realizing a more consistently palatable product to the consumer and more profit to the producer (Weaber and Lusk, 2010).

In the meantime, an opportunity exists to test a random sample of animals and extrapolate results to make informed decisions, and achieve significant return on investment (up to 250%) while testing as few as 10% of the animals (Thompson et al., 2016) in a management group.

With continued research, the potential exists to use genomics in feedlot cattle to manage cattle for performance, health status, and response to certain treatment regimes. Also the possibility to use genomics to understand the interaction of microbiome DNA with host DNA to improve economic traits such as feed efficiency (Roehe et al., 2016).

Avoiding Inbreeding

Hybrid vigor and inbreeding depression are the two measureable factors related to the way that genes combine due to mating decisions that cannot be over-looked both from the standpoint of animal performance as well as the opportunity for genomics to contribute real returns.

Inbreeding is defined as the mating of individuals that share a common ancestor and it has implications because it's been shown to have a deleterious impact on fertility, longevity, disease resistance and other lowly-heritable traits. In addition, inbreeding can increase the risk recessive abnormalities. The ability of genomics to more accurately measure and manage inbreeding is an under-utilized feature of the technology that should yield returns in improved performance and greater return on investment for genomic testing.

Pryce (2014) indicated that a 1% increase in inbreeding decreased milk production by 21 liters, and decreased fat and protein by 0.73 kg and 0.63 kg, respectively. For every 1% increase in inbreeding, these performance reductions were estimated to cost $20 per cow.

Classically, avoiding inbreeding has been managed through pedigree relationships and assuming that relatives shared a certain quantity of their genome due to inheritance from a common ancestor. In fact, relatives may have much more in common than a simple pedigree

relationship would reveal. To do a better job of managing inbreeding Pryce (2014) illustrated that using current high-density and low-density genomic panels could be used to do a better job of managing inbreeding by calculating genomic relationship between animals. Using mating software combined with a threshold level of inbreeding allowable, farmers will be able to manage inbreeding by making wiser mating choices. To date, this has been an under-utilized feature in the beef industry that deserves real consideration.

It should not go without mention that simple process of parent verification has a crucial impact on the accuracy of genetic evaluations and that genomic technology is the basis for this important verification.

Conclusion

Genomic testing in the livestock industry is rapidly becoming more predictable as databases grow, costs per analysis decrease, and more traits are included. Return on investment to the end user is an individualized estimate based on breeding objectives, intended use, and market needs of that specific operation.

Though not explicitly mentioned in this document, testing for genetic conditions, assuming a reasonable gene frequency, is nearly always justifiable (VanEenennaam and Drake, 2012).

However, for genomic trait tests, the answer is a bit more complicated. At the seedstock level, given the accuracy, price, and range of traits covered by current tests, testing is genetically and economically a wise decision, speeding up genetic progress and reducing risk of selecting animals that will under-perform expectations in the market place. As a management tool, genomic analysis is just beginning to be used in the dairy industry for health traits and in the foreseeable future will expand to include how the animal's own genotype interacts with the environment it is exposed to.

The combination of advanced reproductive tools and genomics is revolutionizing products offered to cattle producers, driving genetic progress at a faster pace and to heights only imagined a short decade ago. Along with this revolution, progressive commercial operations will find new ways to access higher performing genetics for their herds than what was previously possible, changing the dynamics of the relationship between seedstock and commercial cattle producers. What role will breed associations and performance recording groups play in the future of the beef cattle industry? Who will own the superior genetics in the future?

Commercial producers already have access to the same advanced genetic tools that seedstock producers have, and can use them to drive their own herd improvement in a much more aggressive way than they are doing today. Genomics combined with their own herd records gives them the opportunity to identify the best animals in their herds and then chart a course for within-herd improvement at a greater magnitude than ever possible before.

The value of genomic technology in returns to the producer is well-documented in dairy and is beginning to be proven in beef cattle as well. The value to bull-studs through reduced progeny testing is especially evident, possibly saving that industry over 90% of the cost

associated with proving bulls (Schaeffer, 2006). Are bull-buyers willing to pay for this technology? In work submitted for publication in 2011, Vestal et al. (2012), found there was no evidence that bull buyers were willing to pay for DNA profile information for beef bulls available at auction. However, those authors did concede that willingness would likely change over time as buyers became more comfortable and confident in DNA test results. Indeed, much has changed since that time. The technology has improved and considerable time and resources have been invested in outreach and education efforts related to genomic technology. There is preliminary evidence that producers investing in commercial replacement females have been willing to pay $200 more per head for those that have been genomically tested (Decker, 2016). Combined with forthcoming results from Short et al., (2016) and MacNeil (2016), that suggest similar values at the commercial and seedstock level, it's becoming apparent that the value proposition for genomic testing in beef cattle is strong.

There does seem to be some fear on the part of breeders that testing may discount some animals with "undesirable" genomic results. Interestingly, Vestal et al., 2012 found that having no information (a blank box) in a sale catalog resulted in steeper discounts for some traits than having information that could be viewed as "bad". Additionally, though genomic testing may reveal some animals that have less-than-desired genetic potential, it also stands to discover others that would not have been deemed as value based on classic evaluation criteria.

At the feed yard level, widespread testing of pens of animals may not be economically advantageous at the moment in the commodity beef market, but may be justifiable in branded beef programs where guaranteeing a positive eating experience for the consumer is paramount.

Continued collection of data and development of new or improved tests focusing on traits that contribute directly to profit is important to support more definitive return on investment for the cow-calf and feedlot sectors. With fertility being the major profit driver at the commercial cow-calf level, a concerted effort needs to be made to gather service and breeding data for use in improvement and development of genomic tests. The field of nutrigenomics, which studies how differences in feed types and gut-microbe DNA interact with genotype of the animal, offers much promise in providing opportunities for efficiency and performance gains in the feed yard.

All sectors of the beef cattle industry could benefit from genomic selection under certain scenarios. Continued cooperation among producers, researchers, breeding and genomics companies, and consumers offers the best opportunity for tools that can be used to increase profits for cattlemen in the months and years to come.

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Genetic evaluation for heat tolerance in Angus cattle

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Introduction

Because beef cattle are raised in extensive conditions, growth can vary across production environments. Within-breed genotype x environment interactions have been reported for weaning weight and yearling weight (Butts et al., 1971; Bertrand et al., 1987). When Hereford cattle were adapted to the Florida or the Montana climate, calves had 20 lb heavier weaning weights when grown in the environment they were adapted to (Butts et al., 1971). Genetic lines within a breed differ in their adaptability to specific regions. Thus, selection would be more accurate when using genetic predictions specific to a given environment.

Part of this genotype x environment interaction could be attributed to differences in heat tolerance, an economically important trait for livestock producers in certain environments. In the beef industry, total economic losses from heat stress are estimated to be greater than $360 million annually (St.-Pierre et al., 2003). Heat stress reduces feed intake, growth, milk production, and pregnancy percentage. Angus experience greater physiological effects of heat stress than *Bos indicus* and tropically adapted *Bos Taurus* breeds (Hammond et al., 1996). With Angus dominating the United States (US) beef industry, improving heat tolerance can have a large economic impact nationally and can increase the use of Angus genetics in regions with greater heat stress.

Livestock populations can be selected for improved heat tolerance if genetic variation exists for the phenotype associated with greater temperatures. Genetic evaluations have been developed to identify those animals that are more robust to changes in temperature-humidity index (**THI**; Ravagnolo and Misztal, 2000; Zumbach et al., 2008b). As weather patterns become more erratic and global warming continues, the more robust animals will be more productive and profitable for farmers. Temperature data can be incorporated into genetic evaluations using reaction norms, which yield EPD based on different THI values. These methods have been applied to dairy, swine, and beef cattle to create selection tools for heat tolerance.

Modeling heat stress

Heat stress was characterized using THI (Zumbach et al., 2008a). These THI data were obtained from public weather station databases, because previous research demonstrated that off-farm weather data was just as useful as on-farm data for assessing heat load (Freitas et al., 2006). Heat stress was based on weather conditions for 30 days before the weaning weigh date. The average THI for this period was used for the analysis. If the average THI was less than 75 °F, then the THI was set to 75 °F, and these animals were not expected to be heat stressed. All

animals in a weaning contemporary group were exposed to the same environmental conditions and had the same amount of heat stress.

Weaning weights from the South region were used to develop a heat tolerance genetic evaluation. Heat stress was incorporated into a reaction norm model resulting in environment-specific EPD for weaning weight and maternal milk. Additionally, weight was evaluated using a univariate model similar to a traditional growth evaluation for comparison.

Results

Heritabilities for weaning weight were greatest for large THI indicating that genetic variation exists to select for heat tolerance. Genetic correlations between THI values of ≤ 75 and ≥ 82 °F were less than 0.50 and were indicative of weaning weights being different traits depending on the environmental temperature. Sire rankings were assessed for bulls with at least 25 progeny with weaning weights. The rank correlation for proven sires was 0.32 between THI of ≤ 75 and 85 °F. Producers would select different bulls depending on the THI for their location for the 30 days prior to weaning. Greater response to selection could be achieved by selecting bulls that were best adapted to the climatic conditions.

Conversely, heritabilities for maternal milk were consistent across heat loads indicating no change in genetic variability across environmental temperatures. Genetic correlations were strong between different heat load values with little re-ranking of proven sires. Possibly, heat stress affects cows by decreasing fertility and body condition but not milk production as measured by calf growth. Thus, milk can be selected across environmental temperatures with similar response to selection.

Reaction norms for the 10 greatest (black) and least (grey) weaning weight proven sires from the univariate model are presented in Fig. 1. This figure presents the EPD for each bull based on THI from ≤ 75 to 85 °F. Bulls with straight lines would be expected to produce progeny with similar growth across THI environments. If the line decreases from left to right, that bull's progeny are expected to grow less as THI increases and have poor heat tolerance. If the line increases from left to right, the bull's progeny are expected to grow more as THI increases and have good heat tolerance. Because the lines for some of the greatest (black) and least (grey) growth sires cross, those sires would be expected to have similar progeny growth in environments with large THI even though the greatest growth sires were clearly superior for lesser environmental temperatures.

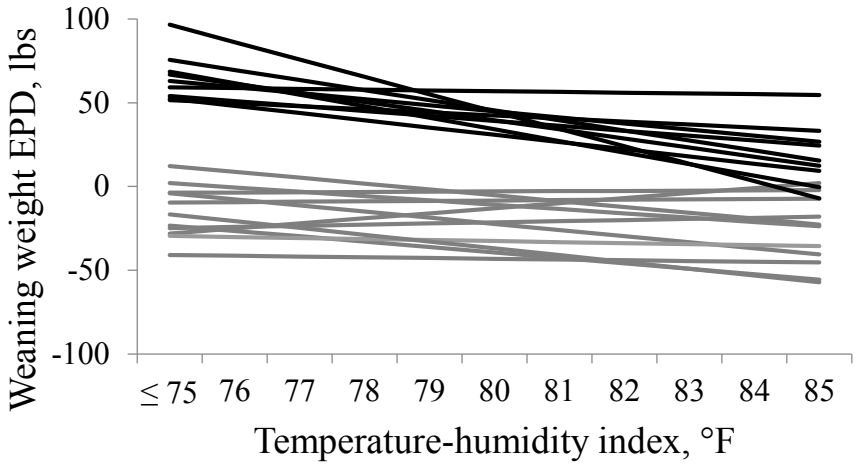

Fig. 1. Reaction norms for the 10 proven bulls with the greatest (black) or least (grey) weaning weight direct EBV from the univariate analysis for Angus in the South region

The genetic trends for weaning weight based on 3 THI values are illustrated in Fig. 2. Weaning weight was less for greater THI indicating growth genetic potential was less in hot environments. Genetic merit has been increasing for THI of ≤ 75 and 80 °F but has started decreasing for THI of 85 °F. Thus, current selection practices in the Angus breed may be qreducing heat tolerance in the South. Angus breeders would benefit from selection tools to improve or maintain heat tolerance in areas affected by heat stress.

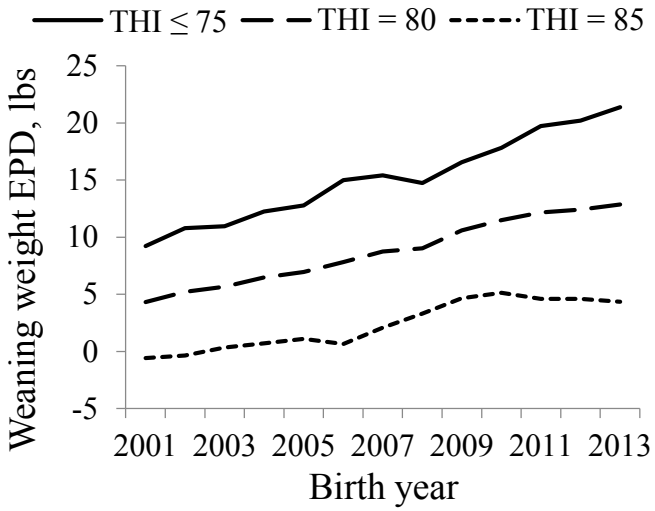

Fig. 2. Genetic trend for weaning weight direct from the reaction norm based on 3 temperature-humidity index (THI) values for Angus in the South region

Conclusions

Genetic variation exists for heat tolerance in Angus, and these cattle can be selected to improve weaning heat tolerance. Proven sires rank differently depending on THI, which has

consequences for selection and mating decisions. Producers in the South region would benefit from environment-specific selection tools to identify the best growth sires for the specific climatic conditions. Additionally, Angus breeders should be concerned about weaning heat tolerance because of the decreasing genetic trend for weaning weight in extreme heat stress.

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Commercial Producer Award Nominees

Hobbs Ranch
Owner: Terry Hobbs Family
Manager: Terry Hobbs
Penokee, Kansas

Hobbs Ranch was established in 1887. After serving his country in the Civil War, Terry' great-grandfather left Missouri and traveled west, homesteading along the north fork of the Saline River near Penokee, Kansas, in southern Graham County.

For 70 years, both registered and commercial Polled Herefords were raised on the ranch. They were a cooperator herd for the American Polled Hereford Association (APHA), progeny testing young sires, recording data and furnishing the association with all the results. They exhibited their cattle at many state fairs and shows during the 1970s and 1980s. Most of the bulls produced were fed and performance-evaluated at central bull tests not only in Kansas, but in Nebraska, Colorado and Oklahoma as well.

In the early 1990s it was decided to incorporate Angus genetics into the herd. They looked to this breed to complement their Hereford cow herd, gaining hybrid vigor, carcass quality and consistency. Presently, they run more than 500 cows on about 12,000 acres of grass and farmland. Calving season begins the first part of February and wraps up about the end of March. They artificially inseminate 100 replacement heifers and 100 cows annually. All the heifers and cows are exposed to natural service sires during the summer. All the calves are weaned, usually in September and October, and backgrounded at the ranch for 60 to 90 days before being sent to a commercial feedyard, where growth and carcass value data is tracked for use in future bull selection. By retaining all, or part, ownership in their calves, they can take further advantage of the genetics they have in their herd.

The Kansas Livestock Association is proud to nominate the Hobbs Ranch.

Lovers Lane Farms
Owners/Managers: Bill and Jim Martin
Moorefield, West Virginia

Headquarted along the south branch of the Potomac River just north of Moorefield, West Virginia, Lovers Lane Farms is a third-generation, diversified livestock and crop farm managed by brothers Bill and Jim Martin along with their father, Leonard. The Martin family operates on 5,000 acres of owned and leased land spanning four counties, including 1,500 acres of crop land, and 2,500 acres of grazing and hay land, with the balance of the acreage being forested.

They calve 600 commercial Angus-cross cows and graze 350 stockers annually. The Angus based cow herd is sorted according to areas of need and specifically mated to top AI and performance tested Angus and Hereford bulls selected to improve each management group's area(s) of weakness. Replacement heifers are selected using reproductive tract scores, pelvic measurements, and health status as well as individual, sire, and dam performance. Steer calves are weaned and preconditioned at least 45-60 days prior to shipment. In addition to their own calves, the Martins will background 2,500-3,000 purchased calves and fully finish an additional 500 annually.

Home-raised and backgrounded calves as well as stockers are sold via local board sales in load lots to farmer feeders in the Eastern Corn Belt, where the Martin's have developed a reputation for healthy, documented, quality cattle. Finished cattle are marketed through local sales where they are procured for harvest in Eastern Pennsylvania. Because of their location within the Chesapeake Bay Watershed, the Martin's follow a comprehensive nutrient management plan on all managed properties to protect water resources and appropriately allocate manure nutrients from their feeding facilities as well as their six poultry houses where they raise around 200,000 pullets annually for Pilgrim's Pride Corporation.

Lovers Lane Farms is committed to maintaining healthy animals, a healthy environment, and a healthy business for their industry, their community and their family.

The West Virginia Cattlemen's Association is proud to nominate the Lovers Lane Farms.

Commercial Producer Award Nominees

Plum Thicket Farms
Owners: Rex & Nancy Peterson, Patrick & Krista Peterson
Manager: Dr. Nancy Peterson
Gordon, Nebraska

Plum Thicket Farms is located in the panhandle of Nebraska. Average annual precipitation is between 14" and 16". They purchased the core of the ranch in January of 1998 along with 200 Angus cows, calving over four months. At that time, the ranch consisted of 2,078 acres of native range, 170 acres of irrigated alfalfa under a side roll system, and 500 dryland acres in a wheat fallow system. The pastures were all season long grazed and the cattle were fed hay for five months of the year. The calves were sold at weaning.

They now control 4,000 acres of native range, grazed in a rest-deferred rotation grazing system. They no-till farm 2,300 acres, including 560 acres under pivot irrigation. They calve 325 Sim-Angus cows for 45 days, starting in late April. Whole herd AI has been a staple of their program. From the outset, they have maintained detailed individual performance records that follow cattle to the rail. Nancy utilized this data to make bull selections and culling decisions. She has steadily improved the genetic quality of their herd. Utilizing annual forages, their cattle live within an eleven-month grazing program. They breed all of the heifers and select their replacements in the spring after they have had their first calf, selling young pairs that will likely go into a fall calving herd. They background all of the steers on forage cocktails and swathed sorghum supplemented with DDG and often retain ownership through the feed lot. They also run a small backgrounding lot. They are currently developing 300 heifer calves, 32 bull calves, and feeding 140 cull cows.

Plum Thicket Farms are a family operation with a passion for raising excellent beef cattle, and improving the range and soil that are their livelihood. Rex and Nancy head the cattle operation. After two tours of duty with the National Guard, Rex and Nancy's son, Patrick, came home to head the farming operation. Patrick is passionate about improving soil health and conserving resources. His wife, Krista, is a large animal veterinarian with a mobile practice in the area. She did a food animal internship at Kansas State Veterinary School and is a welcome addition to their management team.

The Nebraska Cattlemen are proud to nominate Plum Thicket Farms.

SingleTree Ranch
Owners/Managers: Frank and Sheila Daley
New Castle, Colorado

SingleTree Ranch is a family run cow-calf operation started near New Castle, Colorado, in 1979 with the purchase of 106 acres of mostly irrigated land. An adjoining 160 acres were purchased in 1980 along with 80 head of mostly black baldy cows.

More land, cattle, BLM and Forest Service grazing permits have been acquired over the years. They now run close to 600 cows on two ranches near New Castle and another 250 cows on ranches near Wray, Colorado, added in 2005 and 2007. All calves except mountain replacement heifers are backgrounded in a small feedlot on their ranch at Haigler, Nebraska, just across the state line from Wray.

They feed the feeder calves to around 800 pounds at which time they decide whether to sell them or retain ownership while they are fed out at a custom lot. The dairy buy out in 1985 got them started on retained ownership and they have done it off and on since then. They purchased their first Limousin bulls in 1981 and have used primarily Limousin bulls since. They also have used Angus and a few Herefords.

When they have expanded, they have purchased more cows, mostly Angus and Black Baldies, but have primarily raised their own cow herd. Cows on the mountain ranches are bred to start calving March 1, while those in Wray start April 1. For several years they have been keeping the calves in a "natural" (as per USDA guidelines) and have marketed finished cattle to Coleman Natural Meats, Laura's Lean, Meyer Natural Angus,

National, Tyson, and a few others. Selling on a grid has worked well over the years because of the Limousin's excellent carcass traits. They always have a very high yield and a high percentage yield grade 1's and 2's with large ribeye area. Their mountain cattle summer at elevations from 8,500 to 10,500 feet and they have always appreciated how well the Limousins perform at these elevations.

The North American Limousin Foundation is proud to nominate Single Tree Ranch.

Triple M Farm
Owners: Tommy and Rhonda Martin
Manager: Tommy Martin
Moundville, Alabama

Triple M Farm, owned and operated by Tommy and Rhonda Martin, is located in Hale County, Alabama, just south of Tuscaloosa. The farm began in 1943, when 180 acres was purchased by Tommy's grandparents, and has produced beef cattle for three family generations. After his retirement in 2011, Tommy is operating the farm full-time.

The farm consists of 250 acres of owned land, with an additional 90 acres of leased land, made of sandy loam and clay soils. The forage base primarily consists of Bermudagrass, Bahiagrass and Crabgrass, with annual planting of Ryegrass for winter grazing. Soil fertility and weed control are a major focus.

The Triple M herd consists of approximately 90 Simmental and Angus cross cows with a 90-day fall calving system, beginning to calve around September 25 each year. A SimAngus cross is maintained to balance heterosis to capture benefits in fertility, heavier weights and longevity. Artificial insemination, along with estrus synchronization and fixed-time AI, has made a tremendous impact by providing the ability to capture the highest quality genetics. Emphasis is given in balance to calving ease and growth to produce a live calf with solid growth traits and maternal ability. Feeder calves are marketed each August through a cooperative tele-auction sale to seize fall marketing opportunities. Replacement heifers are selected by evaluating heifer and dam performance histories to advance performance. Triple M Farm began maintaining performance records through the Alabama BCIA Commercial Record Keeping Program in 2000. Since then, Triple M Farms has earned a BCIA Gold Star Cow Award each year for the past 13 years, a Most Improved Herd in 2008 and a Top Weaning Weight Award in 2016.

Triple M Farm is proudly nominated by the Alabama Beef Cattle Improvement Association.

BIF Commercial Producer of the Year

Name	State	Year
Woodbury Farms	Kansas	2015
CB Farms Family Partnership	Kansas	2014
Darnall Ranch, Inc.	Nebraska	2013
Maddux Cattle Company	Nebraska	2012
Quinn Cow Company	Nebraska	2011
Downey Ranch	Kansas	2010
JHL Ranch	Nebraska	2009
Kniebel Farms and Cattle Company	Kansas	2008
Broseco Ranch	Colorado	2007
Pitchfork Ranch	Illinois	2006
Prather Ranch	California	2005
Olsen Ranches, Inc.	Nebraska	2004
Tailgate Ranch	Kansas	2003
Griffith Seedstock	Kansas	2002
Maxey Farms	Virginia	2001
Bill & Claudia Tucker	Virginia	2000
Mossy Creek Farm	Virginia	1999
Giles Family	Kansas	1999
Mike & Priscilla Kasten	Missouri	1998
Randy & Judy Mills	Kansas	1998
Merlin & Bonnie Anderson	Kansas	1997
Virgil & Mary Jo Huseman	Kansas	1996
Joe & Susan Thielen	Kansas	1995
Fran & Beth Dobitz	South Dakota	1994
Jon Ferguson	Kansas	1993
Kopp Family	Oregon	1992
Dave & Sandy Umbarger	Oregon	1991
Mike & Diana Hopper	Oregon	1990
Jerry Adamson	Nebraska	1989
Gary Johnson	Kansas	1988
Rodney G. Oliphant	Kansas	1987
Charles Fariss	Virginia	1986
Glenn Harvey	Oregon	1985
Bob & Sharon Beck	Oregon	1984
Al Smith	Virginia	1983
Sam Hands	Kansas	1982
Henry Gardiner	Kansas	1981
Jess Kilgore	Montana	1980
Bert Hawkins	Oregon	1979
Mose Tucker	Alabama	1978
Mary & Stephen Garst	Iowa	1977
Ron Baker	Oregon	1976
Gene Gates	Kansas	1975
Lloyd Nygard	North Dakota	1974
Pat Wilson	Florida	1973
Chan Cooper	Montana	1972

Seedstock Producer Award Nominees

Brink Livestock
Owners/Managers: Bob and Marilyn Brink
Piedmont, Kansas

Bob and Marilyn Brink of Brink Livestock raise Braunvieh cattle on their ranch near Piedmont, Kansas. The Brinks entered into the registered Braunvieh business in 2000, and in 2005 relocated the operation to a grass-based ranch in the Flint Hills near Piedmont, Kansas.

They have a herd of approximately 100 registered Braunvieh cows, calving in both spring and fall. Brink Livestock markets cattle in a number of outlets. They are a founding member of the Braunvieh Herd Builder Group and have sold cattle in all 13 of the group's annual sales. They also promote and sell their Braunvieh cattle at regional and national livestock shows, and have been proponents of performance testing their Braunvieh bulls. Bob and Marilyn have each served two terms on the Braunvieh Association of America's Board of Directors, and have been strong supporters of youth in the Braunvieh breed.

The Brinks utilize native tallgrass prairie as their primary grazing source, and have worked extensively to be good caretakers of the land through rotational grazing and resting pastures, by controlling invasive species in the range and by improving water quality for livestock and wildlife. Bob grew up on the family farm and ranch in northeast Kansas, which included a herd of registered Hereford cattle as well as crop and haying operations. Marilyn was raised on a farm in Illinois and worked for 17 years with the American Polled Hereford and Hereford Associations.

Brink Livestock is proudly nominated by the Braunvieh Association of America.

Hunt Limousin Ranch
Owners: Charles and Nancy Hunt
Managers: Charles Hunt and son Daniel Hunt
Oxford, Nebraska

"Conserve the land for the future generations, keep current and knowledgeable on the leading cattle issues, high quality cattle for a fair price, and treat people with honesty and integrity." The Charles Hunt Family operation began in the 1960's after Charlie attended the University of Nebraska. With a love for God, family, the land, and cattle Charlie and Nancy were ready for the opportunity to do then what they still enjoy doing today, over 56 years later, raising cattle.

Currently, the 6,500 acre diversified operation consists of dryland and irrigated corn, soybeans, alfalfa, wheat and grass land which supports 300 cows, private treaty bulls, and replacement females. Genetics have been placed all over the globe, including Canada, Mexico, Australia and New Zealand. Bulls have been on display at the National Western Stock Show for the past 31 years and the Hunts have attended many BIF, NCBA, and numerous other Ag conferences. Charlie has been the recipient of many awards including the first ever Commercial Marketing Supporter Award from the North American Limousin Foundation. One of the most prestigious awards was being inducted into the Nebraska Cattlemen's Hall of Fame.

The customers and acquaintances the Hunts have met in the beef industry have become some of their best friends. Hunt Limousin Ranch has hosted tour groups and individuals from foreign countries who want to learn the "Hunt Way". All visitors are welcomed with a homemade meal and hot cup of coffee. Hunts take pride in making bull selection a relaxed, low-stress experience.

Charlie and Nancy have four children; David, Susan, Sally and Daniel and nine grandchildren. Their family is always ready to offer a helping hand on the ranch. One of their greatest honors is to have Dan, his wife Melinda, and their children Jenna, Adeline, and Houston living and working beside them, benefiting Hunt Limousin Ranch and the beef industry.

The Nebraska Cattlemen and the North American Limousin Foundation is proud to nominate the Hunt Limousin Ranch.

Seedstock Producer Award Nominees

Little Creek Farm
Owners: Dr. Mikell and Mary Cheek Davis
Manager: Alex Gardner
Starkville, Mississippi

Little Creek Farm, LLC is located in Oktibbeha County, Mississippi near the city of Starkville. Twelve cows (four Polled Herefords, four Purebred Simmentals, and four Fullblood Simmental) were purchased in 1992. Two Full Fleckvieh Simmental heifers were purchased in 1993. Those two heifers began the Fleckvieh journey that continues today.

Red Angus cattle were added to the operation in 2004 with the primary intention to breed the cows to Fleckvieh bulls to demonstrate the impact of Fleckvieh genetics in a crossbreeding program. They made the strategic decision to maintain a Red Angus herd along with the Fleckvieh herd and to produce the Fleck-Angus crossbreds with the goal to retain the crossbred females as recipients for their embryo transfer program.

Little Creek began with a 57-acre home place location. Since 1994 six parcels have been purchased which resulted in a total of 850 acres, of which 100 acres are dedicated to hay production.

Little Creek maintains a two-hundred cow herd: 50 AI quality Fleckvieh cows, 35 AI quality Red Angus cows, and 115 embryo recipients. Embryo donor cows are selected from the two AI herds based on the cows' conformation, structural correctness (with emphasis on feet, legs, and udder), maternal qualities, ease of maintenance, and the quality of their offspring.

The Mississippi Beef Cattle Improvement Association is proud to nominate the Little Creek Farm.

Mill Brae Ranch
Owners: T.D. Steele, Roger Steele, and Mark Nikkel
Manager: Mark Nikkel
Maple Hill, Kansas

Mill Brae Ranch is located in the Flint Hills region of eastern Kansas near Maple Hill. Comprised mainly of warm-season grasses, this region is a portion of the last tallgrass prairie left in North America.

T.D. and Roger Steele purchased the ranch in 1986 in an effort to expand their operation and bull sales. In the spring of 1987, Mark Nikkel was hired as herdsman for Mill Brae and three years later he assumed the day-to-day management of the ranch. In 2001, the Steele family offered Mark and his wife, Janice, the opportunity to join the operation as partners and Mill Brae Ranch LLC was formed. Mark and Janice's daughter, Taylor, is actively involved on the ranch when she is not in school or participating in school, 4-H/FFA or junior breed association activities.

Today, operating on 5,000 acres of owned and leased land, Mill Brae Ranch runs a spring-calving herd consisting of 400 registered Angus and SimAngus cows and 150 commercial cows. The foundation females for the registered Angus cow herd trace back to the highly productive dams the Steele family used to establish their original cow herd in 1950. SimAngus genetics were added in 2013, in response to the needs of their commercial customers.

The registered cows are synchronized and artificially inseminated (AI) to proven high-accuracy bulls that rank in the top 15% in the breed for birthweight and weaning and yearling growth traits. Their main focus is to produce low birthweight, high-growth seedstock, with acceptable carcass traits, excellent udder quality and structural correctness. A portion of the commercial cow herd is used as recipients for the embryo transfer program. About 70 embryos are put in per year out of only highly proven donor cows, which allows them to duplicate their most superior genetics.

Mill Brae Ranch is proudly nominated by the Kansas Livestock Association.

Shaw Cattle Company
Owners: Shaw Family
Managers: Greg, Tucker and Sam Shaw
Caldwell, Idaho

The origin of Shaw Cattle Co. began with a Hereford heifer. Tom Shaw worked weekends and summers throughout high school for a neighbor. After high school and upon his return from the U.S. Navy, the heifer was given to Tom as payment for his summers and a thanks for serving his country. The registered Hereford heifer became the foundation of Shaw Hereford Ranch in 1946. By 1959, Tom had married Mary, started a family and purchased a home near Notus, Idaho. The family moved from the original Shaw homestead to the current headquarters and continued to build a cow herd and raise a family.

Tom and Mary's youngest son, Greg, officially joined the operation after graduation in 1968 and married Cleo two years later. In 1988, the Shaw cow herd was divided into three herds. Greg and Cleo, remained on the original home place at Caldwell to raise their three children Tucker, Sam and Jaime, and subsequently, formed Shaw Cattle Co. The third and fourth generations are continuing the tradition of raising reputable performance cattle. In 1990, Shaw Cattle Co. diversified the Hereford cow herd and added Red Angus genetics. In 1996, black Angus cattle were added to the herd. Today, Shaw Cattle Company maintains over 1,500 registered cows encompassing three breeds. The Shaw's continue to improve the cow herd through the diligent selection of breed leading genetics with a keen eye toward performance, science and technology.

Greg and Cleo's son, Sam, returned to the ranch in 1999, after graduating from the University of Idaho. Sam and his wife, Janel, are raising their three daughters on the ranch. After graduating from the University of Idaho and working in the private sector, Tucker returned with his wife, Angie, in 2003, and are raising their five children on the ranch. Greg and Cleo's daughter Jaime, husband Kelley, and two daughters live in Eugene, Oregon, and enjoy helping out on the ranch when they can.

The American Hereford Association is proud to nominate the Shaw Cattle Company.

Turner Farm
Owners: J.B. and Barbara Turner, Jr.
Manager: J.B. Turner, Jr.
Harvest, Alabama

Turner Farms is a diversified family operation, producing cattle and vegetables and is located in Madison County, Alabama. Turner Farms is owned and operated by J. B. Turner, Jr. and family, and has a firm commitment to producing high quality Angus and SimAngus seedstock and also F-1 Hereford/Angus cross females.

Their breeding program onsists of approximately 80 mature cows and utilizes proven AI sires and embryo transfer to accelerate genetic advancement.Genetic selection emphasizes balanced EPDs along with visual appraisal to produce cattle with longevity and performance. Donor selection is an intensive, ongoing process involving analysis of a potential donor's pedigree, production record and performance of her progeny. The American Simmental Association's Total Herd Enrollment program and also the American Angus Association's AHIR program are used for performance evaluation and analysis.

Turner Farms takes advantage of both a fall and spring calving season to meet the farm's overall marketing goals. Turner Farms has evaluated the performance of their genetics through the Alabama BCIA North Alabama Bull Evaluation for the past 7 years. Top quality commercial replacement heifers from Turner Farms have been a highlight of the North Alabama BCIA Heifer Sale for the past 10 years.

J. B. Turner is a steadfast conservationist and has applied many USDA NRCS programs within his operation since the 1980s. His application of rotational grazing, cross fencing, improved water facilities and nutrient management has increased the land efficiency of his acreage. His commitment to operating in an environmentally sustainable manner was recognized with the honor of the 2016 Alabama NRCS Small Farmer of the Year and the national USDA NRCS Lloyd Wright Small Farmer of the Year Awards.

The Alabama Beef Cattle Improvement Association is proud to nominate the Turner Farm.

BIF Seedstock Producer of the Year

Name	State	Year
McCurry Angus Ranch	Kansas	2015
Schuler Red Angus	Nebraska	2014
Bradley 3 Ranch	Texas	2013
V8 Ranch	Texas	2012
Mushrush Red Angus	Kansas	2011
Sandhill Farms	Kansas	2010
Harrell Hereford Ranch	Oregon	2009
Champion Hill	Ohio	2009
TC Ranch	Nebraska	2008
Pelton Simmental Red Angus	Kansas	2007
Sauk Valley Angus	Illinois	2006
Rishel Angus	Nebraska	2005
Camp Cooley Ranch	Texas	2004
Moser Ranch	Kansas	2003
Circle A Ranch	Missouri	2002
Sydenstricker Angus Farms	Missouri	2001
Fink Beef Genetics	Kansas	2000
Morven Farms	Virginia	1999
Knoll Crest Farms	Virginia	1998
Flying H Genetics	Nebraska	1998
Wehrmann Angus Ranch	Virginia	1997
Bob & Gloria Thomas	Oregon	1997
Frank Felton	Missouri	1996
Tom & Carolyn Perrier	Kansas	1995
Richard Janssen	Kansas	1994
R.A. “Rob” Brown	Texas	1993
J. David Nichols	Iowa	1993
Leonard Wulf & Sons	Minnesota	1992
Summitcrest Farms	Ohio	1991
Douglas & Molly Hoff	South Dakota	1990
Glynn Debter	Alabama	1989
W.T. “Bill” Bennett	Washington	1988
Henry Gardiner	Kansas	1987
Leonard Lodoen	North Dakota	1986
Ric Hoyt	Oregon	1985
Lee Nichols	Iowa	1984
Bill Borror	California	1983
A.F. “Frankie” Flint	New Mexico	1982
Bob Dickinson	Kansas	1981
Bill Wolfe	Oregon	1980
Jim Wolf	Nebraska	1979
James D. Bennett	Virginia	1978
Glenn Burrows	New Mexico	1977
Jorgenson Brothers	South Dakota	1976
Leslie J. Holden	Montana	1975
Jack Cooper	Montana	1975
Carlton Corbin	Oklahoma	1974
Mrs. R. W. Jones, Jr.	Georgia	1973
John Crowe	California	1972

BIF Ambassador Award Past Recipients

Name	Publications	State	Year
E. C. Larkin	Gulf Coast Cattlemen	Texas	2015
John Maday	Drovers CattleNetwork	Colorado	2014
A.J. Smith	Oklahoma Cowman Magazine	Oklahoma	2013
Burt Rutherford	BEEF Magazine	Texas	2012
Jay Carlson	BEEF Magazine	Kansas	2011
Larry Atzenweiler and Andy Atzenweiler	Missouri Beef Cattlemen	Missouri	2010
Kelli Toldeo	Cornerpost Publications	California	2009
Gren Winslow and Larry Thomas	Canadian Cattleman Magazine	Canada	2008
Angie Denton	Hereford World	Missouri	2007
Belinda Ary	Cattle Today	Alabama	2006
Steve Suther	Certified Angus Beef LLC	Kansas	2005
Kindra Gordon	Freelance Writer	South Dakota	2004
Troy Marshall	Seedstock Digest	Missouri	2003
Joe Roybal	BEEF Magazine	Minnesota	2002
Greg Hendersen	Drovers	Kansas	2001
Wes Ishmael	Clear Point Communications	Texas	2000
Shauna Rose Hermel	Angus Journal & BEEF Magazine	Missouri	1999
Keith Evans	American Angus Association	Missouri	1998
Bill Miller	Beef Today	Kansas	1997
Ed Bible	Hereford World	Missouri	1996
Nita Effertz	Beef Today	Idaho	1995
Hayes Walker III	America's Beef Cattleman	Kansas	1994
J.T. "Johnny" Jenkins	Livestock Breeder Journal	Georgia	1993
Dick Crow	Western Livestock Journal	Colorado	1991
Robert C. DeBaca	The Ideal Beef Memo	Iowa	1990
Forrest Bassford	Western Livestock Journal	Colorado	1989
Fred Knop	Drovers Journal	Kansas	1988
Chester Peterson	Simmental Shield	Kansas	1987
Warren Kester	BEEF Magazine	Minnesota	1986

E.C. Larkin (right), Gulf Coast Cattleman, received the 2015 BIF Ambassador Award from Steve Munger, 2014-15 BIF president.

BIF Pioneer Award Past Recipients

Name	State	Year
Paul Genho	Florida	2015
Tom Woodward	Texas	2015
Merlyn Nielsen	Nebraska	2014
Gary Bennett	Nebraska	2014
Steve Radakovich	Iowa	2014
Keith Bertrand	Georgia	2013
Ignacy Misztal	Georgia	2013
Glenn Selk	Oklahoma	2013
Sally Buxkemper	Texas	2012
Donald Franke	Louisiana	2012
Leo McDonnell	Montana	2012
Mike Tess	Montana	2011
Mike MacNeil	Montana	2011
Jerry Lipsey	Montana	2011
Richard McClung	Virginia	2010
John & Bettie Rotert	Missouri	2010
Daryl Strohbehn	Iowa	2010
Glen Klippenstein	Missouri	2010
Bruce Golden	California	2009
Bruce Orvis	California	2009
Roy McPhee (posthumously)	California	2009
Donald Vaniman	Montana	2008
Louis Latimer	Canada	2008
Harry Haney	Canada	2008
Bob Church	Canada	2008
Rob Brown	Texas	2007
David & Emma Danciger	Colorado	2007
Jim Gosey	Nebraska	2007
John Brethour	Kansas	2006
Harlan & Dorotheann Rogers	Mississippi	2006
Dave Pingrey	Mississippi	2006
Jack and Gini Chase	Wyoming	2005
Jack Cooper	Montana	2005
Dale Davis	Montana	2005
Les Holden	Montana	2005
Don Kress	Montana	2005
Frank Felton	Missouri	2004
Tom Jenkins	Nebraska	2004
Joe Minyard	South Dakota	2004
George Chiga	Oklahoma	2003
Burke Healey	Oklahoma	2003
Keith Zoellner	Kansas	2003
H.H. “Hop” Dickenson	Kansas	2002
Martin & Mary Jorgensen	South Dakota	2002
L. Dale Van Vleck	Nebraska	2002
Larry Benyshek	Georgia	2001
Minnie Lou Bradley	Texas	2001
Tom Cartwright	Texas	2001
J. David Nichols	Iowa	2000
Harlan Ritchie	Michigan	2000
Robert R. Schalles	Kansas	2000
Joseph Graham	Virginia	1999
John Pollak	New York	1999
Richard Quaas	New York	1999
John Crouch	Missouri	1998
Bob Dickinson	Kansas	1998
Douglas MacKenzie Fraser	Canada	1998
Larry V. Cundiff	Nebraska	1997
Henry Gardiner	Kansas	1997
Jim Leachman	Montana	1997
A.L. “Ike” Eller	Virginia	1996
Glynn Debter	Alabama	1996
James S. Brinks	Colorado	1995
Robert E. Taylor	Colorado	1995
Tom Chrystal	Iowa	1994
Robert C. DeBaca	Iowa	1994
Roy A. Wallace	Ohio	1994
James D. Bennett	Virginia	1993
M.K. “Curly” Cook	Georgia	1993
O’Dell G. Daniel	Georgia	1993
Hayes Gregory	N. Carolina	1993
Dixon Hubbard	Virginia	1993
James W. “Pete” Patterson	North Dakota	1993
Richard Willham	Iowa	1993
Frank Baker	Arkansas	1992
Ron Baker	Oregon	1992
Bill Borror	California	1992
Walter Rowden	Arkansas	1992
Bill Long	Texas	1991
Bill Turner	Texas	1991
Donn & Sylvia Mitchell	Canada	1990
Hoon Song	Canada	1990
Jim Wilton	Canada	1990
Roy Beeby	Oklahoma	1989
Will Butts	Tennessee	1989
John W. Massey	Missouri	1989
Christian A. Dinkle	South Dakota	1988
George F. & Mattie Ellis	New Mexico	1988
A.F. “Frankie” Flint	New Mexico	1988
Glenn Burrows	New Mexico	1987
Carlton Corbin	Oklahoma	1987
Murray Corbin	Oklahoma	1987
Max Deets	Kansas	1987
Charles R. Henderson	New York	1986
Everett J. Warwick	Maryland	1986
Mick Crandell	South Dakota	1985
Mel Kirkiede	North Dakota	1985
Bill Graham	Georgia	1984

Name	State	Year
Max Hammond	Florida	1984
Thomas J. Marlowe	Virginia	1984
Jim Elings	California	1983
W. Dean Frischknecht	Oregon	1983
Ben Kettle	Colorado	1983
Jim Sanders	Nevada	1983
Carroll O. Schoonover	Wyoming	1983
Gordon Dickerson	Nebraska	1982
Mr. & Mrs. Percy Powers	Texas	1982
F.R. "Ferry" Carpenter	Colorado	1981
Otha Grimes	Oklahoma	1981
Milton England	Texas	1981
L.A. Maddox, Jr.	Texas	1981
Charles Pratt	Oklahoma	1981
Clyde Reed	Oklahoma	1981
Richard T. "Scotty" Clark	Colorado	1980
Bryon L. Southwell	Georgia	1980
Robert Koch	Nebraska	1979
Mr. & Mrs. Carl Roubicek	Arizona	1979
Joseph J. Urick	Montana	1979
James B. Lingle	Maryland	1978
R. Henry Mathiessen	Virginia	1978
Bob Priode	Virginia	1978
Ralph Bogart	Oregon	1977
Henry Holsman	South Dakota	1977
Marvin Koger	Florida	1977
John Lasley	Missouri	1977
W. L. McCormick	Georgia	1977
Paul Orcutt	Montana	1977
J.P. Smith	Missouri	1977
H.H. Stonaker	Colorado	1977
Forrest Bassford	Colorado	1976
Doyle Chambers	Louisiana	1976
Mrs. Waldo Emerson Forbes	Wyoming	1976
C. Curtis Mast	Virginia	1976
Glenn Butts	Missouri	1975
Keith Gregory	Nebraska	1975
Braford Knapp, Jr.	Montana	1975
Reuben Albaugh	California	1974
Charles E. Bell, Jr.	Virginia	1974
John H. Knox	New Mexico	1974
Paul Pattengale	Colorado	1974
Fred Wilson	Montana	1974
Ray Woodward	Montana	1974
Jay L. Lush	Iowa	1973

Paul Genho, president of Farmland Reserve Inc., Salt Lake City, Utah, was awarded the BIF Pioneer Award. Receiving the award in his honor were his two sons, John Genho and David Genho. Pictured are (from left) John Genho; David Genho; Mark Enns, BIF Western Region secretary; and Steve Munger 2014-15 BIF president.

Tom Woodward (left) of Broseco Ranch, Decatur, Texas, received the BIF Pioneer Award from Steve Munger, 2014-15 BIF president.

BIF Continuing Service Award Past Recipients

Name	State/Organization	Year
Joe Cassady	South Dakota State Un.	2015
Andy Boston	Indiana	2015
Lois Schreiner	Kansas State University	2015
Chris Shivers	Am. Brahman Breeders Association	2015
Larry Kuehn	US MARC	2014
Wade Shafer	Am. Simmental Association	2014
Warren Snelling	US MARC	2014
Susan Willmon	Am. Gelbvieh Association	2014
Ben Eggers	Sydenstricker Genetics	2013
Brian House	Select Sires	2013
Lauren Hyde	Am. Simmental Association	2013
Jerry Taylor	University of Missouri	2013
Jack Ward	Am. Hereford Association	2013
Tom Field	Nebraska	2012
Stephen Hammack	Texas	2012
Brian McCulloh	Wisconsin	2012
Larry Olson	South Carolina	2012
Tommy Brown	Alabama	2011
Mark Enns	Colorado	2011
Joe Paschal	Texas	2011
Marty Ropp	Montana	2011
Bob Weaber	Missouri	2011
Bill Bowman	Missouri	2010
Twig Marston	Nebraska	2010
David Patterson	Missouri	2010
Mike Tess	Montana	2010
Darrh Bullock	Kentucky	2009
Dave Daley	California	2009
Renee Lloyd	Iowa	2009
Mark Thallman	Nebraska	2009
Doug Fee	Canada	2008
Dale Kelly	Canada	2008
Duncan Porteous	Canada	2008
Craig Huffhines	Missouri	2007
Sally Northcutt	Missouri	2007
Jimmy Holliman	Alabama	2006
Lisa Kriese-Anderson	Alabama	2006
Dave Notter	Ohio	2006
Jerry Lipsey	Montana	2005
Micheal MacNeil	Montana	2005
Terry O'Neill	Montana	2005
Robert Williams	Missouri	2005
Chris Christensen	South Dakota	2004
Robert "Bob" Hough	Texas	2004
Steven M. Kappes	Nebraska	2004
Richard McClung	Virginia	2004
Sherry Doubet	Colorado	2003
Ronnie Green	Virginia	2003
Connee Quinn	Nebraska	2003
Ronnie Silcox	Georgia	2003
S.R. Evans	Mississippi	2002
Galen Fink	Kansas	2002
Bill Hohenboken	Virginia	2002
William Altenburg	Colorado	2001
Kent Andersen	Colorado	2001
Don Boggs	South Dakota	2001
Ron Bolze	Kansas	2000
Jed Dillard	Florida	2000
Bruce Golden	Colorado	1999
John Hough	Georgia	1999
Gary Johnson	Kansas	1999
Norman Vincil	Virginia	1999
Keith Bertrand	Georgia	1998
Richard Gilbert	Texas	1998
Burke Healey	Oklahoma	1998
Glenn Brinkman	Texas	1997
Russell Danielson	North Dakota	1997
Gene Rouse	Iowa	1997
Doug L. Hixon	Wyoming	1996
Harlan D. Ritchie	Michigan	1996
Paul Bennett	Virginia	1995
Pat Goggins	Montana	1995
Brian Pogue	Canada	1995
Bruce E. Cunningham	Montana	1994
Loren Jackson	Texas	1994
Marvin D. Nichols	Iowa	1994
Steve Radakovich	Iowa	1994
Doyle Wilson	Iowa	1994
Robert McGuire	Alabama	1993
Charles McPeake	Georgia	1993
Henry W. Webster	South Carolina	1993
Jack Chase	Wyoming	1992
Leonard Wulf	Minnesota	1992
John Crouch	Missouri	1991
Robert Dickinson	Kansas	1990
Roger McCraw	North Carolina	1989
Bruce Howard	Canada	1988
Bill Borror	California	1987
Jim Gibb	Missouri	1987
Daryl Strohbehn	Iowa	1987
Larry Benyshek	Georgia	1986
Ken W. Ellis	California	1986
Earl Peterson	Montana	1986
Jim Glenn	IBIA	1985
Dick Spader	Missouri	1985

Name	State/Organization	Year
Roy Wallace	Ohio	1985
James Bennett	Virginia	1984
M.K. Cook	Georgia	1984
Craig Ludwig	Missouri	1984
Art Linton	Montana	1983
J.D. Mankin	Idaho	1982
Mark Keffeler	South Dakota	1981
Glenn Butts	PRI	1980
Jim Gosey	Nebraska	1980
C.K. Allen	Missouri	1979
William Durfey	NAAB	1979
James S. Brinks	Colorado	1978
Martin Jorgensen	South Dakota	1978
Paul D. Miller	Wisconsin	1978

Name	State/Organization	Year
Lloyd Schmitt	Montana	1977
Don Vaniman	Montana	1977
A.L. Eller, Jr.	Virginia	1976
Ray Meyer	South Dakota	1976
Larry V. Cundiff	Nebraska	1975
Dixon D. Hubbard	Washington, DC	1975
J. David Nichols	Iowa	1975
Frank H. Baker	Oklahoma	1974
D.D. Bennett	Oregon	1974
Richard Willham	Iowa	1974
F. R. Carpenter	Colorado	1973
Robert DeBaca	Iowa	1973
E.J. Warwick	Washington, DC	1973
Clarence Burch	Oklahoma	1972

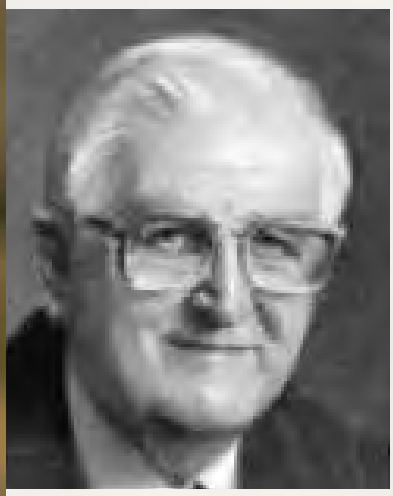
Andy Boston (right), Purdue University Extension, received the Continuing Service Award from Steve Munger, 2014-15 BIF president.

Joe Cassady (left), retired BIF executive director, received the Continuing Service Award from Steve Munger, 2014-15 BIF president.

Lois Schreiner (right), Kansas State University, received the Continuing Service Award from Steve Munger, 2014-15 BIF president.

Chris Shivers (right), American Brahman Breeders Association, received the Continuing Service Award from Steve Munger, 2014-15 BIF president

Baker/Cundiff Award



Frank H. Baker 1923-1993

(Photograph of portrait in Saddle and Sirloin Club Gallery; Everett Raymond Kinstler, artist)

Dr. Frank H. Baker is widely recognized as the "Founding Father" of the Beef Improvement Federation (BIF). Frank played a key leadership role in helping establish BIF in 1968, while he was Animal Science Department Chairman at the University of Nebraska, Lincoln, 1966-74. The Frank Baker Memorial Scholarship Award Essay competition for graduate students provides an opportunity to recognize outstanding student research and competitive writing in honor of Dr. Baker.

Frank H. Baker was born May 2, 1923, at Stroud, Oklahoma, and was reared on a farm in northeastern Oklahoma. He received his B.S. degree, with distinction, in Animal Husbandry from Oklahoma State University (OSU) in 1947, after two and a half years of military service with the US Army as a paratrooper in Europe, for which he was awarded the Purple Heart. After serving three years as county extension agent and veterans agriculture instructor in Oklahoma, Frank returned to OSU to complete his M.S. and Ph.D. degrees in Animal Nutrition. Frank's professional positions included teaching and research positions at Kansas State University, 1953-55; the University of Kentucky, 1955-58; Extension Livestock Specialist at OSU, 1958-62; and Extension Animal Science Programs Coordinator, USDA, Washington, D.C., 1962-66. Frank left Nebraska in 1974 to become Dean of Agriculture at Oklahoma State University, a position he held until 1979, when he began service as International Agricultural Programs Officer and Professor of Animal Science at OSU. Frank joined Winrock International, Morrilton, Arkansas, in 1981, as Senior Program Officer and Director of the International Stockmen's School, where he remained until his retirement. Frank served on advisory committees for Angus, Hereford, and Polled Hereford beef breed associations, the National Cattlemen's Association, Performance Registry International, and the Livestock Conservation, Inc.

His service and leadership to the American Society of Animal Science (ASAS) included many committees, election as vice president and as president, 1973-74. Frank was elected an ASAS Honorary Fellow in 1977, he was a Fellow of the American Association for the Advancement of Science, and served the Council for Agricultural Science and Technology (CAST) as president in 1979. Frank Baker received many awards in his career, crowned by having his portrait hung in the Saddle and Sirloin Club Gallery at the International Livestock Exposition, Louisville, Kentucky, on November 16, 1986. His ability as a statesman and diplomat many awards in his career, crowned by having his portrait hung in the Saddle and Sirloin Club Gallery at the International Livestock Exposition, Louisville, Kentucky, on November 16, 1986. His ability as a statesman and diplomat for the livestock industry was to use his vision to call forth the collective best from all those around him. Frank was a "mover and shaker" who was skillful in turning "Ideas into Action" in the beef cattle performance movement. His unique leadership abilities earned him great respect among breeders and scientists alike. Frank died February 15, 1993, in Little Rock, Arkansas.

Larry Cundiff

(Photograph taken at BIF 2014, by Angus Journal)

Dr. Larry Cundiff retired in January 2007 after 40 years of service as a Research Geneticist with the U.S. Department of Agriculture, Agricultural Research Service. He was Research Leader of the Genetics and Breeding Research Unit at the U.S. Meat Animal Research Center from 1976 until 2005, when he accepted an interim eight-month appointment as Acting Center Director.

Larry Cundiff was born in Kansas in 1939, received his B.S. from Kansas State University in 1961, his M.S. and Ph.D. from Oklahoma State in 1964 and 1966. He married his wife, Laura, in 1960. They have three children. He was on the faculty at the University of Kentucky from 1965 to 1967, before working as a research geneticist in the USDA.

Cundiff has not only designed, conducted and published some of the most important beef breeding research of the 20th century, but also has lead in the transfer of new technology to the beef industry through his continued work in

BIF and his presentations made across the nation and around the world.

His research efforts have involved evaluation and utilization diverse breeds, effects and utilization of heterosis through alternative crossbreeding systems, and evaluation and effectiveness of selection for traits of economic importance in beef production. Since his retirement, he has continued service as a collaborator at the U.S. Meat Animal Research Center assisting with preparation of research reports and speaking at beef industry meetings and conferences. Dr. Cundiff has served as chairman of the Beef Improvement Federation (BIF) Committee on Genetic Prediction from 1973 until 2007, and as the Agricultural Research Service, USDA representative on the BIF Board of Directors from 1981 until 2007. He has served as editor of the Beef Improvement Federation's 9th Edition of Guidelines for Uniform Beef Improvement Programs.

2016 Recipients

Kathleen Ochsner, University of Nebraska-Lincoln
Kashly Schweer, University of Nebraska-Lincoln

Past Recipients

Previously known as Frank H. Baker Memorial Scholarship

Name	University	Year
Justin Buchanan	Oklahoma State Un.	2015
Jamie Parham	South Dakota State	2015
Heather Bradford	Kansas State Un.	2014
Xi Zeng	Colorado State Un.	2014
Heather Bradford	Kansas State Un.	2013
Erika Downey	Texas A&M Un.	2013
Jeremy Howard	Un. of Nebraska-Lincoln	2012
Kristina Weber	Un. of California-Davis	2012
Brian Brigham	Colorado State Un.	2011
Megan Rolf	Un. of Missouri	2011
Kent A. Gray	North Carolina State Un.	2010
Lance Leachman	Virginia Polytechnic Institute and State Un.	2009
Scott Speidel	Colorado State Un.	2009
Devori W. Beckman	Iowa State Un.	2008
Kasey L. DeAtley	New Mexico State Un.	2008
Gabriela C. Márquez Betz	Colorado State Un.	2007
Yuri Regis Montanholi	Un. of Guelph	2007
Amy Kelley	Montana State Un.	2006
Jamie L. Williams	Colorado State Un.	2006
Matthew A. Cleveland	Colorado State Un.	2005
David P. Kirschten	Cornell Un.	2005
Reynold Bergen	Un. of Guelph	2004
Angel Rios-Utrera	Un. of Nebraska	2004
Fernando F. Cardoso	Michigan State Un.	2003

Name	University	Year
Charles Andrew McPeak	Michigan State Un.	2003
Katherina A. Donoghue	Un. of Georgia	2002
Khathutshelo A. Nephawe	Un. of Nebraska	2002
Khathutshelo A. Nephawe	Un. of Nebraska	2001
Janice M. Rumph	Un. of Nebraska	2001
Paul L. Charteris	Colorado State Un.	2000
Katherine A. Donoghue	Un. of Georgia	2000
Janice M. Rumph	Un. of Nebraska	1999
Bruce C. Shanks	Montana State Un.	1999
Patrick Doyle	Colorado State Un.	1998
Shannon M. Schafer	Cornell Un.	1998
Rebecca K. Splan	Un. of Nebraska	1997
Robert Williams	Un. of Georgia	1997
D. H. "Denny" Crews, Jr.	Louisiana State Un.	1996
Lowell S. Gould	Un. of Nebraska	1996
D. H. "Denny" Crews, Jr.	Louisiana State Un.	1995
Dan Moser	Un. of Georgia	1995
Kelly W. Bruns	Michigan State Un.	1994
William Herring	Un. of Georgia	1994

Development of economic selection indices for beef cattle improvement

Kathleen P. Ochsner, University of Nebraska-Lincoln

Introduction

Profitability is the primary goal for most beef cattle producers. The main source of long-term profitability for a beef cattle operation lies in its production efficiency relative to other operations (Harris, 1970). There are numerous approaches to achieve greater efficiency including nutrition, reproduction, management, and genetics. The goal in animal breeding and genetics is to improve animal populations and future generations of animals (Dekkers et al., 2004). Expected progeny differences (EPD) are the traditional genetic tools used to select parents. A drawback to EPD is that they represent genetic merit in only one trait while in reality multiple traits influence an animal's value (Hazel, 1943). With EPD as a sole selection tool, producers are left to individually determine their optimal use and ultimately the economic importance of each trait (Bourdon, 1998). Selection indices account for multiple traits simultaneously and consider both biological production levels and economics (Parish, 2011). Falconer and Mackay (1996) recommend the use of selection indices for multi-trait selection in animal populations.

According to Hazel and Lush (1942), selection for an index which gives proper weight to each trait is more efficient than tandem selection or selection for multiple traits with independent culling levels. Tandem selection involves selection for one trait at a time until all traits have been improved to the desired level. This method is inefficient because selection pressure is placed on only one trait at a time, making genetic progress slow. Additionally, progress made in one trait could be eroded as selection pressure is placed on a different trait. When selection is based on independent culling levels, a certain level of merit is established for each trait and all individuals below that level are culled regardless of their performance in other traits. The main concern with this method is that an animal with superior performance in many traits may be culled if it is barely under the thresh hold level for just one trait. In this situation selection indices are an appropriate alternative because they allow for superior performance in one trait to compensate for poor performance in other traits.

Review of Literature

To achieve progress towards any breeding goal, it is important to determine which animals should be chosen as the parents of the next generation. Selection may differ between production systems and goals set forth for a particular operation. It is first important to specify the goal of a particular operation, and then develop a breeding program specific to this goal. Harris et al. (1984) presented an eight-step process for developing a breeding program: (1) describe the production system (2) formulate the objective (3) choose a breeding system and breeds (4) estimate selection parameters and economic values (5) design an animal evaluation system (6) develop selection criteria (7) design mating for selected animals (8) design a system for expansion.

Breeding Objective

The breeding objective is a combination of economic weighting factors and genetic information for traits to be improved (Falconer and Mackay, 1996). Selection on a breeding objective should result in increased profit of the firm that is investing in a breeding program (Goddard, 1998). Defining a breeding objective and developing selection criteria based on that breeding objective should be the primary step in developing a structured breeding program (Ponzoni and Newman, 1989). Defining an objective is critical because highly efficient selection for the wrong objective may be worse than no selection at all (James, 1982). To develop the most appropriate breeding objective several pieces of information are needed: (1) the management and production system of a group, (2) the return and cost of the production system, and (3) the economically relevant traits (ERTs) which influence returns and cost of production.

The breeding objective for a beef cattle breed may vary depending on the production system being used (Phocas et al., 1998). Dickerson et al. (1974) suggested that the breeding objective for efficient beef production should be more efficient growth accompanied by earlier sexual maturity to reduce replacement cost, lengthen productive life and minimize increase in mature body size. Efficiency should be measured as cost per unit of product from females and their progeny over a given period of time. Traits considered for market animals by Dickerson et al. (1974) were carcass composition, meat quality, and optimum weight at slaughter. Traits considered for cows were mature size, milk production and calving difficulty.

Garrick and Golden (2009) suggest that the goal of the beef industry as a whole should be to produce beef that is nutritious, healthful and desirable in a manner that is respectful of the resources used in its production. For a cow-calf system, Garrick and Golden (2009) describe the principal determinants of income as the number of females of breeding age, reproductive performance, calf survival, replacement rate, and the sex, weight and age of sale animals. Downstream factors which may potentially influence income are aspects of meat quality (e.g., marbling and tenderness) and management factors (e.g., adaptability, disease resistance, and docility). Expenses include feed costs,

veterinary costs, and labor. For a feedlot system, income is associated with the weight and carcass attributes of sale animals. Expenses include feed, yardage, labor and animal health.

Literature suggests that breeding objectives should be divided into groups depending on the emphasis of a breed or a specific operation. MacNeil et al. (1994) stated that the breeding system could be divided into three categories: general purpose, maternal and terminal. The U.S. beef production system can generally be divided into two sectors, seedstock and commercial. In seedstock operations, self-replacement is required to keep the breeding system stable so a maternal index can be used for producing reproductively proficient parents. Terminal selection indices can be used for commercial producers looking to purchase animals for use as parents in a system where progeny will be harvested.

It has been argued that biological efficiency should be used in defining breeding objectives instead of economic efficiency to assure sustainability of genetic improvement (Dickerson, 1982). However, difficulties in the expression of costs and revenues in terms of energy or protein consumption and lack of differentiation between values of products when biological efficiency is considered render this criterion unable to describe the overall objective of the producers (Harris and Newman, 1994). In general, even if future economic conditions can be difficult to foresee, the definition of the breeding goal according to an economic criterion allows a more complete description of the production system by also taking into account non-food costs (Dickerson, 1970; Goddard, 1998). Albera et al. (2004) stated that the use of biological rather than economic efficiency would lead to the formation of a different breeding goal. However, Albera et al. (2004) ultimately concluded that improvement in economic efficiency also leads to improved biological efficiency in most traits studied.

Determining traits in the breeding objective

A strong relationship between the breeding objective and changes in profitability is highly desirable, implying that all traits associated with profitability of an animal should be included (Pearson, 1982). Choice of traits to be included in the breeding objective should be based on relative contribution of each trait to the overall efficiency of production, which is usually evaluated from an economic perspective (Goddard, 1998). If efficiency is to be evaluated from an economic perspective, traits to be considered for use should be those which affect the income and cost of the system. Income is related to the number and value of sale animals, while cost is associated with the quantity and price of the resources required for production (Garrick and Golden, 2009).

For selection to be most efficient for individual producers, a comprehensive and systematic way of relating changes in individual performance levels to changes in profitability at the enterprise level must be developed (MacNeil et al., 1997). As such, relative weighting of each contributing trait must be determined. Harris (1970) indicated that the relative emphasis placed on each trait in a selection program depends on the combination of economic importance of the trait, potential for genetic improvement of the trait, genetic interrelationships between the trait and the cost of measurement in labor, facilities and time. Potential for genetic improvement is also highly dependent on genetic variability and accuracy of selection decisions. In most species, using a complete breeding objective would result in including a large number of traits. Gjedrem (1972) considered the definition of the aggregate breeding value and concluded that all traits of economic importance should be included. The disadvantage to this is that it would require estimation of a large number of genetic parameters and economic values. In some cases, these parameters cannot be estimated accurately, and the resulting selection will produce less than maximum change in profitability (Harris, 1964; Vandepitte and Hazel, 1977). A more practical approach may be to include only those traits which account for a significant (perhaps 10%) proportion of the variation in profit (Pearson, 1982).

When determining traits to be included in the selection criteria during development of a selection index, it is important to differentiate between ERT and indicator traits. An ERT is a trait directly associated with profitability, and can be identified by considering whether a change in performance of the trait will result in a change in either income from or cost of production (Golden et al., 2000). If income or expenses change independently of the trait in question, the trait is likely an indicator trait. For example, consider calving ease and birth weight which are two EPD associated with dystocia. Calving ease is the ERT because selection on this trait will result in greater calf survival and heifer rebreeding rates, resulting in greater income. Conversely, birth weight is only an indicator of calving difficulty. Birth weight itself cannot explain all the differences in calving difficulty, and therefore should not be the focus of selection decisions designed to reduce dystocia. When information is available for the ERT, information on the correlated indicator trait need not be considered when calculating a selection index. The concept of ERT can help focus selection pressure on what will directly influence profitability (Enns, 2013).

In practice, some traits in the objective are not readily observed, hence our need to use indicator traits for predicting traits that do hold economic relevance. For some ERT, data collected on the trait may misrepresent the population, and thus prediction on an indicator trait may be more accurate. For example, genetic evaluation for

carcass traits is problematic in seedstock herds because few young animals are harvested. Animals that are harvested are likely individuals deemed unsuitable for breeding, and not representative samples of offspring. It is also most appealing to incorporate traits for which data already exists, which often leads to incorporation of a number of indicator traits rather than ERT. The methodology to develop selection indices from a list of traits including some correlated indicator traits is well-accepted, but requires a priori knowledge of the genetic correlation between the indicator traits and ERT (Garrick and Golden, 2009).

Sivanadian and Smith (1997) showed that response to selection is improved as additional traits are added to the selection criteria, given that the parameters are known without error. They further demonstrated that the change in response increased as the heritability and/or the economic weight of each added trait increased. The magnitude of the change was influenced by the product of the heritability and the economic weight. Hazel (1943) confirmed that information collected on a greater breadth of traits for a greater number of animals will improve the response to selection when using indices based on that information. This was demonstrated through a swine breeding program using individual phenotypic data, productivity of the dam and average weight and score of the litter simultaneously in order to increase genetic progress expected when using an index to make selection decisions. Using an index which combined all three sources of information improved efficiency by 11.3 percent as compared to a selection index based only on an individual's own phenotypic records. Since time and effort expended in keeping records is but a small portion of total labor in a breeding program, it may be worthwhile to collect additional data on a larger number of animals in order to improve response when implementing index selection.

Estimation of relative economic values

Economic values are necessary for each trait in the breeding objective to ensure that selection emphasis is proportional to the economic importance of each trait. Considering that most beef production systems have generation intervals greater than five years and significant genetic improvement requires more than one generation, it is obvious that relative economic values must pertain to the long run (MacNeil et al., 1997). When developing a selection index utilized in pursuit of a breeding objective, prices of concern are those several years into the future when the outcome of selection will be realized in the commercial industry. Selection choices are dependent on the relative prices of inputs and outputs and are therefore essentially unaffected by the general inflation of prices common to all inputs and outputs (Pearson, 1982). When choosing prices, previous price trends must be combined with a prediction of whether or not the trend will continue at a steady rate, intensify, or weaken. Frequent changes in price relationship can have a devastating effect on genetic change. In traits for which prices vary drastically over short periods of time, particularly in a cyclic fashion, considering prices from a larger range of time may be beneficial. Economic values should be changed infrequently, and only after substantial evidence for changing these price relationships has accumulated. Relative economic values should not be influenced by year-to- year fluctuations in prices of inputs or outputs (MacNeil et al., 1997). Further supporting this conclusion, Balaine et al. (1981) found correlations ranging from 0.98 to 1.0 between estimates of profit using widely divergent prices over a 15 year period.

The profit equation is a widely used method to derive the relative economic value. Moav and Moav (1966) presented a profit equation to integrate the cost and returns from production to compare the profitability of animals. In animal breeding, the profit equation is a mathematic form of the production system and the breeding objective. Garrick and Golden (2009) discussed measuring profit of a cow-calf production system in terms of 'profit per unit land', and in a feedlot system in terms of 'profit per pen'. Thus, the specific profit perspective must be chosen in the initial stages of objective development.

Relative economic values recognize that economic return from a one standard deviation increase in one trait will not be equal to the same increase in another trait. Only economically important traits and indicator traits that will respond to selection are ultimately used by the seedstock producer. It is not efficient to measure or base selection on traits without economic value. Ponzoni and Newman (1989) outlined and implemented a method for determining relative economic values for beef production. In their example, they calculated relative economic values for the biological traits as partial derivatives of profit with respect to each trait holding the other traits constant at their mean levels.

The relative economic value for any one trait may differ depending on the goal of the breeding objective and the subsequent markets that the particular breeding objective targets. Melton (1995) discovered that a breeding objective generated specifically for a non-integrated cow-calf producer resulted in greater relative economic value for maternal and reproductive traits and lower relative economic value for retail product than an objective encompassing the entire beef industry. MacNeil et al. (1994) found that for Canadian beef production, cow weight, female fertility and maternal weaning weight had economic importance in maternal lines but not in terminal lines. Additionally, it was discovered that growth had higher relative economic value for the finishing phase than for the backgrounding phase. In the U.S. beef system, MacNeil (2005) found a high correlation among breeding objectives for four terminal sire lines.

This study demonstrated the importance of increasing calf survival, weight gain, dressing percentage and marbling score while decreasing feed intake and back fat. Quantifying the importance of each trait in the breeding objective is essential not only to effectively select animals with higher rank, but also to determine the priority of traits in relation to future research and to develop systems for data collection and evaluation of these traits (Garrick and Golden, 2009).

While studying effects of production conditions on economic values, Koots and Gibson (1998) found that changes in some specific conditions resulted in large shifts in economic values. Reducing fertility and survival rate caused the largest changes to economic values. The economic value for mature weight was affected by practically all alternatives considered in the study. These results suggest that economic values will differ between production and marketing circumstances. MacNeil et al. (1997) pointed out that resources available for production and level of production vary among production units resulting in different economic structures. Thus, a customized approach to estimation of economic values, as described by Upton et al. (1988), may be warranted. Still, in practice the effects of changes of economic values on selection response depend on which traits appear in the index. Additionally, it has been shown that small changes in economic values do not significantly affect selection response (Vandepitte and Hazel, 1977; Smith, 1983). As such, a relatively small number of selection indices should cover a wide range of production and economic circumstances.

Selection Index Construction

In his seminal paper, Hazel (1943) outlined the following statistics which are necessary for selection index construction:

A. Phenotypic constants
    1. Standard deviation for each trait
    2. Phenotypic correlation between each pair of traits
    3. Phenotypic correlations between the traits of relatives
B. Genetic constants
    1. Heritable fraction of the variance in each trait
    2. Genetic correlation between each pair of traits

Hazel (1943) introduced the analytical method for calculating a selection index. The aggregate value (H) of an animal is defined as the sum of its genotypes for each economic trait (Gi), with each genotype being weighted according to the relative economic value of that trait (ai). An animal's genotype for a specific trait is the sum of the average additive effects of genes which influence the trait. Therefore, aggregate genotype is defined as:

$$(1) \qquad H = a_1G_1 + a_2G_2 + \ldots + a_nG_n$$

Recognizing that environmental factors, dominance and epistasis may influence phenotypic performance, selection for improved breeding value must be practiced indirectly by selecting for a correlated variable (I) based on the phenotypic performance of each individual for several traits. Hazel (1943) defines I as:

$$(2) \qquad I = b_1X_1 + b_2X_2 + \ldots + b_nX_n$$

where Xi represents the phenotypic performance for the several traits which influence the goal trait and bi represents the multiple regression coefficients designed to make the correlation between H and I as large as possible.

MacNeil et al. (1997) demonstrated how to calculate the vector (b) of weighting coefficients for each source of information in the index using the equation:

$$(3) \qquad b = P^{-1}Gv$$

where P is a n x n matrix of the phenotypic (co)variances among the n traits measured and available as selection criteria, G is a n x m matrix of the genetic (co)variances among all m objective traits, and v is a m x 1 vector of relative economic values for objective traits.

Indices using EPD

Bourdon (1998) pointed out two serious drawbacks in applying index weighting factors to phenotypic values for an individual. First, this method lacks accuracy because it does not incorporate information on relatives. Second, it is biased because genetic differences among contemporary groups are not accounted for. These issues can be overcome by using genetic predications derived from best linear unbiased prediction (BLUP) instead of individual phenotypic performance. Henderson (1963) demonstrated that if genetic predictions derived from multitrait BLUP

are available for all traits in the breeding objective, genetic predications can simply be substituted for true breeding values in the breeding objective. Schneeberger et al. (1992) reconfirmed the equivalence of weightings derived using BLUP and conventional selection index. Further, they presented the models needed to compute index weights for the more likely case in which traits in the breeding objective differ from those for which genetic predictions are available. The equation to estimate index weights to be applied to EPD is:

b= G11-1G12v

where G11 is a n x n matrix of genetic (co)variances among the n selection criteria, G12 is a n x m matrix of the genetic (co)variances among the n selection criteria and m objective traits, and v is a m x 1 vector of relative economic values for all objective traits. Index weights calculated in this way account for potentially large amounts of information on relatives. The index will also be unbiased because predictions derived from BLUP procedures are themselves unbiased (Bourdon, 1998).

Improving accuracy of selection indices

Information gleaned from large scale genetic evaluation has led to an ever increasing number of EPD being made available to producers. The amount of information available is often overwhelming to producers when trying to make the best selection and purchase decisions. The increase in the number of EPD was based on the presumption that EPD for more traits helped better characterize the genetic capability of animals (Bourdon, 1998). In many cases, little consideration was given to the value of EPD and instead they were produced simply because data were cheaply and easily collected. Improvements in current selection indices still need to be made by increasing the number of ERT that have EPD reported. Spangler (2015) expressed his concern that many ERT are not currently evaluated nor collected routinely in the seedstock sector, even though they drive value downstream. Some ERT that fall into this category are reproductive performance, disease, tenderness, primal yield and dark cutters. In the future it is recommended that enterprise-level profitability moves closer to industry-level profitability.

Generally, some and perhaps most traits in the breeding objective are not observed so predictions for them must be calculated through covariances with measured traits. Since the relationships between observed traits and traits in the breeding objective are defined by covariances, they are assumed linear. While the use of covariance matrices is mathematically straightforward, it is not without problems (Bourdon, 1998). The linearity between some of these traits is questionable. Evans (1996) reported a nonlinear genetic relationship between scrotal circumference and heifer pregnancy. Scrotal circumference is an easily measured trait likely to be used as selection criteria while heifer pregnancy is an ERT likely to appear in a breeding objective. The accuracy of selection based on an index including scrotal circumference as selection criteria could be greatly improved if instead EPD for heifer pregnancy were reported and could be included in the selection criteria.

Conclusions and Implications to Genetic Improvement of Beef Cattle

Enns and Nicoll (2008) determined the long-term genetic change in a commercial beef breeding program resulting from selection for indices developed for an economic breeding objective. Changes in each of the breeding objective component traits were applied to the breeding objective equation to estimate average change in the aggregate breeding value (H). Selection based on an economic breeding objective in a New Zealand Angus nucleus herd described by Nicoll et al. (1979) was initiated in 1976, and significant improvement in H was realized from 1976 through 1993. During this time, the increase in net income at an annual rate was equated to US$24.68 per cow lifetime. This study was among the first to report genetic improvement in commercial beef cattle breeding programs resulting from selection for an economic breeding objective and using indices that did not contain all traits of economic importance. Traits included in the index were weaning weight, yearling weight, mature cow weight and cow fertility. Results support the use of multi-trait selection indices to predict an economic breeding objective in beef cattle genetic improvement programs.

Livestock industries have relied increasingly on selection indices as a tool for maximizing profitability in individual livestock operations. Many breed associations have produced and published selection indices for use by producers. Literature provides ample evidence that selection indices are an efficient tool to utilize when making selection decisions. The power of selection indices can be improved by the willingness of producers to adopt selection index technology through guidelines for deriving relative economic values and implementing selection index technology in national cattle evaluation (MacNeil et al., 1997). The key to successful use of a selection index lies in identifying the index that best suits a particular operation while keeping in mind the goal to improve multiple traits simultaneously (Enns, 2013). Recognizing that the beef industry is dynamic and ever-changing, the selection index is a versatile tool to increase profitability of an operation by selecting for multiple traits of economic importance.

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Genomic selection for feed efficiency traits

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Introduction

Feed costs comprise the majority of variable expenses in beef cattle systems making feed efficiency an important economic consideration within the beef industry (Koch et al., 1963; Dickerson et al., 1974). Aside from the direct economic impact of this trait complex at the individual producer level, the projections of global population growth provide extra pressure for efficient beef cattle production as producers try to combat the growing food demand with limited resources (Eggen, 2012). Improved feed efficiency also has an environmental impact through a decreased carbon footprint as more efficient cattle have fewer days to finish, emitting less methane throughout their lifetime (Freetly, 2013).

There are multiple measures of feed efficiency. The most common used in the fed cattle sector is feed conversion ratio (FCR), the ratio of feed to gain (F:G), or gain to feed (G:F). This ratio is simply the raw pounds of feed required for raw pounds of weight gained, or the reciprocal. It makes no adjustments for age and weight differences of the cattle or energy content differences of the diet being fed. For these reasons, unadjusted FCR should be limited to use within contemporary groups. Due to the positive genetic correlation between feed intake and gain, selection to improve FCR has the potential to lead to larger, more maintenance intensive animals in the breeding herd (Archer et al., 1999).

One proposed alternative to FCR is residual feed intake (RFI). The concept of RFI was introduced by Koch et al. (1963) by suggesting that feed intake should be adjusted for body weight and weight gain, making RFI the difference between actual feed intake and the predicted feed intake of an animal based its requirements for maintenance and gain. More desirable or efficient animals will have a negative RFI value with an average individual having an RFI of zero (Koch et al., 1963; Archer et al., 1999). The prediction equation is developed by regressing actual feed intakes, gains and weights of the animal's contemporaries, meaning the sum of RFI values across the contemporary group in which it was calculated should equal zero and thus contemporary group definition becomes vital. It is sometimes considered the preferred definition of feed efficiency because RFI is phenotypically independent of the production traits (growth and body weight) used in the prediction equation (Kennedy et al., 1993). Ultimately, selection on RFI is equivalent to using a restricted selection index containing the component traits. Since genetic variation in RFI exists, genetic progress towards more efficient cattle through selection on this trait is possible.

The use of RFI as a measure of feed efficiency is occasionally contested for a variety of reasons including difficult interpretation and differences in the frequency of recording for the component traits. Additionally, if any genetic or residual correlations exist between feed intake and maintenance traits, the resulting heritability estimates can be flawed (Lu et al., 2015; Kennedy et al., 1993). In the dairy industry, Lu et al. (2015) proposed a multi-trait model as an alternative approach to feed efficiency. This may represent a more robust measure of feed efficiency and comprehensive investigation into the genetic relationship between intake and gain.

Feed intake, and consequently feed efficiency traits, are difficult to obtain and expensive to measure. Consequently a genomics approach seems warranted. Although it is an expensive initiative, the detection of genetic markers for feed efficiency has the potential for great returns in the beef industry.

Review of Literature

Genetic Parameters for Feed Efficiency Traits

Moderate heritability estimates for average daily gain (ADG), dry matter intake (DMI), metabolic mid-test body weight (MMBW; lb0.75) and RFI suggest genetic variation exists and genetic progress can be garnered. Average daily gain is defined as the difference between the start and end test weights divided by the total number of days on feed. Arthur et al. (2001a) used data from 1,180 young Angus bulls and heifers on performance tests to estimate genetic and phenotypic parameters. Direct heritability of ADG was estimated as 0.28 (Arthur et al., 2001a). Heritability estimates were higher from data on young Charolais bulls. The heritability of ADG was calculated at 15 and 19 months of age on Charolais bulls. Heritability estimates were moderate at 0.34 and 0.41, respectively, for the two ages (Arthur et al., 2001b). These estimates are similar to previous reports from Robinson and Oddy (2004) and Schenkel et al. (2003) of 0.23 and 0.35, respectively.

Daily DMI is the cumulative on-test feed intake on a dry matter basis divided by the total days on feed. Nkrumah et al. (2007) estimated the heritability of daily DMI as 0.54 using crossbred beef steers, which is higher than a previous estimate of 0.44 by Schenkel et al. (2003). Feed intake can also be measured on an as-fed basis. Heritability estimates for feed intake as total feed consumed (as-fed) are also moderate with reports of 0.27, 0.48 and 0.39 from Robinson and Oddy (2004), Arthur et al. (2001b) and Arthur et al. (2001a), respectively.

Mid-test body weight (MBW) can be calculated by the average of the initial and end weights or through regression techniques. Metabolic mid-test body weight (MMBW) is MBW0.75. Arthur et al. (2001a) reported the direct heritability estimate of 0.40 for MMBW. This agrees with the estimates of 0.35 and 0.41 from Schenkel et al. (2003), and Robinson and Oddy (2004), respectively.

Direct heritability estimates are moderate for RFI. Arthur et al. (2001a) estimated a heritability of 0.39. Schenkel et al. (2003) used two definitions of RFI. The first was the classical definition of the trait, the difference between actual feed intake and expected feed intake required for body weight and growth (RFIP), and the second included an adjustment for end of test backfat thickness (RFIb). Heritability estimates for both versions of RFI were very similar at 0.38 and 0.39 for RFIP and RFIb, respectively. Robinson and Oddy (2004) reported heritability estimates much lower for RFI (0.18) when cattle from varying breed types (temperate and tropical) at near market-ready weights were fed an ad libitum feedlot diet. Estimates for other feed efficiency related traits including FCR, feeding time and number of eating sessions per day are also moderate (Robinson and Oddy, 2004; Herd and Bishop, 2000; Arthur et al., 2001a; Arthur et al., 2001b).

Two of the main causes for genetic correlations between traits are the existence of pleiotropy and linkage (Bolormaa et al., 2014). Genetic and phenotypic correlations exist among feed efficiency traits and between feed efficiency and production traits. Phenotypic and genetic correlations between MMBW and ADG were 0.24 and 0.53, respectively (Arthur et al., 2001a). Moderate-to-strong positive genetic correlations exist between ADG and feed intake (as-fed or dry matter basis) with estimates of 0.54 (Arthur et al., 2001a), 0.87 (Nkrumah et al., 2007) and 0.50 (Schenkel et al., 2004). Several authors have reported moderate phenotypic correlations between gain and feed intake ranging from 0.41 to 0.60 (Arthur et al., 2001a; Nkrumah et al., 2007; Schenkel et al., 2004). Additionally, MMBW has been reported to be positively correlated with feed intake both phenotypically (rp=0.77), and genetically (rg=0.71) by Schenkel et al. (2004). By definition, RFI should be phenotypically independent of its component traits (Koch et al., 1963). Estimates from Arthur et al. (2001a) illustrate this with reported phenotypic correlations between RFI and MMBW (rp=0.02) and between RFI and ADG (rp=-0.06). Nkrumah et al. (2007) reported RFI was also genetically independent of its component traits, ADG and MMBW, with estimates close to zero (rg=-0.04, rg=-0.06). Nkrumah et al. (2007) reported that the genetic correlation between RFI and feed intake was 0.72, while feed intake was genetically correlated with F:G to a lesser degree (rg=0.31). Schenkel et al. (2003) also found RFI to be more strongly genetically correlated with feed intake than F:G, thus suggesting selecting for low RFI could decrease feed intake more substantially than selecting for FCR.

Feed intake tends to be positively genetically correlated with postweaning growth traits including 200-d weight direct and 400-d weight direct with estimates of rg =0.28 and 0.56, respectively (Arthur et al., 2001a). Additionally, RFI was negatively correlated with 200-d weight direct (rg=-0.45) and 400-d weight direct (rg=-0.26; Arthur et al., 2001a). Both FCR and RFI are negatively correlated with longissimus muscle area (LMA). This suggests more efficient cattle have larger LMA (Schnekel et al., 2003). More efficient cattle may also produce a leaner product, as RFI is genetically correlated with intra-muscular fat percentage (rg=0.22) and rump fat (rg=0.72) (Robinson and Oddy, 2004). Robinson and Oddy (2004) further investigated the association between RFI and fat by holding age and carcass weight constant. Regardless of adjustment, the magnitude and sign of the relationships were similar.

Methods for genomic prediction

Traditionally, genetic selection to improve economically relevant traits in livestock has been based on phenotypic records and pedigree information. Estimated breeding values (EBV) are an estimate of the additive genetic merit of an individual for a given trait. The genetic value of a parent is one-half of its EBV, referred to as an expected progeny difference (EPD) in the U.S. beef cattle industry. The calculation an EPD combines pedigree information, the individual's own performance records and the performance records of one's offspring or relatives. Selection based on EPD has been successful. For animals to have EPD with high accuracy, many offspring with performance records are typically needed. In terms of feed intake, this is often not plausible due to the expense of recording phenotypes. The length of the generation interval is also a limiting factor on the timeliness of the genetic progress. The concept of identifying genes to improve certain traits and selecting candidates for breeding based on the presence of favored alleles is advantageous (Goddard and Hayes, 2009).

One of the primary hurdles which must be overcome with the current genomic advances is continuing to develop methodology to accurately estimate marker effects in a computationally efficient manner. The evolution of methodology is almost as vast as the changes in technology, or possibly parallel to some degree. Historically, BLUP has given animal breeders a powerful tool for the prediction of breeding value based on performance records. Henderson (1984) realized the advantages of prediction with BLUP over least squares, regressed least squares or selection index due to the reduction of error and the greater correlations between the predictors and the predictions.

The BLUP methodologies were augmented to include maker effects into breeding value predictions through mixed models for the introduction of genomic BLUP (GBLUP; Fernando and Grossman, 1989). With BLUP, pedigree information is used to derive the relationship matrix making full sibs have the same EBV (parent average value). If instead, genomic information (i.e. SNP genotypes) is used to form the relationship matrix, the Mendelian Sampling term is taken into account and allows for individual deviation from the parent average. This increases the accuracy of the EBV and consequently, the response to selection (Hayes et al., 2009). As with most linear predictions, GBLUP assumes that all markers contribute to the overall genetic variance therefore meaning each of the SNP have small effects (VanRaden, 2008).

Regression techniques were also used as a method for MAS where least square analysis was used as a way to estimate marker effects. Lande and Thompson (1990) found MAS to be feasible through the multiple regression of phenotype on genotype at a given marker loci to determine markers associated with a given trait due to LD with the QTL. If a sufficient amount of markers are linked with the QTL and a large enough sample size of individuals exist, the regression should be able to account for most of the additive genetic variance within the trait due to a particular QTL (Lande and Thompson, 1990). In reality, the massive amount of marker effects cannot be estimated to be included into the standard regression model. With the advent of high-density genotyping platforms, the number of makers exceeds the number of genotyped individuals within the population. In order to overcome the challenge of dimensionality, only a subset of the marker effects are estimated to be included in the regression model and results in larger errors and poor estimates of the genetic value of an individual (Zhang and Smith, 1992; Whittaker et al., 2000).

Ridge regression is a method that has better predictive ability than when only a subset of markers can be used (Breiman, 1995) as more markers are able to be included with the estimates of marker effects shrunk towards zero by a constant factor ($\boldsymbol{\lambda}$) known as the smoothing factor (Whittaker et al., 2000). However, Xu (2002) demonstrated that this penalty approach may not be a valid method for QTL mapping when genome-dense SNP are used. Through a simulation study, Whittaker et al. (2000) showed ridge regression outperformed regression with a subset of marker effects estimated and traditional phenotypic selection.

Perhaps the most appealing method for genomic prediction lies within the “Bayesian alphabet.” Bayesian analysis has captured the attention of animal breeders for a number of reasons. First, Bayesian procedures have the ability to handle situations where the number of markers exceeds the number of observations (Gianola et al., 2009). Meuwissen et al. (2001) demonstrated how to make the transition from traditional BLUP estimation to analysis of marker effects with each SNP having a specific variance through Bayesian techniques. Bayesian analysis takes into account the degree of uncertainty revolving around each of the unknowns within the model (Gianola et al., 2009). Nonlinear equations, such as those within Bayesian methods, assume a prior distribution of SNP effects. This may be a more realistic approach as the effects from each marker may not all contribute small effects as assumed with linear predictions. In fact, major genes may exist on some chromosomes therefore having corresponding markers that explain a greater amount of genetic variance (VanRaden, 2008).

In Bayesian models, all unknown parameters are treated as random variables each with its own distribution. Variables are further classified as observables or unobservables. The observable variables include the phenotype (yi for i=1,…,n where n number of individuals) and the marker information. The QTL effect (bj) and the variance of each marker effect ($\boldsymbol{\sigma}$2j for j=1,…,p where p is the total number of markers) are considered unobservable. The distribution of the unobservable variables is referred to as the prior distribution, f($\boldsymbol{\Theta}$). The distribution of the observable variables is a function of the unobservables; the likelihood function, f(y|$\boldsymbol{\Theta}$). The likelihood function represents the contribution of the phenotypic information to knowledge of the prior ($\boldsymbol{\Theta}$). The posterior distribution is the conditional distribution of the parameters given the observable variables or simply the combination of the likelihood function and the prior distribution, f($\boldsymbol{\Theta}$|y). The Markov Chain Monte Carlo (MCMC) sampling technique draws samples from the posterior distribution to estimate the posterior means and variances (Xu, 2002; Gianola and Fernando, 1986).

Meuwissen et al. (2001) proposed two Bayesian methods with the advent of genomic selection; BayesA and BayesB. BayesA shares similarities with the previous regression models as it assumes that all markers have an effect and the prior distribution of the marker effects is normal with a marker-specific variance from a scaled inverse chi-square distribution. The normal distribution of SNP effects allows for some SNP to have larger effects than others, but with BayesA every SNP is treated as though it has a non-zero effect. However, if the number of QTL is substantially less than the number of markers and, given the multitude of SNP on current genotyping arrays, it seems logical to assume some markers will have no effect (Meuwissen et al., 2001; Goddard et al., 2010). For this reason, BayesB was introduced. BayesB allows for a proportion of the makers to have an effect (1-π) following a normal distribution and a proportion of the markers to have no effect (π). The proportion of markers that have no effect (π) is assumed a priori. The variance of the marker effects is sampled from a scaled inverse chi square distribution similar to the BayesA approach. One of the criticisms of BayesA and BayesB is the magnitude of influence the prior has on the shrinkage of

the marker effects (Gianola et al., 2009). BayesC assumes that every marker will not have an effect parallel to BayesB, but BayesC uses an equal variance for all SNP. BayesC can be extended by assuming that pi is not known and instead is estimated from the data (BayesCπ). Estimating π requires additional samples (Habier et al., 2011). The Bayesian alphabet continues to expand for animal breeding prediction.

Methods of genomic prediction primarily exploit linkage disequilibrium (LD) between SNP markers and QTL. Although SNP-based models offer promise to discover genomic regions associated with traits of interest, models utilizing haplotypes consisting of multiple SNP markers may provide greater power for association experiments. This is primarily justified as haplotypes may be in greater LD with the QTL than the individual SNP marker. As the number of SNP markers within a chromosomal segment increase, the likelihood that identical haplotypes carried by different animals are identical by descent increases as well. Given haplotypes are identical by descent, QTL alleles would be conserved within the haplotype (Hayes, 2013).

Inclusion of Genomic Information into National Cattle Evaluations

The augmentation of genomic information into National Cattle Evaluations (NCE) is critical for the progression of breeding programs. The advent of SNP panels to genotype large numbers of animals at a reasonable cost has made genomic prediction feasible. The QTL can be detected through LD with the markers, even though in practice the position of the QTL and the effects are not known. Summation of the product of the marker effects and SNP genotypes across all loci can estimate the breeding value of an individual based on markers effects only, or the molecular breeding value (MBV). This estimation focuses on the total genetic value of the animal instead of the precise discovery of QTL (Goddard et al., 2010).

Molecular breeding values have been augmented into NCE for the majority of popular beef cattle breeds. Genomically-enhanced expected progeny differences (GE-EPD) are calculated similarly to traditional EPDs with the addition of genomic test results. The way the genomic information is augmented into EPDs differs and can be divided into multi-step and single-step approaches. The multi-step approach requires the estimation of marker substitution effects, the prediction of the MBV and the combination of MBV with EPD. Single-step approaches include all phenotypic, pedigree and genomic information by modifying the relationship matrix of the mixed model equations (Fernando and Garrick, 2013).

In order to augment genomic information into NCE for one succinct value for selection decisions, a method referred to as “blending” was proposed. Blending is an index-like approach that utilizes traditional matrix calculations to establish the weighting factors b from Pb=g. These weightings will differ for each trait according to the accuracy of the MBV and for each animal according to the EBV reliability (Garrick and Saatchi, 2013). For most breeds, belnding is done post-evaluation and thus the MBV only influences the genotyped individual (Spangler, 2013).

Kachman (2008) introduced methodology to incorporate marker scores into NCE by integrating MBV as a correlated indicator trait in a multi-trait model. This approach was very adaptable for breed associations. Contrary to the blended approach, treating the MBV as a correlated trait had the ability for the genomic information to influence other animals in the pedigree that did not have genotypic data (Spangler, 2013). This approach was later adopted by MacNeil et al. (2010) for the use of incorporating ultrasound data and MBV as indicator traits for predicting carcass EBV. Exploiting the knowledge of genetic correlations among traits and between traits and MBV allow for multiple sources of information to be used to predict hard to measure traits, such as carcass traits that can only be obtained after an animal is slaughtered.

Recently, a single-step approach to GBLUP has been adopted. The single-step approach combines phenotypic, pedigree and SNP data in a single analysis. It creates the G relationship matrix using animals with genotypic data as with GBLUP and a sub-matrix using pedigree data for individuals without genotypic information. It combines those matrices into a relationship matrix, H. Evidence shows that single-step GBLUP (ssGBLUP) produces the same or improved accuracies of other genomic prediction models. It allows combined phenotypes from nongenotyped animal into the analysis. The limitations of ssGBLUP are the massive computing power needed. For large datasets, the inversion of the H matrix can be computationally expensive. Additionally, the G and A matrices need to be scaled appropriately (Misztal et al., 2013). Several breed associations are moving toward this single-step approach for their genetic analyses.

As with any method of genomic augmentation, animals with preexisting high accuracy EBV do not notice additional gains in accuracy by incorporating molecular information for a given trait. However, lowly accurate animals (i.e. those without progeny) do see gains in accuracy. The increase in accuracy through the incorporation of genomic information is directly related to the correlation between the phenotype and the MBV as the amount of genetic variance explained is equal to the square of the correlation. This is best illustrated by an example adopted from

Spangler (2011) using results reported by MacNeil et al. (2010). Assuming the correlation (r) for marbling score was 0.37, 13.7% (r2x100) of the additive genetic variance of marbling score was explained by the genomic test. Moreover, if the heritability of marbling is known to be moderate (h2=0.3), the gain in accuracy for an animal with no ultrasound record or progeny information is now equivalent to the accuracy of having 5 progeny with carcass records in its pedigree or ultrasound information on the individual itself through the incorporation of genomic data (Spangler, 2011).

The primary justification for incorporating molecular information into traditional selection methods is the faster rate of genetic gain than could be achieved by phenotypic data alone (Meuwissen et al., 2001). Meuwissen and Goddard (1996) predicted 8-38% extra genetic gain through the incorporation of marker information into BLUP breeding values. Additional advantages of genomic selection include improved accuracy of young, unproven animals as selection candidates (Kachman et al., 2013) such as yearling bulls who have not produced offspring. In the dairy industry, it is estimated that the use of genomic selection with reduce the costs of bull testing by upwards of 90% (Eggen, 2012). The ability to make more accurate selection decisions at a younger age will in turn reduce the generation interval, speeding the rate of genetic progress as Meuwissen et al. (2001) anticipated. Within the beef industry, genomic predictors allow for selection of economically relevant traits that have phenotypes that are only expressed late in life, phenotypes that are expensive or difficult to measure, traits that are limited by sex, lowly heritable traits or phenotypes that can only be collected once the animal has been harvested (Dekkers, 2004; Bolormaa et al., 2013).

Conclusions and Implications to Genetic Improvement of Beef Cattle

In regards to feed efficiency, genomic prediction is conducted as the association between genotypic data and measures of feed efficiency such as FCR, RFI or component traits including DMI or ADG. Multi-trait models have been proposed in the dairy (Lu et al., 2015) and swine (Strathe et al., 2014) industries as a more comprehensive investigation of feed efficiency. Lu et al. (2015) modeled DMI with energy sink traits including milk and MMBW. The classical calculation of RFI assumes relationships at the genetic and nongenetic levels are constant. The proposed multi-trait model allows these relationships to differ. Aside from the gains in genetic prediction accuracies with the multi-trait model over RFI, the multi-trait model allows the inclusion of all animals, even those with missing records (Lu et al., 2015).

Given multi-trait models can be deployed for genetic merit prediction, it seems possible to use the same approach with genomic prediction. A multi-trait model for GWAS including intake and gain is currently an unexplored area in the beef cattle industry. The frequency of intake and gain phenotypes differ considerably with gain measured more routinely on-farm. Since a strong genetic correlation exists between the two traits, a bivariate model would exploit the knowledge of the highly recorded trait to inform the limited phenotype.

Genomics has proven to be an exciting time within the beef industry; however, it is not a cure-all type of solution. With expensive to measure phenotypes, such as feed intake, it is practical to assume that only superior animals will be chosen for feeding trials. This non-random selection creates a bias in the genomic predictions (Spangler, 2013). Genomic prediction requires a large number of animals with phenotypic and genotypic data for training. For traits that are routinely recorded and have existing EPD, the transition to GE-EPD has been made. However, novel traits require greater effort to build resource populations of thousands of animals representing multiple breeds to establish genomic predictions that are robust across beef cattle populations. This has been the focus of a multi-institutional research effort in beef cattle (Saatchi et al., 2014). Genomic information could also be improved by having a greater understanding of the underlying biological mechanisms of distinct phenotypes (Eggen, 2012). Molecular breeding values work well when used within the same cattle breed as training, but lose efficacy when applied across breeds (Kachman et al., 2013).

At its current state, genomics serves as a tool to compliment selection techniques in order to gain higher accuracies. Although genomics was unable to serve as the magic bullet for animal breeding, it does bring forth advantages. Aside from the expected genetic gains through greater accuracies and decreased generation intervals, genomics has the ability to aid in parent identification and traceability. As industry and social demands continue to increase, it is vital for livestock producers to implement all possible selection techniques to produce the most efficient animals. The world population is expected to increase 40 to 50% by 2020 to 2030. To accommodate the growing demand for protein with the decreasing land resources, cattle must be more efficient in converting feed to consumable product. Increased environmental awareness also drives the demand for greater feed efficiency with concerns of the carbon footprint resulting from livestock production (Green, 2008). Cattle producers will face these contests and many others in years to come, but the opportunities through beef cattle genomics are considerable.

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Roy A. Wallace BIF Memorial Scholarship

The Roy A. Wallace BIF Memorial Fund was established to honor the life and career of Roy A. Wallace. Mr. Wallace worked for Select Sires for 40 years, serving as vice-president of beef programs and devoted his life to beef-cattle improvement. He became involved with BIF in its infancy and was the only person to attend each of the first 40 BIF conventions.

Roy loved what BIF stood for – an organization that brings together purebred and commercial cattle breeders, academia and breed associations, all committed to improving beef cattle. Wallace was honored with both the BIF Pioneer Award and BIF Continuing Service Award and co-authored the BIF 25-year history, Ideas into Action. This scholarship was established to encourage young men and women interested in beef cattle improvement to pursue those interests as Mr. Wallace did, with dedication and passion.

Proceeds from the Roy A. Wallace Beef Improvement Federation Memorial Fund will be used to award scholarships to graduate and undergraduate students currently enrolled as fulltime students in pursuit of a degree related to the beef cattle industry. Criteria for selection will include demonstrated commitment and service to the beef cattle industry. Preference will be given to students who have demonstrated a passion for the areas of beef breeding, genetics, and reproduction. Additional considerations will include academic performance, personal character, and service to the beef cattle industry.

Two scholarships will be offered in the amount of $1,250 each. One will be awarded to a student currently enrolled as an undergraduate and one will be awarded to a student currently enrolled in a master of science or doctoral program.

2016 Recipients

Ryan Boldt, Colorado State University
Will Shaffer, Oklahoma State University

Past Recipients

Name	University	Year
Joshua Hasty (graduate)	Colorado State University	2015
Matthew McIntosh (undergraduate)	University of Connecticut	2015
Heather Bradford (graduate)	Kansas State University	2014
Maci Lienemann (undergraduate)	University of Nebraska-Lincoln	2014
Loni Woolley (graduate)	Texas Tech	2013
Tyler Schultz (undergraduate)	Kansas State University	2013
Ky Polher (graduate)	University of Missouri	2012
Natalie Laubner (undergraduate)	Kansas State University	2012
Jessica Bussard (graduate)	University of Kentucky	2011
Cassandra Kniebel (undergraduate)	Kansas State University	2011
Paige Johnson (graduate)	Texas Tech University	2010
Sally Ruth Yon (undergraduate)	South Carolina	2010

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Past BIF Commercial Producer of Year Tour

Tailgate Ranch, Tonganoxie, Kansas

Tailgate Ranch is a commercial cow-calf operation consisting of about 1,500 acres of cool-season grass and legume pastures, 390 acres of brome hay meadows, and 60 acres of alfalfa. Tailgate was formed in 1962 by Paul McKie and grew into its present state. The ranch is located at Tonganoxie, KS, about 30 minutes west of Kansas City.

The ranch currently runs about 280 females (including 80 replacement heifers) in its spring calving herd and 120 cows in the fall calving herd. Their main focus over the last seven years has been developing and breeding high-quality replacement females following a strict culling regime in order to build a superior maternal cow herd. Feedlot and carcass data have been collected to help improve feed efficiency and product quality.

Bred heifers begin calving February 10, and are through in 45 days. Heifers are estrus synchronized and artificially inseminated (AI) one time, then cleaned up by proven, easy calving Angus / Red Angus bulls. Spring cows, consisting mostly of Red Angus or Angus crossbreds, begin calving March 1 and are through by April 15. Calves are pre-wean vaccinated, then weaned September 20 and put on growing ration and pasture until steers are either sold or sent to a feedlot. Heifers continue developing on pasture for the AI breeding program. Fall calving cows, mostly straight Angus, begin September 1 and finish by October 15. Fall calves are generally creep fed 60-80 days, weaned at 150 days of age, preconditioned and sold as grass cattle. Angus, Red Angus, and Red Angus x Simmental bulls are used on the spring herd with Angus, Red Angus and Braunvieh bulls used on fall cows.

Woodbury Farms, Quenemo, KS

Woodbury Farms is located in Osage County, Kansas, on the eastern edge of the Flint Hills. Their operation was started in 1881 when Fred H. Woodbury purchased his first 80 acres near Olivet, Kansas.The headquarters of the farm was moved 25 miles northeast in 1968, as the original homeplace was flooded to make way for the Melvern Reservoir.

The fourth generation of Woodburys now operates land in four counties, consisting of 5,000 acres of native and tame grasses and 400 acres of cropland. The cow herd is made up of 400 spring-calving cows, of which 175 are registered Angus and 225 are commercial Angus and black baldies, along with a few red baldies that stem from a Hereford cow base.

The Woodburys market calves through many avenues. All calves are backgrounded after weaning, with a majority of the steers being sold through the local sale barn. About 1/3 of the heifer calves are retained for replacements and a majority of the remainder are sold in a production sale in March, along with about 40 yearling bulls from the registered herd.

A small number of steers and heifers also are entered in the annual Flint Hills Beef Fest held in Emporia, Kansas. Cattle are summer grazed on the Flint Hills, then finished at a commercial feedyard where carcass data is gathered. Over the past several years, Woodbury cattle have won the grandstand show in both the steer and heifer divisions and placed high in the grass futurity contest. They also won the steer carcass contest in 2012.

With a long-standing tradition behind them, the Woodburys are focused on continuing the operation into the next generations.

Kniebel Cattle County, White City, Kansas

The year 2013 marked the 135th anniversary of Kniebel Farms and Cattle Company, a diversified family operation that has grown from a single homestead to encompass 7,000 acres of Flint Hills grass and farmland. Great-grandfather Kniebel started raising cattle in 1878. Like most operations, the base herd was Hereford; but unlike most operations, there were never any calves sold, only market-ready cattle. Originally, finished cattle were driven to the railhead. As years passed, these cattle were trucked to Kansas City, sold to packing houses through local sale barns and, eventually, bought directly by packers.

The current operation, owned and managed by Charles and sons Kevin and Chuck and their families, consists of 500 spring-calving cows and 60 fall-calving cows. They utilize a three-breed rotation, consisting of Red Angus, Angus and horned Hereford, in the crossbreeding program for their commercial herd. All the calves are finished in their family-owned feedyard. The farming portion of the ranch raises all the feed for the feedlot. It truly is a "conception to consumption" operation.

In 1996, they joined U.S. Premium Beef (USPB), a progressive group of ranchers and feeders that purchased part of the National Beef packing plant. USPB pays for harvested cattle on a grid, which rewards the quality we strive to produce.

Kniebel's raise cattle that are thick, moderate-framed, easy-keeping, pound-producing, and also happen to be higher grading, choice cattle. Through USPB, carcass data is collected and added to culling criteria. Kniebel Farms and Cattle Company believe in developing a well-rounded program and they do not chase any single trait or fad. They continue to try to find ways to be more efficient and currently are incorporating different grazing varieties and techniques to hold down costs.

Past BIF Seedstock Producers of the Year Tour

McCurry Angus Ranch, Burrton, KS

McCurry Angus Ranch is a family owned and managed operation located in south central Kansas in the Sandhills area of Reno and Harvey counties. McCurry Angus Ranch utilizes 2,000 acres for home-based operations, with satellite operations in Chase and Greenwood counties, which consists of primarily native tallgrass prairie in the Flint Hills. Buffalo, SD, is the ET base for 150 commercial Angus-based cows.

McCurry Angus consists of 400 registered Angus cows split evenly between spring- and fall-calving herds, and 250 spring-calving commercial Angus cows. About 175 bulls are sold yearly in a spring production sale and private treaty sales throughout the year. The target customers are commercial cattle producers. Currently, females are marketed primarily private treaty. In addition, spring-born commercial steer calves are marketed through Superior Livestock's online auction.

The ranch got its start in 1977, with the marriage of two third-generation Angus breeders. Andy and Mary McCurry began their first-generation start-up operation with seven registered Angus heifers representing pedigree lineage of seven distinct cow families, no land, no facilities, and no equipment. Today, 95% of the current herd traces back to those foundation females. Upon completion of college in 2004, the McCurrys' son, John, joined the operation full time and expansion occurred. The firsthand knowledge of developing a business from the ground up, with no external financial backers or financial means beyond themselves, has provided the McCurrys with a unique insight of the overall business structure required for profitability and sustainability.

Tours

Mushrush Red Angus, 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.

Fink Beef Genetics, Randolph, Kansas

Completely unique may be the best way to describe the beginning and day-to-day operations of Fink Beef Genetics (FBG), located near Manhattan, Kansas. Faced with two low paying, full time jobs, one Angus cow, no land and very little money in 1977, Fink Beef Genetics has grown to a seedstock operation that today includes Angus, Charolais and F1s. The business incorporates all segments of the beef industry from conception to consumption.

Since 1991, owners Galen and Lori Fink, along with their daughter Megan, have devoted their efforts to FBG. The business operates entirely with rented land, purchased feeds and basically no outside labor. The operation has used AI exclusively since 1977 and implants more than 1,000 embryos each year.

Cooperator herds were devised in 1990 to utilize the commercial producers' land ownership and management and form a profitable relationship for both parties. High accuracy sires dominate the breeding program and all pedigrees are stacked several generations deep to prevent surprises for customers.

Seedstock, embryos and semen are sold nationwide through public auctions, ecommerce and private treaty. The concept of pre-contracted bulls was developed by FBG in 1991. Customer service is a major part of the FBG program. Types of services available include the longest running sponsored calf sales in the United States, commercial female sales, seedstock cooperators in five beef alliances, credit for carcass data and working relationships with various feedlots. Fink Beef Genetics has co-founded two companies, Genetics Plus and Integrated Genetic Management, that focus on providing customers complete genetic assistance.

Since 1992, Finks have owned and developed the Little Apple Brewing Company Restaurant in Manhattan. This experience has provided insight into the beef industry from conception to consumption.

Moser Ranch, Wheaton, Kansas

The spring of 1987 saw the Moser Ranch market four bulls as breeding stock to local cattlemen, and in their 11th annual sale on February 8, 2003, 118 head of Simmental, Angus and Red Angus bulls sold into seven states and one Canadian province. Harry, a native of North Dakota and graduate of North Dakota State University in agriculture/animal science, and Lisa, a native Kansan with a degree in agriculture/animal science from Kansas State University, have been in the cattle business all of their lives. Along with their children, Cameron, Kendra and Kayla, the Mosers own and manage the Moser Ranch, located approximately 40 miles northeast of Manhattan in the northern Flint Hills of Kansas.

With the use of proven, predictable genetics, and extensive artificial insemination (AI) and embryo transfer (ET) program, utilizing every available economic and performance measurement as much as possible, the Mosers have built a very strong genetic base in their cow herd, while at the same time developing a strong customer service program. 150 spring and 20 fall-calving Simmental females, 40 spring and 10 fall-calving Angus, 25 Red Angus spring-calving females, and 50 fall-calving commercial Angus females make up the cow herd numbers on the Moser Ranch. Currently, seven producers are cooperator herds for the embryo transfer program, which began in 1991 and this enables the Mosers to produce approximately 150 additional calves per year. Bulls are sold primarily to commercial cattlemen in the annual bull sale, and females and embryos are sold private treaty.

The Mosers are very “hands-on” with respect to their entire operation. Whether it be day-to-day care of the cow herd, sire selection and mating decisions, all heat detection and AI work, weaning and development of bulls and replacements, putting up and grinding feed, all aspects of sale management and promotion, financial and breed association bookwork, computer time and web site updates, customer service and consultations or developing marketing options and feeding alliances, the family works together and utilizes the strengths each person brings to the operation.

In the past five years, the commitment to helping market customer calves through various avenues has been especially rewarding. Two alliances with which they are involved provide feedlot and carcass data on each individual animal that goes through each program. In addition, a Moser Influence Preconditioned Calf Sale held each fall gives still other customers a very lucrative option. Continued customer and consumer education is addressed regularly by holding seminars and hosting tours to enhance understanding of the beef industry.

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