



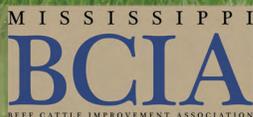
• BEEF. •

20 **IMPROVEMENT** **15**
FEDERATION

Biloxi, MS | June 9-12

Annual Convention

EXPANDING FOCUS





47TH BEEF IMPROVEMENT FEDERATION ANNUAL MEETING AND RESEARCH SYMPOSIUM



**MISSISSIPPI STATE
UNIVERSITY.**

**DEPARTMENT OF
ANIMAL AND DAIRY SCIENCES**
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June 1, 2015

Welcome to the Magnolia State!

On behalf of the Mississippi State University Extension Service and the Mississippi Beef Cattle Improvement Association it is my pleasure to welcome you to the 47th Beef Improvement Federation Annual Meeting and Research Symposium. Over the course of the next few days, I hope that you will get a taste of Southern hospitality as you interact with some of the world's best researchers, producers, and allied industry partners. The BIF Conference planning committee has worked hard to insure that this event will be extremely worthwhile and valuable.

With a growing population, fewer cattle, and resources, increasing efficiency and identifying superior genetics to rebuild the nation's cow herd has become extremely important. The Southeastern U.S., and Mississippi in particular, offers great weather, abundant forage, and great opportunities for growth of the beef industry. Finding the balance of profitability and sustainability will be an ongoing challenge for our industry, and this year's speakers should shed light on that focus.

This conference would not be possible without the support of our sponsors. Please take the time to thank each of them for their contributions. We would also like to thank the Mississippi Cattlemen's Association staff for their assistance in the planning, promoting, and volunteering at BIF. We hope you enjoy all the amenities of the Beau Rivage and city of Biloxi. Enjoy your week on the Mississippi Gulf Coast!

Sincerely,

Brandi B. Karisch, Ph.D.
Meeting Coordinator
Assistant Professor, Beef Cattle Specialist
Mississippi State University

BUILDING THE FUTURE OF ANIMAL AGRICULTURE



47TH BEEF IMPROVEMENT FEDERATION ANNUAL MEETING AND RESEARCH SYMPOSIUM

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47TH BEEF IMPROVEMENT FEDERATION ANNUAL MEETING AND RESEARCH SYMPOSIUM

SCHEDULE OF EVENTS

Tuesday June 9, 2015

10:00 a.m. - 12:00 p.m. BIF Board Meeting, *Azalea A/B*

12:00 p.m. - 7:30 p.m. Registration

1:00 p.m. – 4:00 p.m. Beef Improvement Federation Young Producers Symposium *Azalea C/D*

1:00 BIF History, Mission, and Meeting Orientation
Dr. Twig Marston, Red Angus Association of America

1:30 Current DNA Technology
Dr. Bob Weaber, Kansas State University

2:00 What's Your Motivation in the Genetics Business?
Dr. Jane Parish, Mississippi State University

2:30 Panel
Clint Berry, Joe Epperly, and Garrett Thomas

3:00 Social Meet and Greet
Sponsored by Southern Ag Credit 

5:00 p.m. – 7:00 p.m. Mississippi Welcome Reception *Magnolia A/D* *Sponsored by Geneseek*



7:00 p.m.–8:15 p.m. NAAB Symposium *Camelia Ballroom*

7:00 Welcome

7:15 Assessing the Economic Impacts of Estrus
Synchronization and Fixed-Time AI in Beef Production
Systems – *Dr. G. Cliff Lamb, University of Florida -
North Florida Research & Education Center*

7:45 Temperament and Acclimation to Human
Handling Impact Productive and Reproductive
Efficiency in *Bos indicus*-Influenced Cattle
Dr. Reinaldo F. Cooke, Oregon State University

Wednesday June 10, 2015

7:00 a.m. - 6:00 p.m. Registration

7:00 a.m. - 8:00 a.m. Breakfast
Sponsored by Mississippi Land Bank



8:00 a.m. Shuttle departs for spouse's tour

8:00 a.m. - 12:30 p.m. General Session I: Rebuilding a Cowherd *Camelia Ballroom*

8:00 Welcome

8:30 Setting the Stage
Dr. John Paterson, NCBA

9:00 Sustainability: What Does it Mean?
Dr. Sara Place- Oklahoma State University

Wednesday June 10, 2015 (continued)

8:00 a.m. - 12:30 p.m. General Session I: Rebuilding a Cowherd *Camelia Ballroom*

9:30 Sustainability: What Does the Data Say About
the Beef Industry?
Dr. Kim Stackhouse-Lawson, NCBA

10:00 Break

10:30 How Do Current Market Incentives Affect
Genetic Selection Decisions?
Dr. Lee Schulz, Iowa State University

11:30 Profitability: Looking to the Future of Your
Operation
Dr. John Michael Riley, Oklahoma State University

12:30 p.m. - 2:30 p.m.: Awards Luncheon- Seedstock and Commercial Producer of the Year Awards *Magnolia A-D - Sponsored by Zoetis*

2:30 p.m. - 5:00 p.m.: Technical Breakout Sessions *Azalea A/B, Azalea C/D, Magnolia E/F/G*

- Advancements in Selection Decisions - *Azalea A/B*
Chair: Dr. Bob Weaber, Kansas State University
 - o 2:30 Decoupling of Feed Intake & Measures of
Gain in Feed Efficiency Trials to Improve Selection
Ms. Kelli Retallick, Kansas State University
 - o 3:05 Improving the Ability to Utilize Multiple
Breeds in Commercial Beef Production: Breed
Specific Heterosis and Across Breed Calving Ease
EPD Adjustment Factors
Dr. Matt Spangler, University of Nebraska
 - o 3:40 Genomic Discovery of Bovine Respiratory
Disease Traits Using Commercial
Data and DNA Pooling
Dr. Larry Kuehn, USDA-ARS, U.S. MARC
 - o 4:15 How Whole-Genome Sequencing Will
Impact Selection Decisions
Dr. Jared Decker, University of Missouri
- Advancements in Emerging Technology - *Azalea C/D*
Chair: Mr. Jack Ward, American Hereford Association
 - o 2:30 National Genetic and Genomic Evaluations
- Present and Future
Dr. Dorian Garrick, Iowa State University
 - o 3:20 Updates on Feed Efficiency, Heifer Fertility
and whole genome sequencing
Dr. Jerry Taylor, University of Missouri



47TH BEEF IMPROVEMENT FEDERATION ANNUAL MEETING AND RESEARCH SYMPOSIUM

SCHEDULE OF EVENTS

Wednesday June 10, 2015 (continued)

- Advancements in Producer Applications - *Magnolia E/F/G*
Chair: Dr. Jane Parish, Mississippi State University
 - o 2:30 eBEEF: A New Educational Website on Beef Cattle Genetics
Dr. Alison Van Eenennaam, University of California, Davis
Dr. Darrh Bullock, University of Kentucky
 - o 3:20 Phenotypic Data Collection for Reproductive Traits in Heifers
Dr. David Patterson and Dr. Jared Decker, University of Missouri
 - o 4:10 Phenotypic Data Collection for Bovine Respiratory Disease
Dr. Mark Enns, Colorado State University

6:00 p.m.–10:00 p.m. Shuttle to and return to headquarters hotel

7:00 p.m.–8:00 p.m. Awards Dinner (Seedstock Producer of the Year) and Night at the Museum- Maritime & Seafood Industry Museum

Thursday June 11, 2015

7:00 a.m. - 6:00 p.m.: Registration

8:00 a.m. - 12:30 p.m. General Session II:

**Rebuilding a Cowherd
Focused on the Female**

Sponsored by Merial, Camelia Ballroom

8:00 Balancing Novel and Proven Applications for Female Selection

Ken Stewart, Rollins Ranches

C.J. Blew, Blew Partnership

9:00: Cow Lifetime Productivity Task Force

Dr. Mike McNeil, Delta G

10:00: Break - Sponsored by NAAB

10:30: Adaptability Panel

Moderator: Dr. Trent Smith, Mississippi State University

11:30: Charge and Session Wrap-up

11:45 a.m. Annual meeting, regional caucuses and election of directors *Magnolia A/D*

12:30 p.m.- 2:30 p.m.: Awards Luncheon: presentations of Pioneer awards, Continuing Service awards and President's address, *Magnolia A/D*

2:00 p.m.- 5:00 p.m.: Technical Breakout Sessions
Azalea A/B, Azalea C/D Magnolia E/F/G

Thursday June 11, 2015 (continued)

- Advancements in Cow Herd Efficiency and Adaptability and Live Animal, Carcass, and End Product *Magnolia E/F/G*,
Chair: Dr. Mark Enns, Colorado State University
Chair: Dr. Robert Williams, American International Charolais Association
 - o 2:30 BIF Feed Intake Guidelines Revision
Dr. Mark Enns, Colorado State University
 - o 2:50 BIF Feed Intake Guidelines Revision Challenges
Dr. Matt Spangler, University of Nebraska
Dr. Bob Weaver, Kansas State University
 - o 3:25 Water Intake in Beef Cattle
Dr. Megan M. Rolf, Oklahoma State University
 - o 4:00 Commercial Phenotyping
Alison Sunstrum, GrowSafe Systems Ltd.
 - o 4:35 Heterosis Effects on Stayability -
Dr. Scott Speidel, Colorado State University

- Advancements in Genetic Prediction
Committee Chair: Dr. Mark Thallman, USDA-ARS, U.S. Meat Animal Research Center, Azalea C/D
 - o 2:30 Genomic Evaluation Using Single-step GBLUP in Angus
Dr. Daniela Lourenco, University of Georgia
 - o 3:15 What Do SNP Chips Say About Sequence Variation?
Dr. Warren Snelling, U.S. MARC
 - o 3:45 Efforts in Developing Decision Support Software for the Beef Industry
Dr. Matt Spangler, University of Nebraska
 - o 4:30 Discussion on Using GPE and the Across Breed EPD Program to Help with Parameterization of Multibreed Evaluation -
Dr. Wade Shafer, American Simmental Assn.
Dr. Larry Kuehn, U.S. MARC

5:30 p.m.: BIF Board Meeting - *Azalea A/B*

Friday June 12, 2015

7:00 a.m.– 6:00 p.m.: Tour
Grand Bay National Estuarine Research Reserve
Seward Farms
Tanner Farms
Rocking B Cattle

GENERAL SESSION SPEAKERS

John Paterson serves as an Executive Director of Education for the National Cattlemen's Association. This team is part of a group which has focus in research, education and innovation in the beef industry. Specifically, educational programs are aimed at areas of animal welfare, sustainability, beef safety, increased production efficiencies, and beef quality assurance certification. Paterson received his Ph.D. in Beef Cattle Nutrition from the University of Nebraska, and from 1979 to 1993 was on the faculty of the Animal Science Department at the University of Missouri. He was a beef extension specialist at Montana State University from 1996 to 2012. Paterson was raised on a ranch in SW New Mexico and continues to ranch with his brother Tom in Alma, NM.



Among the numerous industry awards Paterson has received are the Pfizer Animal Health National Extension Award from the American Society of Animal Science and the Distinguished Service Award from the Western Section of the American Society of Animal Science. He was recently named a Fellow in Extension from the American Society of Animal Science and an Emeritus Professor from Montana State University. He has authored and co-authored more than 200 peer-reviewed and proceedings papers and given more than 200 invited presentations. Paterson and his wife, Diana, have three children; Courtney, a pediatrician in Billings, MT; Terrill, a Ph.D. candidate at Montana State University; and Cameron, an Instructor at Mercer College in Macon, Georgia.

Sara Place is an Assistant Professor of Sustainable Beef Cattle Systems in the Department of Animal Science at Oklahoma State since February 2013. Her research program focuses on the sustainability (environmental, economic, and social) of cattle production systems, and the measurement and mitigation of enteric methane emissions.



Prior to Oklahoma State, she worked with the Innovation Center for US Dairy and Winrock International as a Live-stock Production Consultant. She received her Ph.D. in 2012 from University of California, Davis in Animal Biology where her work focused on measurement and mitigation of greenhouse gas emissions from cattle. She earned a B.S. in Animal Science from Cornell University in 2008 and an A.A.S. degree in Agriculture Business from Morrisville State College in 2006. Place is originally from Upstate New York where she grew up on her family's dairy farm.

Kim Stackhouse-Lawson is the Executive Director of Global Sustainability at the National Cattlemen's Beef Association. She received her Ph.D. in Animal Science from the University of California, Davis. Kim leads the NCBA sustainability program. She is responsible for the beef checkoffs sustainability research program which is most well noted for



the completion of the first and largest sustainability assessment in agriculture. The assessment provides the beef community with its first sustainability benchmark and a path forward to improve sustainability along the entire value chain. In addition, Kim is a board member for the Global Roundtable on Sustainable Beef, administrator of the US Roundtable for Sustainable Beef, chair of the Five Nations Beef Alliance sustainability sub-committee, and a member of the International Meat Secretariat sustainability sub-committee. She was recently recognized in the 2013 UC Davis alumni spotlight for her leadership and career accomplishments in the area of sustainability.

Lee L. Schulz is an assistant professor and extension livestock economist in the Department of Economics at Iowa State University. Lee grew up on a diversified crop and livestock farm in Wisconsin. He obtained a B.S. in Agricultural Business from the University of Wisconsin River Falls, a M.S. in Agricultural Economics from Michigan State University and a Ph.D. in Agricultural Economics from Kansas



GENERAL SESSION SPEAKERS

State University. Schulz's integrated research, teaching, and extension program provides leadership in the study of, and develops educational programming for, critical issues facing the livestock and meat industries. These issues include animal identification and traceability, animal handling, commodity market analysis, consumer demand, economics of animal disease, financial analysis, producer perceptions and preferences, and risk management. Schulz is also known for his development of decision support tools that producers can use to help them make decisions that will improve the profitability of their operations.

John Michael Riley recently transitioned from the Mississippi State University Extension Service to Oklahoma State University's Department of Agricultural Economics. Throughout his career he has focused his efforts in the areas of commodity marketing, price analysis, risk management and agricultural policy. His undergraduate and M.S. work was done at Mississippi State University and his doctorate is Kansas State University. He was raised in Quitman, Mississippi on a small commercial cow-calf operation. He and his wife Jennifer live in Stillwater along with their 2 children, Landon and Emery.



Ken Stewart of Okeechobee, Florida attended Davenport College and studied general business management. Ken is general manager for Rollins Ranches, which has been a large commercial cow-calf producer for more than 40 years. The operation runs more than 10,000 cows at its 4 Florida locations, and uses Red Angus, Gelbvieh & Charolais genetics. Ken and his wife, Jenny, have one daughter, Keighly and two sons, Jimmy and Jacob.



C.J. Blew farms and ranches in a family partnership headquartered in Hutchinson Kansas. The operation is spread throughout South Central Kansas and consists of a commercial cow calf and diversified crop operation. The Blew family's Red Angus cow herd produces data driven, value added feeder cattle and commercial replacement heifers. The operation uses an extensive AI and carcass testing program with partnered Red Angus seed stock producers.



C.J. is an active leader in the ag cooperative system, currently serving on the CHS board of directors and as chairman of Mid Kansas Cooperative Association. C.J. also serves on the Kansas Red Angus Association board of directors and on the Hutchinson Community College Ag Advisory Board. C.J. is a member of the Red Angus Association of America, Kansas Livestock Association, and the Texas Cattle Feeders Association.

Michael MacNeil is an internationally recognized expert in the field of breeding and genetics research. His personal research has focused on practical avenues through which sophisticated animal breeding technologies can impact selection decisions by beef producers. He is author, co-author or editor of more than 350 scientific and technical publications (123 in refereed journals). The value that others attached to his work is evidenced by more than 75 national and international invitations, consultancy, offices held and committee assignments in professional societies, numerous citations in the scientific literature, and use of the results by action agencies, beef producers, breed associations, and others. From 1988 - 2011, Dr. MacNeil was the steward of the Line 1 Hereford population at Fort Keogh. During this time, Line 1 germplasm has impacted the Hereford breed in every country where Hereford cattle are raised. At the end of 2011 Dr MacNeil retired from USDA Agricultural Research Service after a career of more than 30 years. He is currently engaged in several significant partnerships to enhance genetic evaluation of livestock and improve profitability of production. In addition, he continues working to train the next generation of scientists both in the USA and in developing countries.



Drought Was Just One Reason the US Cow Inventory Declined

John Paterson, PhD

Executive Director of Education, National Cattlemen's Beef Association

Introduction.

It is widely expected that the next two decades will be bright for the beef industry because there will be more people who will have more money and who will want more beef. Worldwide, as medium incomes of consumers increase from \$500/yr to \$2000/yr, it is projected that yearly meat expenditures will increase from \$19 to \$170. Likewise, increasing income from \$2000/yr to \$9000/year will further increase total meat expenditures to a projected \$397/year. The rise in ethnic populations will have an impact on beef consumption because Hispanics are anticipated to increase from 16% to 30% of households, Asians from 5% to 9% and African-Americans from 14% to 15%. What this means for beef is that producers must maintain and broaden beef's appeal to all ethnic groups because culinary tastes will continue to shift. Remember, that the customer is always right. But also consider that the customer is not always informed, scientifically literate, interested in the truth or concerned about the livestock producer's well-being (Anderson, 2015).

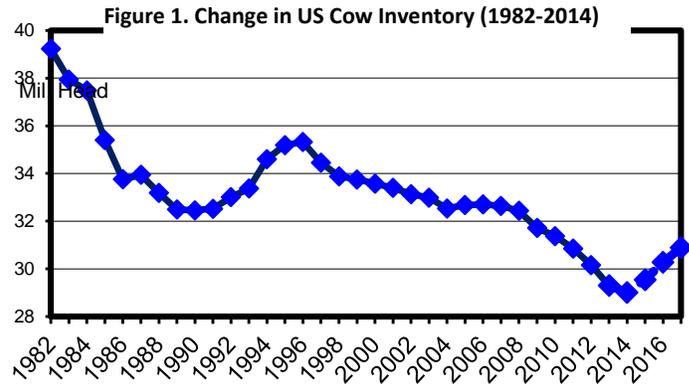
Demand for all beef has increased but it has especially increased for ground beef. Since 2009 the price of hamburger has increased more than 60% and much of the carcass is now ground. Although ground beef is very important, it will remain a secondary-targeted product (Brink, 2015, NCBA Cattlemen's College, San Antonio). It has been predicted that the future of the industry will be in the production of big, high value cattle to maximize revenue per unit. The beef industry will facilitate this by exporting some of our premium product and importing low cost, lean trim for grinding and the production of hamburger.

How has the population of the US cowherd changed?

Historically, since the early 1950's the beef industry has witnessed four large spikes in calf prices; 1951, 1973, 1979 and 2014 (Brester, 2014, MT Nutrition Conference). The commonality of these years is that they were years of low cattle numbers and were the start of herd expansion. During the 1951 spike there were concerns about food security following supply disruptions after WWII and also concerns about a new world war. However, by 1954 calf prices had declined below the long run average. In 1973 the price rise was partially due to declines in world food production and the 1972 Russian grain deal. By 1975 prices once again declined, in response to demand decline and this was also a year for record cattle inventory. Between 1975 and 1978 there was a 15% decline in cattle numbers and herd rebuilding began in earnest. However, rebuilding only lasted a couple of years because of the 1979 OPEC oil shock hurt demand.

Most recently, the beef cow inventory has declined from approximately 40 million head to a 50 year low of approximately 28 million head (Figure 1). There are probably at least six reasons for the decline; prolonged drought, high feed costs, high operating cost, age of the producer, competition with crops which have been more profitable and unbelievable prices for calves, heifers and cows which have slowed rebuilding.

From about 1982 until 1991 there was sustained liquidation of the cow herd (39 million to 32 million cows). Starting in 1991 there was herd expansion which continued until 1996 when liquidation started again. However, due to drought liquidation (2000), recession (2009) and continued drought (2012-2014) the inventory dropped to less than 29 million beef cows.



Cornell researchers have predicted that a “mega drought” will occur late in this century and could last for three decades. One pundit (Durden, 2015) observed that California has no contingency plan for a persistent drought (let alone a mega drought) except to stay in an emergency mode and “pray for rain”. As an example of the devastating effects of drought during the years of 2007-2014, Texas lost 25% of its cow inventory, Oklahoma lost 12% and New Mexico lost 16%.

Although huge in inventory losses, drought wasn’t the only reason for a decline in cow inventory. Approximately 18% of farms operated by producers between the ages of 35-54 saw an exit from the industry between 2007 and 2012. This represented approximately 24,000 operators. Presently, 64% of cow ownership is held by producers older than 55 and 65% of pastured acres are owned by producers older than 55 (2012 Census of Agriculture).

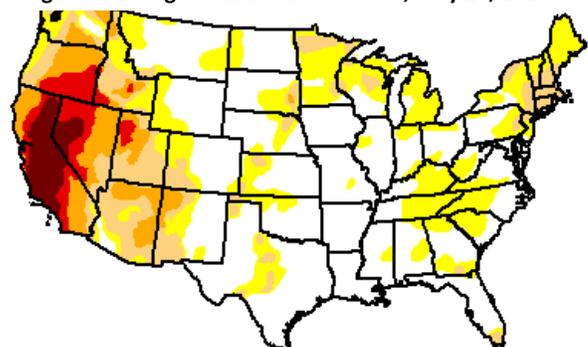
The result of a shrinking calf crop means that as prices go up, feedyards close, packing plants close (Tyson, Cargill, National Beef) and final weights of fed cattle go up. Management at the feedyard level has seen an aggressive use of implants and beta agonists. With the decline in feeder calf numbers, genetic capability of the cattle has improved because less productive cows were sold in response to high prices and consequences of drought.

Interestingly, part of the cow inventory loss was due to competition for additional crop land. Peel (Oklahoma State University) reported that cropland used for pasture declined 64% from 35.8 million acres to 12.8 million acres (2007- present) because farmers tilled additional acres in order to exploit high grain prices. Ringwald (2014, Drovers Journal) showed that the average net return for wheat, corn, soybeans and sunflowers was \$65/ac vs. \$16/ac for the cow-calf operators. This may be one major reason why the decline in cow inventory has ranged from 12% in IA to 23% in TN.

What are the predictions for the future?

Parts of Texas and Oklahoma have received almost two feet of rain over the past couple of months which has stopped the drought. But, California and parts of the Southwest continue to be either extremely dry or abnormally dry (Figure 2).

Figure 2. Drought Conditions in the US, May 26, 2015



Last year, in anticipation of herd rebuilding, Troy Marshall (2014) asked the question “Are producers going to add 100 cows and invest \$100,000 to do it or will they use that money to pay off debt, upgrade the tractor or remodel the kitchen?” Chandler Keyes (2014) wrote an Op Ed entitled “The Industry’s Future is Positive but Partly Cloudy” (BEEF, June 17). He said that 70% of our beef comes from 30% of our producers. If this trend continues, then “If you’ve got 200 mother cows, I think you’re in the business and will try and find ways to expand. However, if you have less than 200 cows and you do it by yourself, I’m not so sure you’re going to run out there and try and find pasture, buy cattle and find a hired hand”. Randy Blach from CattleFax was quoted as saying “The beef cowherd must expand in the next 1-4 years and if it doesn’t, we will have a smaller industry and we will move beef from the center of the plate to more of a specialty item”.

Expansion of the cow herd at present is occurring at a faster than expected rate with 72% of the growth occurring in the Southern Plains. Sixty-six percent of the retained beef replacement heifer growth is also in the Southern Plains. When beef cattle producers have been asked why they are optimistic in rebuilding their cowherds they responded that 1) supply and demand fundamentals encourage rebuilding, 2) there is international demand for beef, 3) with the lessening of the drought, there is available feed and forage and 4) there is less volatility in input costs. However, when producers were asked what would make them pessimistic about the future they responded that 1) government regulations and oversight would hinder expansion, 2) lessening consumer demand, 3) industry consolidation and concentration and 4) credit availability to purchase replacement heifers.

Dr. Pete Anderson (2015, NCBA Cattlemen’s College, San Antonio) summarized the challenge to cow herd growth as “North America must get in, stay in and dominate the worlds high quality beef market. Exports are a key because no other countries can do that as well, it is a best use of our resources, and it is a more profitable way to export grains”. Finally, Derrell Peel (2014) summarized the psychology of the current cattle business: “Cattle producers thrive on adversity but sometimes they seem ill-equipped to handle prosperity”.

Sustainability: What does it mean and why does it matter?

Sara E. Place

Oklahoma State University

Introduction

The global population is expected to grow to between 9 and 10 billion persons by the year 2050, with much of the population growth occurring in developing nations and the global south (United Nations, 2013). There has been a major migratory shift of population from rural to urban environments, and now more than 50% of the world's population lives in cities (United Nations, 2014). In addition to a growing population, incomes are increasing around the world. Both growing numbers of people and increasing affluence will drive growth in demand for animal protein by an estimated 70% over the next few decades (Gerber et al., 2013). Simultaneous to increasing animal protein demand, the productivity of agriculture faces the constraints of limited resource availability (e.g., water) and global climate change and variability. With the convergence of increasing demand for food and global environmental changes, interest in sustainability and sustainable intensification of agriculture has grown.

Does sustainability equal carbon footprint?

While many agree sustainable food systems are needed, agreement on what “sustainable food systems” are remains elusive. Much of the recent interest in sustainability pertaining to beef production has been driven by concerns regarding the environmental impact of beef production. A 2006 United Nation's Food and Agriculture Organization (UN FAO) report titled “Livestock's Long Shadow” (LLS; Steinfeld et al., 2006) was particularly influential in driving media interest in the environmental impact of beef and animal agriculture more generally. The executive summary of the 416 page report contained the following two sentences:

“The livestock sector is a major player, responsible for 18 percent of greenhouse gas emissions measured in CO₂ equivalent. This is a higher share than transport.”

The 18% of greenhouse (GHG) emissions figure has been extensively quoted in popular media articles and documentaries (see: <http://www.cowspiracy.com/facts/>). LLS used a life cycle assessment (LCA) to determine the 18% figure. LCA is essentially an accounting system that sums all GHG emissions from the entire production chain of a given product, from “cradle-to-grave.” For an LCA of beef production, the GHG emissions sources can include emissions from feed production (e.g., nitrous oxide emissions from soil), emissions from the animals themselves (e.g. methane emissions from enteric fermentation), and emissions from processing and transportation (e.g., carbon dioxide emissions from burning fossil fuels). Included in LLS' LCA of global livestock production was land use change, which included desertification and deforestation. Land use change accounted for over 35% of the total estimated GHG emissions attributed to livestock in LLS (Steinfeld et al., 2006). For land use change, the lost potential of photosynthetic organisms (e.g., trees, grasses) to sequester carbon dioxide from the atmosphere is counted as a source of GHG emissions, along with any emission of carbon stored in the soil.

While land use change is a serious environmental issue, animal agriculture has not been a major driver of land use change in the United States in the past several decades (Pitesky et al., 2009). Additionally, the transportation and energy sectors in the United States generate far more GHG emissions as a percent of total GHG emissions as compared to the whole of U.S. animal agriculture. According to the most recent U.S. GHG emissions inventory, animal agriculture contributes approximately 3.6% of GHG emissions (considering enteric methane and manure methane and nitrous oxide emissions; US EPA, 2014). Fossil fuels burned for transportation and electricity contribute 30.6% and 25.8%, respectively, of total U.S. GHG emissions (US EPA, 2014). Clearly, the 18% of GHG emissions statistic from LLS is not appropriate to apply uniformly across all regions and nations around the world. To better represent the geographic variability in GHG emissions from animal agriculture, the UN FAO conducted a follow-up report that disaggregated GHG emissions from animal agriculture by region. The report found that 14.5% of global anthropogenic GHG emissions were from animal agriculture, and there was significant variation from region-to-region (Gerber et al., 2013). Indeed, the average GHG emission intensity (i.e., carbon footprint) was 46.2 kg of CO₂-equivalents¹ per kg of carcass weight of beef; however, the range was 14 to 76 kg of CO₂-equivalents per kg of carcass weight, with the lowest GHG emissions intensities found in developed nations with intensive production systems (Gerber et al., 2013; Opio et al., 2013).

Carbon footprints of beef production not only vary based on geographic location (due to differences in production systems, technologies, animal genetics, etc.), but also temporally. In the United States, advances in animal genetics, nutrition, reproduction, etc. have led to improvements in the production efficiency of beef production. Simply, production efficiency can be defined as minimizing the amount of inputs (e.g., feed, fossil fuels) and outputs (GHG emissions) to produce a given quantity of beef (Place and Mitloehner, 2010). In many, but not all cases, improvements in efficiency that beef producers have pursued to improve their business profitability and viability have translated into reductions in the carbon footprint of U.S. beef production. Rotz et al. (2013) simulated the U.S. Meat Animal Research Center's beef production system and found that the carbon footprint was reduced 6% from 1970 to 2011. Capper (2011) estimated that the U.S. beef carbon footprint was reduced by 16% from 1977 to 2007. However, environmental sustainability encompasses more than just carbon footprint, (both Rotz et al. (2013) and Capper (2011) did estimate other categories environmental and resource use footprints, e.g., water footprint of beef), and sustainability more broadly must consider economic and social factors relating to beef production.

¹ Different greenhouse gases have different radiant forcings, or abilities to trap heat in the Earth's atmosphere, and different atmospheric lifetimes. To account for these differences, the Intergovernmental Panel on Climate Change (IPCC) has established global warming potentials (GWP) for each GHG on a carbon dioxide basis for a 100-year time horizon, often referred to as carbon dioxide equivalents (CO₂-equivalents). The 100-year GWPs from the 2013 IPCC report for methane and nitrous oxide are 28 and 265 respectively, without the inclusion of climate-carbon feedbacks, and 34 and 298, respectively, with the inclusion of climate carbon feedbacks (IPCC, 2013). Climate carbon feedbacks relate to the positive feedbacks during warming. For example, increased warming caused by GHG emissions can accelerate methane release from the Arctic, further accelerating the warming process.

Beef sustainability: What is it?

Sustainable development was defined in 1987 as meeting “the needs of the present without compromising the ability of future generations to meet their own needs” (Brundtland, 1987). Others have defined sustainability as meeting a triple-bottom line of balancing people, planet, and profit (Elkington, 2004). Combining these concepts, sustainable beef production can be defined as meeting current and future demand for safe, nutritious beef products while maintaining long-term business viability, stewardship of natural resources, and responsibilities to community, family, and animals. The optimum balance of the economic, environmental, and social aspects of sustainability will not be the same for each operation, due to differences across production systems including varying climates, available resources (financial capital, human capital, natural resources), and value judgements of both producers and consumers. The social aspects of sustainability are particularly hard to quantify, and thus, many of the tradeoffs and synergies between the different areas of sustainability remain unquantified, and in some cases are unquantifiable.

The definitional and quantification challenges of beef sustainability stem from beef sustainability being a “wicked problem.” Peterson (2013) outlined four distinguishing characteristics that make problems wicked as the following: (1) no definitive formulation of the problem exists, (2) its solution is not true or false, but rather better or worse, (3) stakeholders have radically different frames of reference concerning the problem, (4) the underlying cause and effect relationships related to the problem are complex, systemic and either unknown or highly uncertain. In essence, the wickedness of sustainability is due to scientific uncertainty of individual and inter-related aspects of sustainability (e.g. methane emissions from grazing beef cattle – few data exist) and differences in perspectives and values across stakeholders. For beef production, stakeholder groups are broad and extend the entire beef value chain, from beef producers, processors, retailers, consumers, as well as governmental and non-governmental organizations (e.g. World Wildlife Fund, The Nature Conservancy). Each of these stakeholders may prioritize a certain aspect of sustainability above others. For example, a consumer may value food safety and affordability as the highest priorities of beef sustainability, while an environmental group may value lowering the environmental footprint of beef production as the highest priority for beef sustainability. Transparently delineating the different values stakeholders bring to a beef sustainability discussion before advancing to sustainability “solutions” is critical to avoid intractable debates.

Context for Beef Sustainability

One of the arguments against the sustainability of beef production is that cattle are inefficient converters of feed to body weight gain, and our food systems would be more sustainable and feed more people if they included less ruminant meat products (Cassidy et al., 2013; Heller and Keoleian, 2014; Stehfest et al., 2009). The trade-offs of dietary switches are often calculated by assuming pasture and cropland used for livestock production would be abandoned (Stehfest et al., 2009) or the forage component of livestock diets is simply ignored (Cassidy et al., 2013). Additionally, the byproducts of ruminant meat production (e.g., leather) are often assumed to be replaced without consideration of the environmental impact of the

alternatives (Stehfest et al., 2009) or are not considered (Cassidy et al., 2013). These assumptions and omissions likely limit the usefulness of the conclusions that can be drawn from such analyses, though, to be fair, accurately modelling the environmental impacts of the global food system or consequences of dietary shifts is a nearly impossible task due to the complexities and uncertainties involved. Nonetheless, improving feed conversion efficiency is a key area of opportunity to improve the sustainability of beef production. Enhancing feed conversion efficiency has often focused on improving individual animal performance of confined feedlot cattle fed total mixed rations. However, improving and selecting for more feed efficient cattle in the feedlot may increase mature cow size and increase the feed requirements of the U.S. cow herd. Considering the entire beef value chain's feed conversion efficiency (total feed resources required by all animals in the seedstock, cow-calf, stocker, and feedlot phases/total live weight gain of animals destined for slaughter), improving feed conversion efficiency may become more complex. For example, the reproductive efficiency of cow herd could significantly impact the size of the supporting herd (cows, heifers), and consequently feed resources, required to produce a given amount of beef; therefore, improvements in the calf crop should have positive implications for whole herd feed conversion efficiency.

Fundamentally, the beef industry is about converting natural resources of lower human value to higher human value products. Less than 1% of the solar energy that reaches Earth is captured by photosynthetic organisms, which is the energy that allows all heterotrophic life (i.e., non-photosynthetic, from bacteria to cattle to humans) to exist. Much of the solar energy captured by photosynthesis is in the form of the compound cellulose. Ruminants play a unique role in the food system by converting cellulose, which is indigestible by humans and the most abundant organic (carbon-containing) molecule on Earth, into high quality animal protein and ancillary products (e.g., leather). The monogastric animal industries (e.g., poultry, swine) have a limited capacity to use high cellulose-containing forages and by-product feeds (e.g., almond hulls, cottonseed), so while those species (and fish) may be more efficient when expressing feed efficiency as feed-to-gain, consideration should be given to the conversion of human inedible-to-human edible energy and protein.

Oltjen and Beckett (1996) evaluated dairy and beef cattle systems using a costs and returns analysis of humanly edible energy and protein. Humanly edible returns for digestible energy ranged from 37 to 59% and returns to digestible protein ranged from 52 to 104% depending on the time spent in the feedlot and the feedstuffs used (increasing amounts of corn in the diet lowered the returns on humanly edible inputs, and increasing the use of by-products increased the return to humanly edible inputs; Oltjen and Beckett, 1996). Wilkinson (2011) found similar results when evaluating the human edible energy and protein conversion efficiencies of U.K. beef systems, with increasing incorporation of cereal grains into the diets of beef cattle resulting in poorer conversion efficiencies. A tradeoff of increasing forage in the diets of cattle is those diets result in higher enteric methane emissions (Johnson and Johnson, 1995). Additionally, ruminants can add value to agricultural systems by preventing permanent grasslands from being converted to cultivated cropland and by incorporating forages into crop rotations, both of which can improve soil conservation and health. Rangelands (approximately 50% of the Earth's land surface, much of which is unsuitable for cultivation) and human inedible

by-products will always be an important part of our agricultural system; therefore, cattle and other ruminants play an important role in enhancing nutrient recycling in our food system.

The argument that beef production, due to its inefficiencies, negatively impacts food security misses many of the complicated factors that influence food security. Food security for current and future generations is often used as a major justification for increasing the productivity of agricultural production. Indeed, food security is a critical issue in the United States and around the world. In 2013, 14.3% of all U.S. households and 19.5% of U.S. households with children were estimated to be food insecure (Coleman-Jensen et al., 2014). Food insecurity in the United States is defined as reduced food intake and disrupted eating patterns at times during the year due to a lack of money and other resources for food (Buzby et al., 2014). Globally, approximately 1 in 9 persons, or 802 million people, suffer from chronic undernourishment (FAO, IFAD and WFP, 2014). A logical conclusion upon first observing the number of food insecure persons is that we must produce more food to meet their needs. Increased food production is certainly a component of the solution to food insecurity; however, food security is far more complicated than simply producing enough food to meet the needs of the global population. For example, it is estimated that 30% of edible food and approximately 20% of the global meat supply is wasted throughout the production chain (UN FAO, 2015). In the United States, an estimated 31% of the edible food supply and 27% of meat is wasted (Buzby et al., 2014). Based on the proportion of food wasted, it seems current levels of food production in the world would be able to meet the needs of the global population if there was no waste. However, food security is more complicated than a simplified equation of food security = [calories produced]/ [calories required by the human populace]. Food and nutritional security depend on availability and access to food. Physical infrastructure (transportation systems, refrigeration), market infrastructure, incomes, political stability, etc. all play important and interrelated roles in determining how food secure a population is, whether considering the United States or any other nation in the world. Consequentially, during discussions of the role of intensification and increasing productivity of beef production, and agriculture more broadly, the nuance and complicated nature of food security should not be ignored to justify certain production systems or technologies.

Conclusion

Clearly, sustainability is important to the beef industry, with the U.S. Dietary Guidelines Advisory Committee including sustainability in their draft report of the 2015 Dietary Guidelines and major retailers like Wal-Mart seeking sustainable products to sell in their stores. Improvements in production efficiency are associated with decreases in environmental footprints, which translates into potential win-win scenarios where producers can improve economic and environmental sustainability simultaneously. In the face of increasing global protein demand, further improvements in the production efficiency of the beef system will be necessary to meet demand and minimize the environmental footprint of beef. However, the social acceptability of production practices must be considered. Approximately 2% of Americans are agricultural producers, but 100% of the population are eaters – the values and concerns of the public cannot be ignored. Finally, there are significant data gaps and uncertainties related to beef

sustainability, particularly related to the tradeoffs and synergies across the economic, social, and environmental indicators of sustainability, which should be remedied with research and respectful dialogue among members of the beef value chain.

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Sustainability

Executive Summary



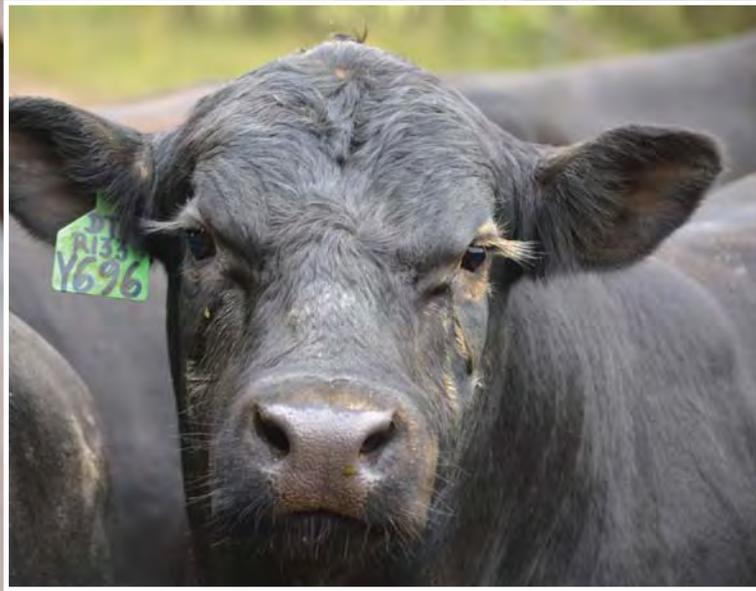


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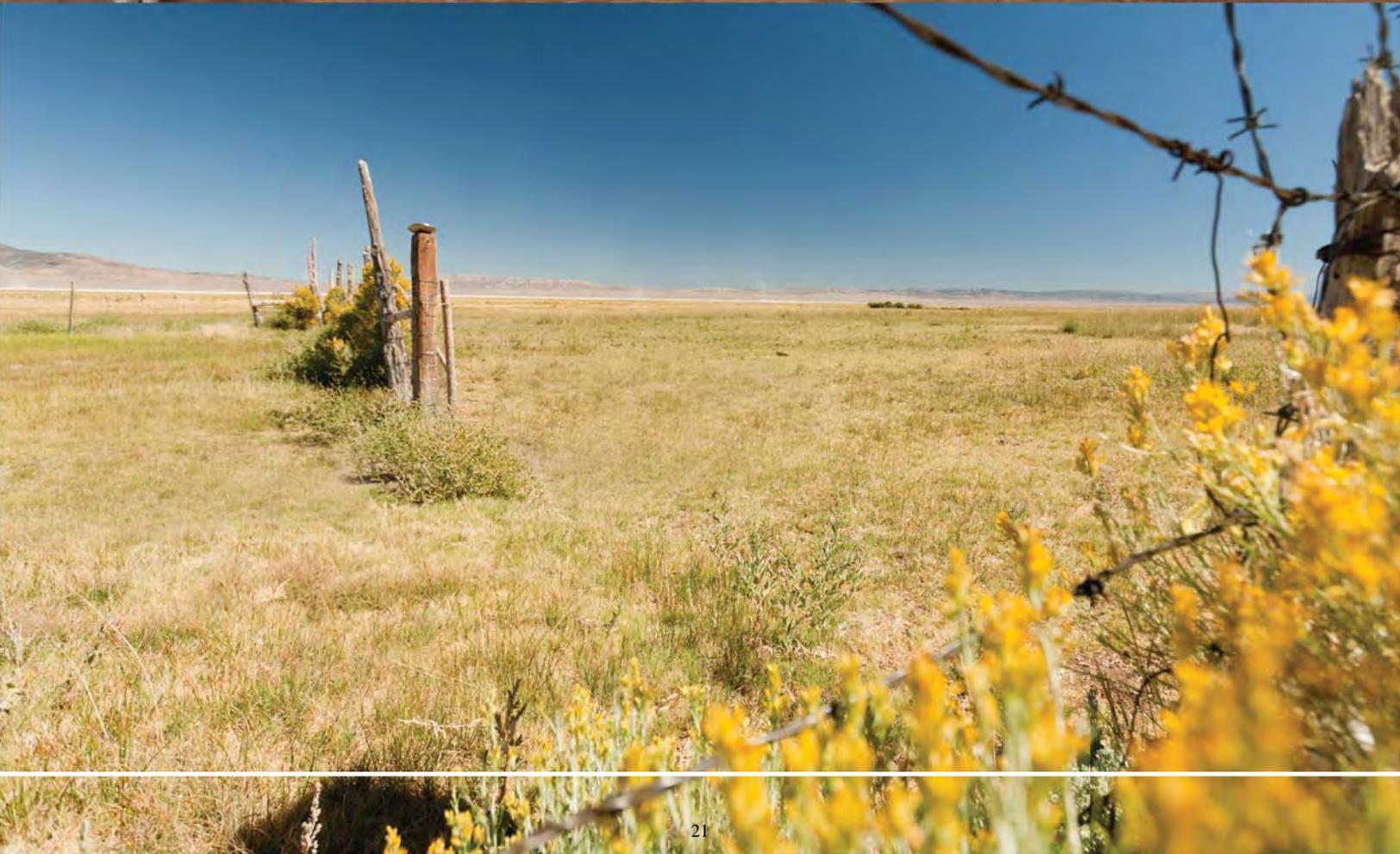
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Introduction

Beef Industry Sustainability: Meeting growing global demand by balancing environmental responsibility, economic opportunity and social diligence throughout the supply chain.





A Journey of Continuous Improvement

Ensuring a sustainable food supply is undoubtedly one of the greatest societal challenges. By 2050, 70 percent more food will be required to feed the growing population and all agricultural production will be needed to meet the increasing demand.

Today, a sustainable food supply includes balancing efficient agricultural production with environmental, social and economic attributes. The beef community recognizes the important role it plays in contributing to more sustainable food and has committed to a journey toward more responsible beef production. As a first step, the Beef Checkoff Program launched a comprehensive assessment to quantify and benchmark environmental, social and economic aspects of beef industry sustainability.

This beef industry life cycle assessment is not intended to compare one beef production practice to another. Instead, it is designed to provide a benchmark which will help all beef operators along the supply chain find individual means of improving the efficiency and sustainability of their operations.

The beef industry is the first food system to benchmark its current status in a holistic manner that encompasses all three aspects of sustainability. The research included an evaluation of thousands of data points to quantify the industry's progress since 2005. By documenting that progress, the beef community can for the first time provide science-based answers to questions about its sustainability.

Page Five



Approach



Beef production involves more complex biological processes than any other food system. The completion of this life cycle assessment required the entire value chain to work together to account for inputs and outputs. That cooperation between segments marks a new chapter for the beef community and demonstrates the industry's commitment to a path of continuous improvement.



Conducting a Sustainability Assessment

Defining sustainability is challenging because it means different things to different stakeholders. In an effort to determine the most relevant of these attitudes about the sustainability of beef, the research team and contractor BASF Corporation conducted a perception analysis, which gathered opinions about beef production practices from a wide swath of stakeholders and thought-leaders.

The compilation of these perceptions (Figure 1) allows beef producers to focus their improvement efforts in areas with the greatest perceived importance. For example, because animal welfare was ranked as highly important by stakeholders, the industry can focus on making progress toward improved

sustainability by focusing its efforts on initiatives such as Beef Quality Assurance.

A sustainability assessment requires the use of life cycle assessment methodology to measure the impacts of production. A life cycle assessment is essentially an accounting system that uses complex models to quantify all inputs and outputs involved in producing beef, from birth of the animal to the consumer's plate (Figure 2). Inputs along the entire value chain were included, from the pre-chain production of fertilizer, packaging, chemicals and others; to primary inputs like feed and water, through consumption and disposal of packaging materials by the consumer. These impacts were quantified against a consumer benefit (CB) of one pound of boneless, edible, consumed beef.

The Beef Industry Sustainability Assessment was designed to capture how industry changes and improved management practices have affected beef's long-term sustainability. Significant changes in industry practices led to the selection of benchmark years. The 1970s were chosen because they reflect the shift to the production of boxed beef. The benchmark year of 2005 was selected to reflect the widespread use of distillers grains in feedlots. The final benchmark year, 2011, represents the present day beef value chain.

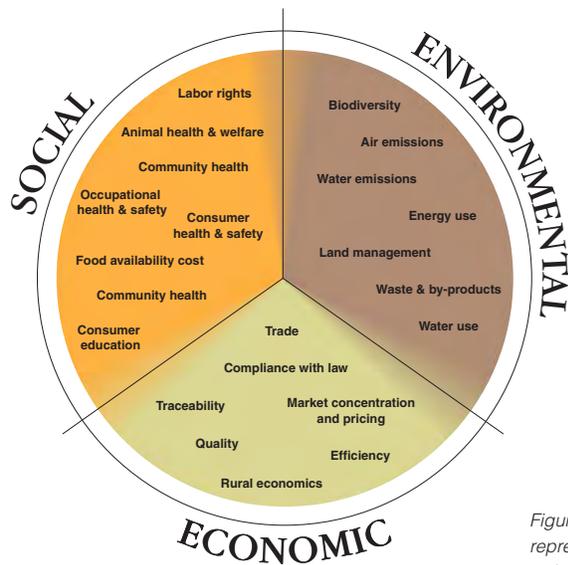


Figure 1 | Perception Analysis

Figure 1: Stakeholders were asked to define beef sustainability. This Figure represents the most common definitions given by stakeholders. The beef industry definition of sustainability, "balancing environmental responsibility, economic opportunity and social diligence," encompasses stakeholder perceptions.



Approach



Figure 2 | Beef Life Cycle

Beef production is extremely complex and conducting a thorough life cycle assessment required the development of new methods to account for the inputs and outputs of the entire production process. Two independent models were used to quantify the sustainability of the beef value chain. One model was used to simulate biological processes on-farm; the other was used to quantify impacts in the post-harvest sector.

Pre-harvest Data Collection

For Phase 1 of the Beef Industry Sustainability Assessment, the data used to simulate the pre-harvest sector, which includes cow-calf and feedlot segments, were gathered from the United States Department of Agriculture's (USDA) Meat Animal Research Center (MARC) in Clay Center, Nebraska. Utilizing the MARC records, which date back to the 1970s, the research team was able to predict all on-farm processes (for example, crop and animal performance, irrigation, etc.) through use of the Integrated Farm System Model (IFSM).

By combining MARC data with the simulation capacity of the IFSM, the research team gained the benefits of a transparent system, with years of research-proven accuracy to back it up.





The model was used to simulate 25 years of weather and its impact on crop production, feed use and animal performance, as well as the return of nutrients back into the land at the MARC facility. For example, growth and development of crops were predicted for each day of the growing season based on soil, water, nutrient availability, ambient temperature and solar



Figure 3 | Pre-harvest: IFSM

radiation. In the case of cattle predictions, the IFSM model was used to simulate animal growth; lactation requirements for cows; maintenance requirements for cows, calves, replacement heifers and finished cattle; and the nutrient content of any manure produced (Figure 3).

Some of the results comparing model accuracy to actual data collected can be seen in Table 1.

Table 1 | Actual reported vs. IFSM-simulated feed production at USDA MARC for 2011

Feed Type	Actual tons Dry Matter	Simulated tons Dry Matter	% Difference
Alfalfa / grass hay silage	6,096	6,102	0.0
Corn silage	5,444	5,422	0.4
High-moisture corn	3,092	3,109	0.5
Corn grain	1,834	1,820	0.8
Distillers grains	1,841	1,837	0.2
Total	18,307	18,290	0.0





Approach

Although the MARC data and IFSM were demonstrated to be highly accurate and representative of beef cattle production systems in the United States, some significant differences exist between MARC production practices and those elsewhere in the country. Therefore, further research is needed to regionalize the data to better represent average production systems in other parts of the country, which will be included in Phase 2 of this project.

Post-harvest Data Collection

The life cycle assessment for post-harvest considered the packing, case-ready, retail and consumer segments of the beef supply chain. The packing and case-ready segments contributed significant resources, including a robust data set, to allow for the completion of the analysis.

For the purpose of conducting Phase 1 of this life cycle analysis, all beef was assumed to be packaged in a case-ready system. Data from the consumer and retail segments were derived from publicly available sources (the U.S. Environmental Protection Agency, USDA, Food Marketing Institute and the U.S. Bureau of Labor Statistics) as no primary data were available from retail sources. As a result, the life cycle assessment showed no improvements from 2005 to 2011 for the consumer and retail segments.

BASF Corporation's life cycle assessment model, the Eco-efficiency Analysis (EEA), provided the framework required to

analyze the environmental, social and economic impacts of the post-harvest segments of the beef value chain. The model was then populated with data from the pre-harvest simulations to allow the entire life cycle to be benchmarked. Beef supply chain sustainability was compared over time against the consumer price of beef in accordance with ISO 14040 and 14044 for life cycle assessment and 14045 for eco-efficiency analysis.

It is important to recognize that the science of life cycle assessment requires analyzing all production inputs, including pre-chain impacts, that contribute to producing one pound of boneless, edible, consumed beef. Due to the beef industry's inability to influence changes in pre-chain impacts, gaining efficiencies in this area is a challenging prospect. However, because many of those industries are also on a path of continuous improvement, the beef industry benefits from pre-chain progress. For example, as diesel engines are improved to lower emissions and improve fuel efficiency, the beef industry benefits and shows a decrease in both air emissions and resource use.

Third-party Certification

The completed Beef Industry Sustainability Assessment has been subjected to extensive third-party and peer review. The pre-harvest segment results are published in the *Journal of Animal Science* and The U.S. Beef – Phase 1 Eco-efficiency Analysis, which examined the entire beef value chain, was certified by NSF International in July 2013.





Findings

The EEA portfolio shows the present-day U.S. beef value chain is more sustainable than in 2005 (Figure 4). While there was a 6 percent increase in the price of beef between 2005 and 2011, there was a simultaneous decrease in the overall environmental and social impacts from the U.S. beef value chain of approximately 7 percent. Following weighting and normalization, the EEA portfolio showed a 5 percent improvement in overall sustainability.



All impacts are quantified against a consumer benefit (CB) of one pound of boneless, edible, consumer beef.

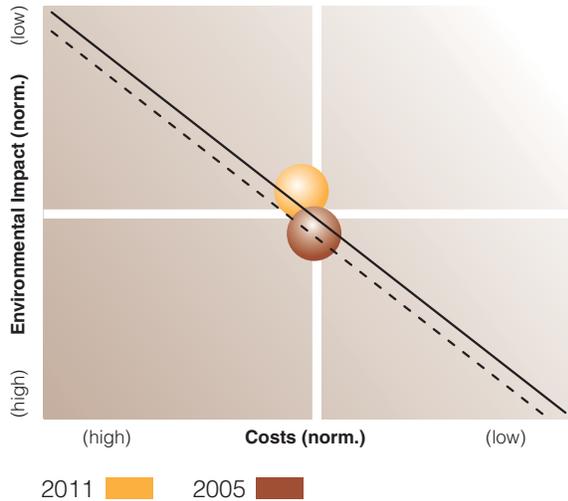


Figure 4 | Eco-efficiency Portfolio: U.S. Beef

Economic Impact Category

The importance of economic benefits to the beef industry cannot be overstated and is a critical component of sustainability. However, measuring the economic benefit of one pound of boneless, edible beef is challenging due to the complexity of the industry. To measure the economic sustainability of the entire beef value chain, the consumer price of beef is utilized. The researchers acknowledge the economic benefit of beef extends beyond just consumer price and further research in this sustainability category is required.

The results of the life cycle cost analysis were adjusted to reflect current market conditions and pricing; therefore, 2005

pricing was adjusted to 2011 dollars. The results of the life cycle cost analysis showed a price increase of 6 percent between 2005 and 2011 (Figure 5).

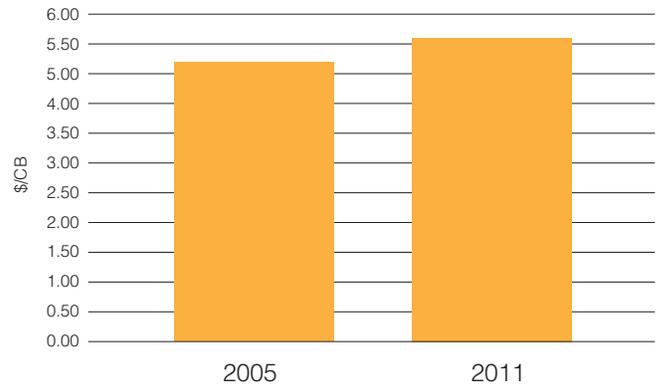


Figure 5 | Life Cycle Costs

Environmental and Social Impact Categories

Improvements in efficiencies have driven the majority of the increases in overall beef value chain sustainability. Because it is difficult to improve biological processes in short time periods, enhancements to pre-chain manufacturing processes, as well as major innovations and investments in infrastructure by the packing and case-ready sectors, contributed heavily to the recent improvements in industry sustainability.

Environmental and social impact categories shown in this fingerprint highlight areas important when measuring

sustainability. In this report seven impact categories are highlighted; five are environmental (energy use, consumptive water use, emissions, resource use and land use) and two are social (toxicity potential and occupational illnesses and accidents). Overall, improvements were seen in nearly all impact categories between 2005 and 2011 (Figure 6).

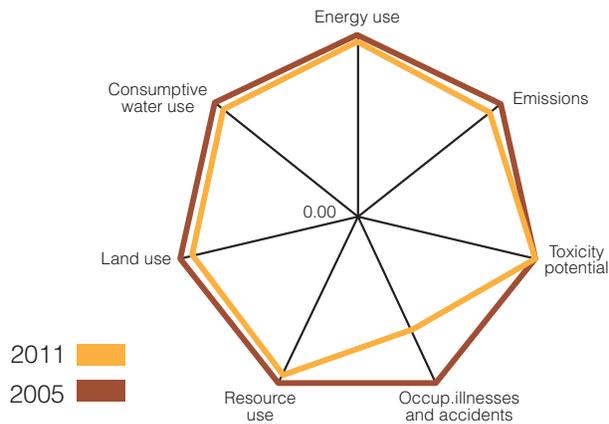


Figure 6 | Environmental Fingerprint

Environmental Impact Categories

Energy Use

The greatest energy impacts for the beef industry are the result of embodied energy requirements dictated as standard practice by life cycle assessment protocols. Embodied energy is how life cycle assessments level the playing field for all energy sources. In order to compare energy sources,

the energy source must be calculated by converting it to its most efficient use. In the case of corn, that most efficient use is combustion. Because most of the corn utilized in beef production is utilized as a feed source, the beef industry showed a larger than expected cumulative energy demand. Nearly 80 percent of the industry's cumulative energy demand is the result of embodied bioenergy in the form of animal feed (Figure 7).

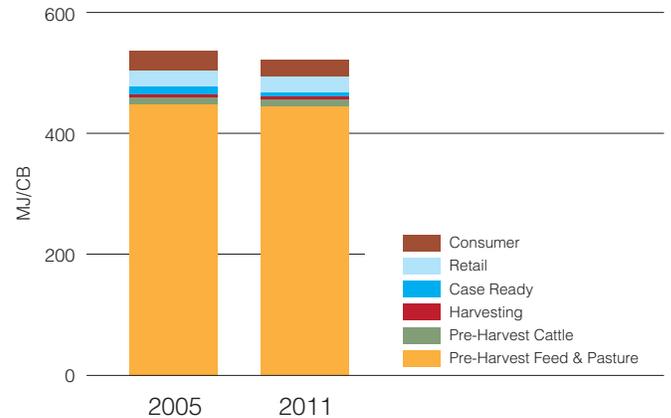


Figure 7 | Cumulative Energy Demand

Since embodied energy from feed sources such as corn is not easily reduced, it is important to recognize that the main opportunities for reduction in this category are found in the non-renewable energy associated with the current U.S. energy grid and transportation system, as seen in Figure 8. Between 2005 and 2011, the beef value chain lowered its

energy use by 2 percent (Figure 7 & 8). The reductions in energy use can be attributed to the following factors:

- Reduced use of utilities and transportation energy throughout the value chain
- Increased crop yields and less fuel use to produce required feed resources
- Increased use of biogas capture and conversion by packing plants, leading to lower electricity requirements
- Conversion of boilers at packing plants from diesel to natural gas
- Reduced packaging requirements through the use of right-size packaging which reduced the pre-chain impacts of packaging production

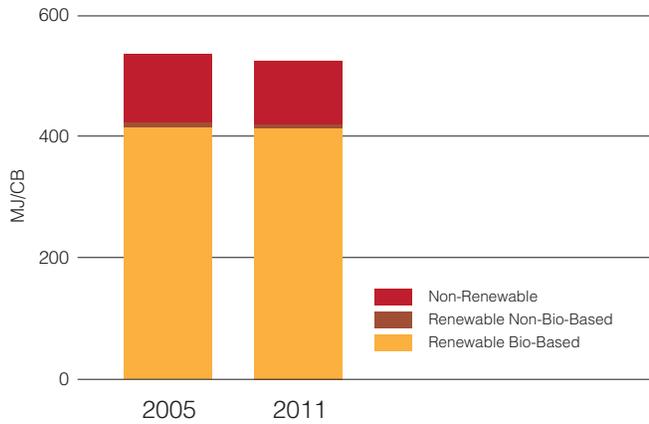
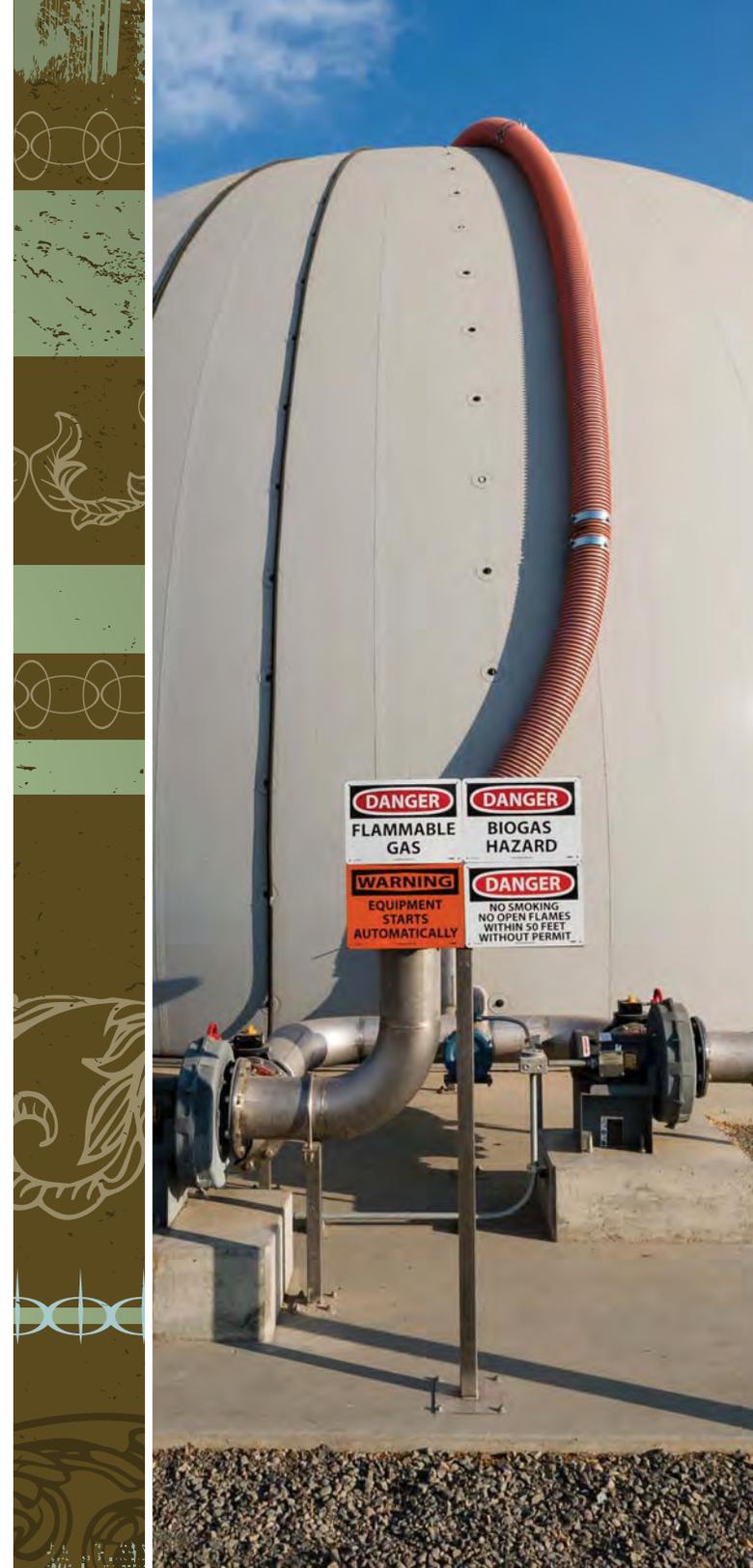


Figure 8 | Renewable and Non-Renewable Energy Breakout





Consumptive Water Use

Crop irrigation accounts for 95 percent of water use by the beef value chain. In this impact category a 3 percent reduction in use was achieved between 2005 and 2011 (Figure 9).

Reductions in consumptive water use were the result of several factors, including:

- Improved crop yields and reduced water use to produce required feed resources
- Improvements in packing plant water efficiency
- Optimizations in the case-ready phase that lead to packaging reductions and reduced pre-chain water use

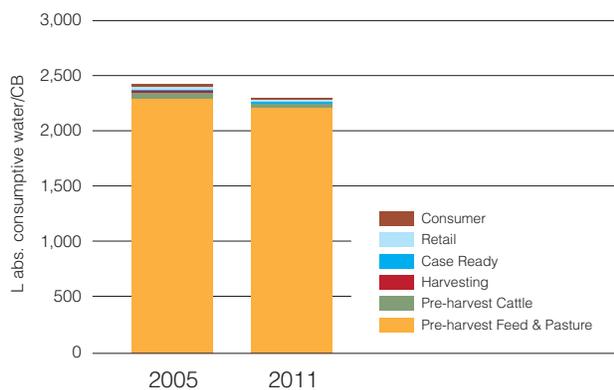


Figure 9 | Consumptive Water Use

Emissions

The emission impact category measures emissions to water, soil and air.

Emissions to Water

The life cycle assessment attributed 78 percent of emissions to water to run-off in 2005 and 81 percent in 2011, largely due to nutrient leaching from cropland. However, the beef value chain has a positive story to tell in this category. In the six years between 2005 and 2011, emissions to water decreased 10 percent (Figure 10) as a result of several improvements in production and management practices, including:

- Increased crop yields which decreased fertilizer use and associated run-off per unit of feed produced
- Installation of gray water recycling equipment in packing plants and increased use of right-size packaging
- Associated reductions in pre-chain emissions and increased usage of wet distillers grains



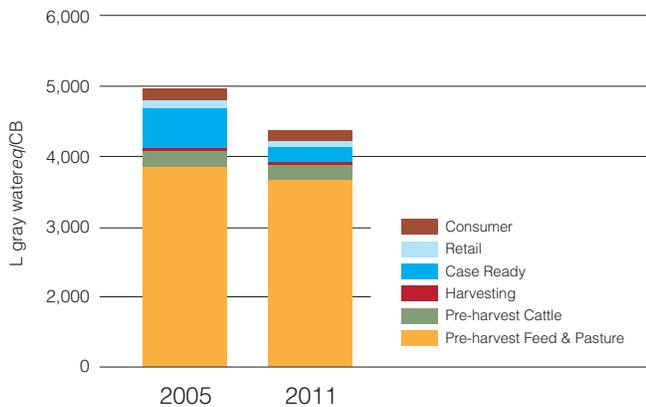


Figure 10 | Emissions to Water

Emissions to Soil

Emissions to soil are measured as solid waste generation and analyzed according to ultimate disposal method—recycling, incineration or landfill. Nearly all solid waste accounted for in Figure 11 was the result of pre-chain waste. Solid waste generated by pre-chain production declined 7 percent between 2005 and 2011 (Figure 11) as a result of:

- Greater use of biogas at packing facilities
- Improved crop yields

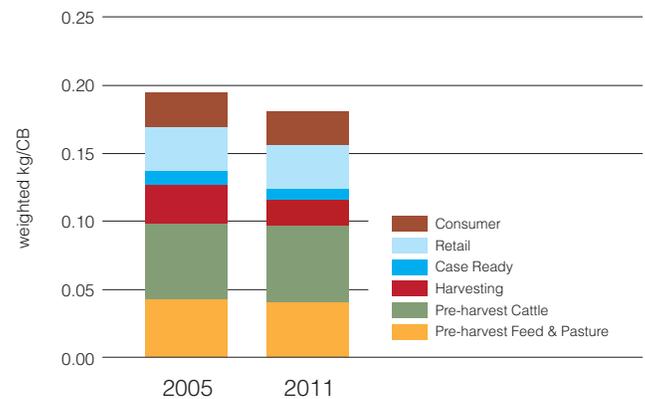


Figure 11 | Solid Waste Generation

Emissions to Air

There are four primary sub-categories of air emissions measured by the life cycle assessment. Those sub-categories include greenhouse gases, acidification potential, photochemical ozone creation potential and ozone depletion potential.

Greenhouse Gases

Enteric methane from cattle is the largest contributor to the global warming potential (GWP) of the beef value chain,



accounting for 42 percent of the total. Nitrous oxide (N₂O) from manure in feedlots and pastures was the second-largest source of GWP, accounting for 20 percent of the total. Other significant contributors include field emissions from fertilizer, refrigerant leakage from the retail sector and cooking of beef products by consumers. Some improvements in greenhouse gases achieved over the last six years were canceled out by the increased use of wet distillers grains which have a higher GWP as a result of the pre-chain ethanol distillation process. However, the beef supply chain has still reduced its carbon footprint by 2 percent since 2005 (Figure 12) through:

- Increased use of recovered biogas and right-size packaging which results in less fossil fuel use
- Increased crop yields resulting in less fossil fuel inputs to feed production
- Improved animal performance which maximizes feed-to-gain ratios

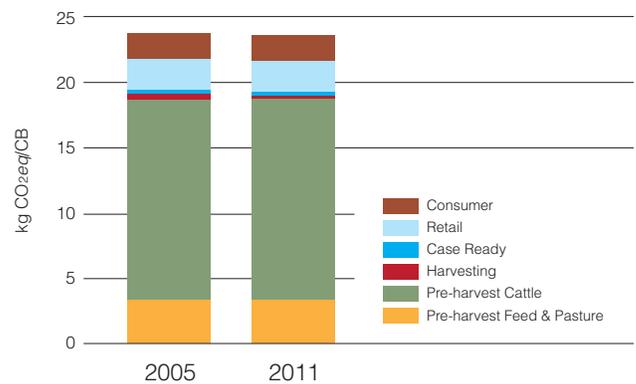


Figure 12 | Greenhouse Gas Emissions

Acidification Potential

The major contributors to acidification potential come from the pre-harvest phases of cattle production. Manure and urine from cattle and the use of fertilizer in feed production are the primary contributors. Emissions from the combustion of fossil fuels for transport, production of electricity, on-site boiler use and pre-chain impacts of corrugated cardboard production also contributed to the beef industry's acidification potential emissions.

The inclusion of wet distillers grains in cattle feed rations increased ammonia emissions, which contributes to acidification potential. However, decreased fertilizer and fossil fuel combustion from feeding distillers grains offset the increased ammonia production. Overall acidification potential was reduced 3 percent since 2005 (Figure 13) from:

- Increased crop yields resulting in more efficient utilization of applied nitrogen from fertilizer or manure

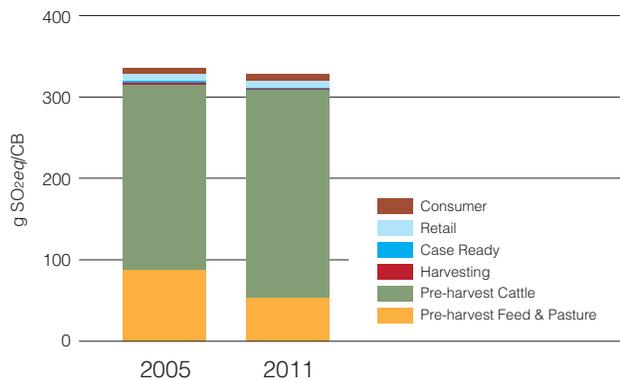


Figure 13 | Acidification Potential

- Increased energy efficiency, use of captured biogas and packaging optimizations which lower pre-chain acidification potential emissions

Photochemical Ozone Creation Potential (POCP)

The main contributors to POCP, also known as summer smog, are volatile organic compounds which are emitted primarily from the use of feed resources such as silage and wet distillers grains, as well as fossil fuel combustion and the pre-chain emissions created by the use of corrugated cardboard and plastic. The results of the life cycle assessment show a slight reduction in POCP emissions in the post-harvest sector between 2005 and 2011 due to the increased use of biogas capture and conversion technology, as well as increased use of right-size packaging. However, those improvements were nearly offset by the increased usage of high-moisture corn and silage by the pre-harvest sector at MARC during the same time period (Figure 14).

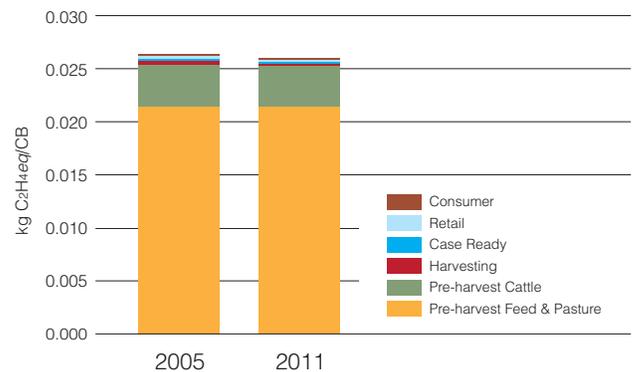


Figure 14 | Photochemical Ozone Creation Potential

Ozone Depletion Potential (ODP)

Halogenated hydrocarbons utilized by commercial refrigeration systems at retail are the most significant contributors to the ODP emissions measured in the life cycle assessment. Because of the lack of primary data submitted by retail and restaurant stakeholders, the only available data were open-source data from the U.S. Environmental Protection Agency. These data are not updated frequently enough to capture improvement during the timeframe of the assessment. Other contributors to ODP include the use of low-density polyethylene (LDPE) packaging (Figure 15).

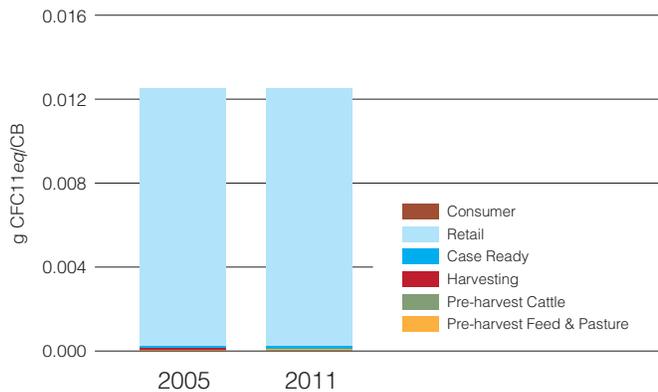


Figure 15 | Ozone Depletion Potential

Resource Use

Resource use impacts are weighted, with more finite resources being assigned a higher weighting than more plentiful resources. Zinc is one of the world's most finite resources. As a result, even though it is used in small quantities by the beef

industry, it adds significant burdens to the beef value chain's overall resource use impact, accounting for half of the total. Fossil fuel use also factors heavily into the industry's resource use and can be primarily attributed to pre-chain production processes for transport, processing and feed production. The production-related (the distillation process) impacts of the distillers grains used in cattle rations also contributed slightly to resource use as well.

The beef value chain's resource use has improved by 2 percent during the past six years (Figure 16). Although the reduction may appear small, the beef industry has made significant efficiency improvements. For example, farmers and ranchers are producing more total product per animal. The result is an improvement in industry efficiency and a lowered overall resource use impact. Other improvements in the resource use category were realized as a result of:

- Improved crop production practices and increased crop yields
- Increased use of recovered biogas from wastewater lagoons at packing plants, thereby lowering the need for fossil fuel use

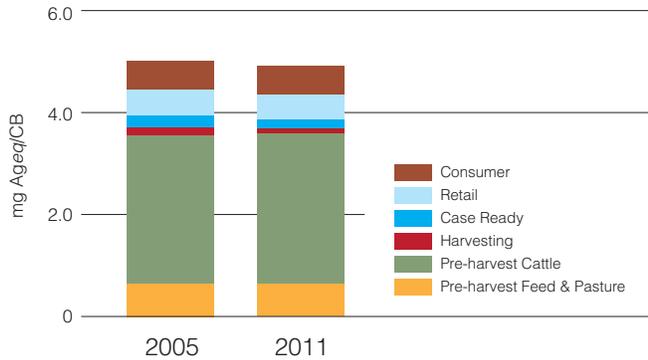


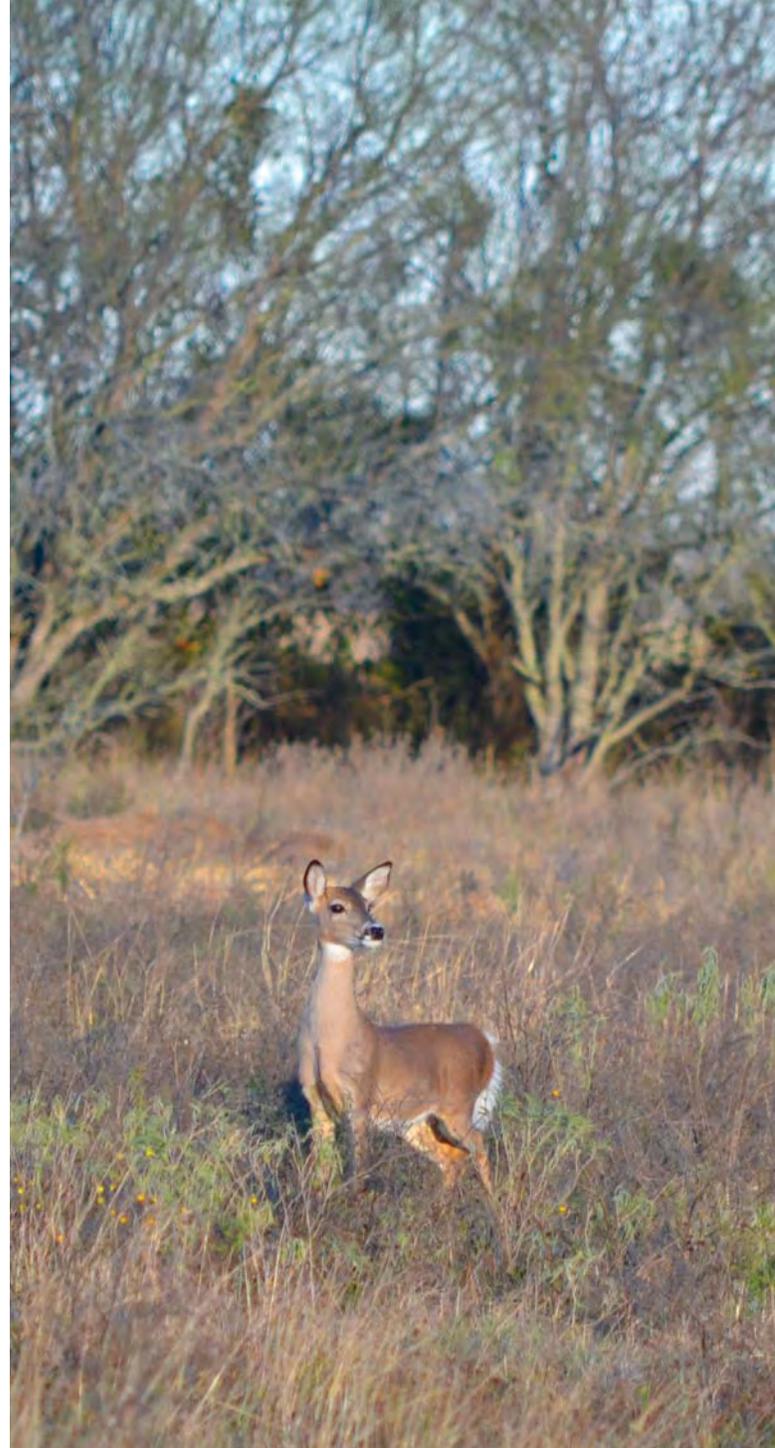
Figure 16 | Resource Use

Land Use

The beef value chain has reduced land use by 4 percent from 2005 to 2011 (Figure 17). The beef industry's use of farm land, pasture and rangeland accounts for the bulk of land use impact, accounting for 95 percent of the category. The majority of the remaining land use is the result of pre-chain processes such as the production of corrugated cardboard and diesel consumption.

Future research on land use was identified as a significant priority for the beef value chain, as grazing ecosystems are complex and not well represented by current life cycle assessment methodology. Overall reductions in land use can be attributed to:

- Increased crop yields, which resulted in a decline in the total number of acres required for feed production
- Use of distillers grains, which reduced the need for additional crop acres used for feed production





- Right-size packaging which lower the industry's use of cardboard and other packaging products
- Improvements in energy efficiency across the entire beef value chain

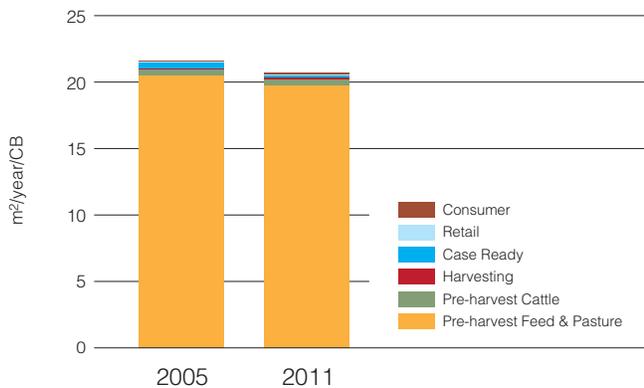


Figure 17 | Land Use

Social Impact Categories

Toxicity Potential

Agricultural chemicals and fertilizers are the primary contributors to toxicity potential because they can pose a human health risk. Fossil fuel energy, pre-chain utilization of chemicals, utilities and transportation also contribute to this category.

In the six years measured in the life cycle assessment, toxicity potential was essentially unchanged (Figure 18). Reductions in toxicity potential were achieved due to the increased use of recovered biogas from lagoons at harvesting facilities, which reduced energy and fossil fuel consumption. A decreased use of plastics in packaging lowered pre-chain toxicity potential. In addition, other energy efficiency improvements throughout the value chain resulted in lower fossil fuel use. However, the increased use of distillers grains increased ammonia releases from urine and effectively neutralized these improvements.

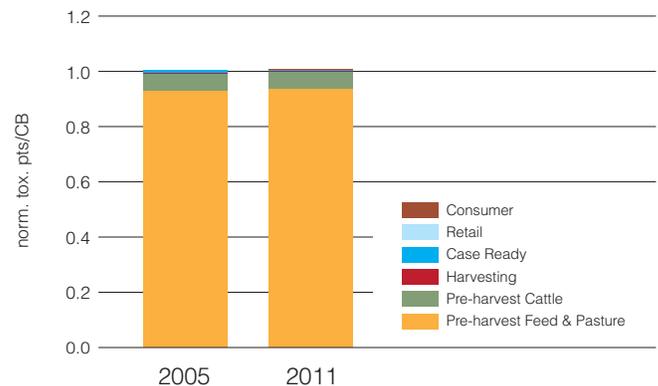


Figure 18 | Toxicity Potential



Occupational Illnesses and Accidents

The single-largest categorical reduction came in occupational illnesses and accidents, which declined 32 percent in the six years between 2005 and 2011 (Figure 19). The data was compiled from the U.S. Bureau of Labor Statistics and showed improvements in the numbers of working accidents, fatalities, illnesses and diseases associated with industries related to the production of beef. Other categories in this social metric include animal welfare, food safety and community nuisance odors and emissions. Significant improvements in these areas resulted from:

- A decline in the numbers of pre-chain and packing sector occupational accidents, illnesses, injuries and diseases
- Improvements in animal welfare, as reflected in a third-party audit result of packing plants and adoption of Beef Quality Assurance at the feedyard and cow-calf sectors
- The installation of covered lagoons, which lowered community nuisance odors and reduced packing plant dependence on fossil fuels (which reduced pre-chain occupational accidents and illnesses)

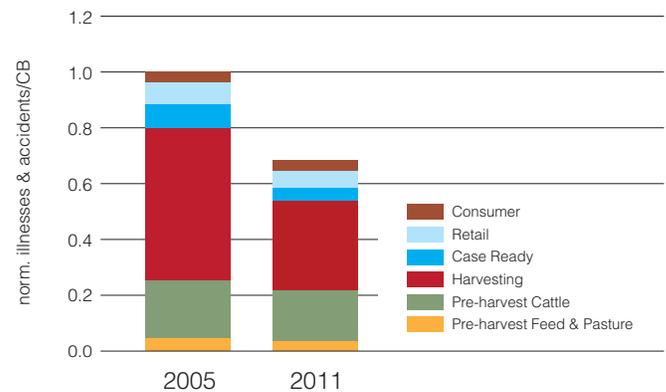


Figure 19 | Occupational Illnesses and Accidents

1970s Pre-harvest Data

Initially, the intent of this project was to benchmark the 1970s, which represented a time in the industry of increased carcass utilization and fabrication, known as the “shift to boxed beef.” While high-quality data for the pre-harvest sector is available dating back to the 1970s, data is not available from the post-harvest segment. Therefore, the following benchmark data focuses solely on the pre-harvest sector between 1970, 2005 and 2011. Since the 1970s, efficiencies improved overall sustainability.

The pre-harvest sector achieved a 10 percent reduction in environmental and social impact between 1970 and 2005 (Figures 20 and 21). A 12 percent reduction was

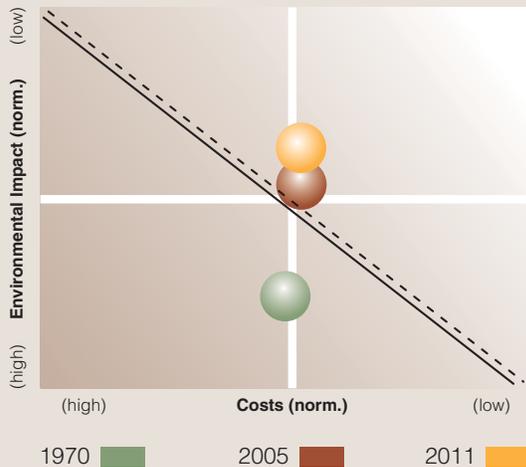


Figure 20 | Eco-Efficiency Analysis Portfolio for 1970 pre-harvest scenario

achieved between 1970 and 2011 (Figures 20 and 21). These improvements were primarily the result of improved efficiency of crop and animal production.

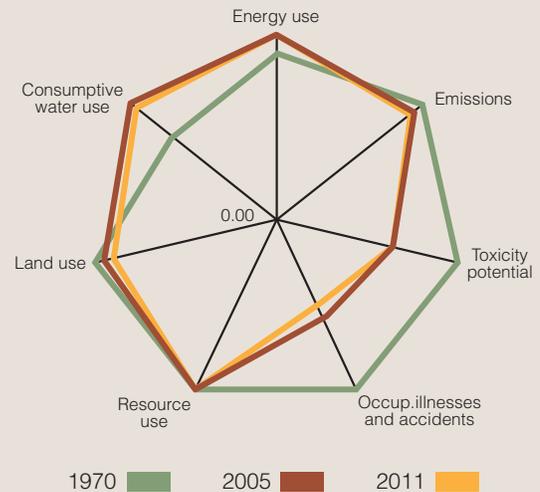
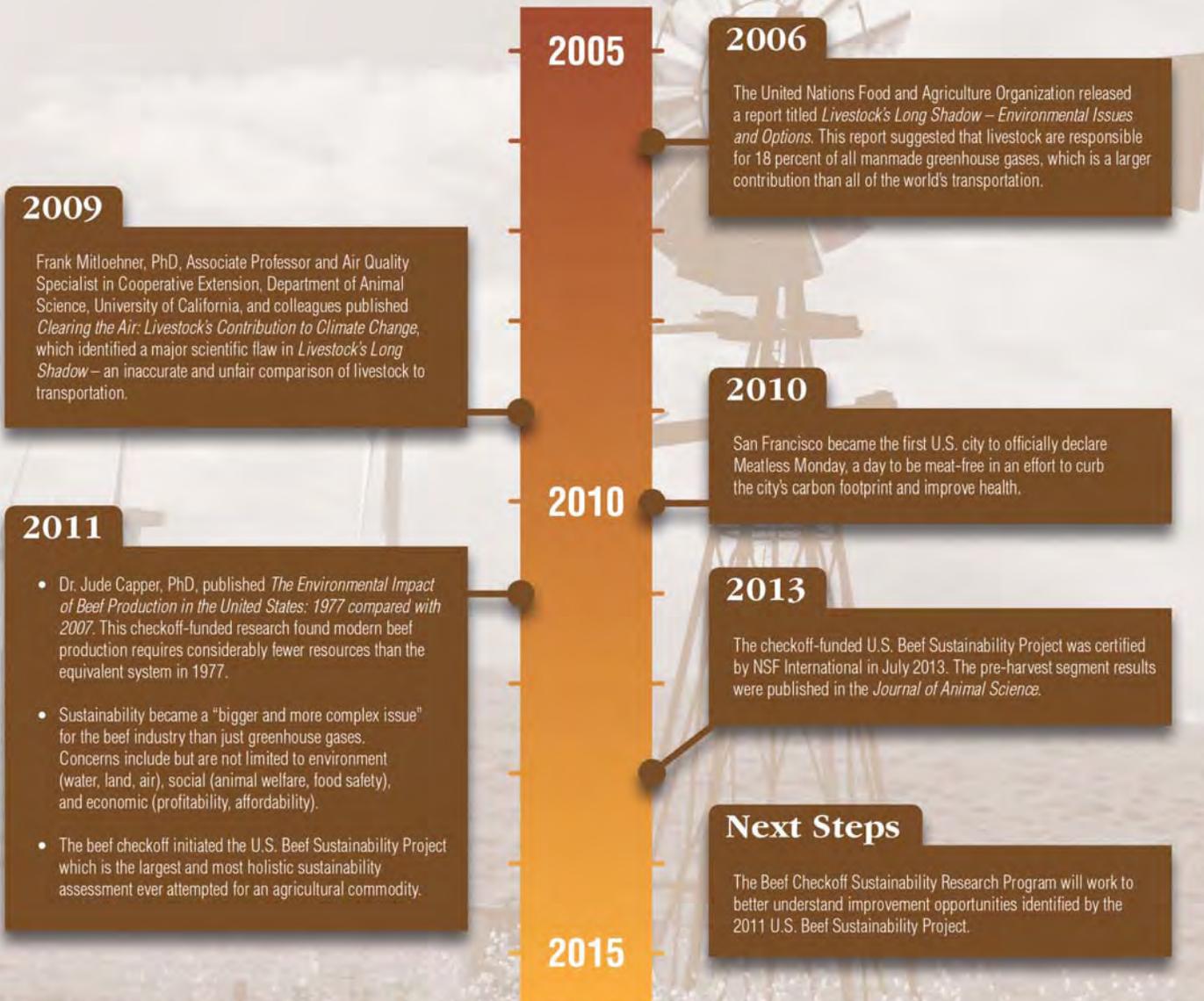


Figure 21 | Environmental Fingerprint for 1970 Pre-harvest Scenario

In some cases an increased impact resulted since the 1970s. This is primarily from increases in crop inputs including fertilizer, energy and water at the MARC. In many instances, the adoption of these practices led to the improvements in efficiency that we see today. For example, the installation of irrigation-driven water and energy use since the 1970s has helped improve crop yields, offsetting other inputs and resulting in an overall improvement of sustainability since the 1970s (Figure 21).

Sustainability Timeline





*Opportunities for
Continuous Improvement*



The checkoff-funded Beef Industry Sustainability Assessment serves as a guidepost for continuous improvement across the full beef value chain. The industry has demonstrated a commitment to continually improving how beef is produced and is constantly searching for new and better methods to lower its environmental footprint while improving its social and economic contributions to communities across the country.

That dedication to improvement has persisted for generations in the United States and it drives the beef industry to look openly at its production practices to find new ways to innovate. The results of the life cycle assessment highlight the industry's significant achievements over time and help identify areas for future progress and innovation. As a result of this work, the beef value chain has identified several target areas to focus its efforts, outlined in Table 2.

These target areas provide high-level opportunities for each segment to contribute to industry-wide improvement. The list is not meant to be exhaustive; instead, it outlines priorities for future improvement identified by the life cycle assessment. There is no one-size-fits-all approach for improvements in beef industry sustainability and each individual along the value chain has a role to play. Increased efficiency is undoubtedly the greatest contributor to increased sustainability and it will continue to be the beef value chain's best opportunity for future progress.

Several of the opportunities for improvement identified in this assessment require additional research to better understand how changes and improvements can be adopted by individual producers. For example, region-specific research is needed to identify management practices and other solutions to help producers evaluate and improve the sustainability of their individual operations.

The realized and existing opportunities table captures factors which are primarily focused on improvements in the environmental metric. However, it is important to note that social sustainability, while not yet well understood, is just as critical to overall industry sustainability and should continue to be a key focus. This is an area where individual efforts at the local level can make a big difference. Local contributions could include, but are not limited to, donations to food banks, participation on school boards, or providing internships and tours for members of the local community.

In addition to further research, there is also a need to capture and quantify some of the less tangible benefits of the beef value chain. These intangibles include important attributes of beef production such as the preservation of open space and wildlife habitat. As the science of life cycle assessments continues to improve over time, improvements being made by the beef value chain may be more fully understood and quantified in the future. That work will further showcase the industry's contributions to responsible beef production.

Table 2 | Realized and existing opportunities by sector

Realized Opportunities	Existing Opportunities
Crop farm <ul style="list-style-type: none"> Improvements in crop yields Increased adoption of precision farming techniques Improved nutrient management 	<ul style="list-style-type: none"> Continue to improve crop yields Continued adoption of more water-efficient irrigation systems Continue to optimize nutrient application to soil
Cow-calf/Stocker <ul style="list-style-type: none"> Higher performing cattle through improved genetics and health Improved nutrition 	<ul style="list-style-type: none"> Continue to improve management of cattle and resources to promote improved efficiencies
Feedlot <ul style="list-style-type: none"> Improved cattle performance through better management, nutrition, genetics, health and technology Improved manure management 	<ul style="list-style-type: none"> Optimize the use of distillers grains in diets Continue to improve efficiencies Continue to optimize manure management techniques to reduce fertilizer inputs
Packer <ul style="list-style-type: none"> Biogas recovery Closed loop water cooling systems Waste water recovery 	<ul style="list-style-type: none"> Continue to optimize biogas recovery systems, closed loop water cooling systems and waste water recovery systems in plants
Case Ready <ul style="list-style-type: none"> Right-size packaging Plant optimization 	<ul style="list-style-type: none"> Explore new packing alternatives that further reduce inputs and are accepted by the consumer
Retail <ul style="list-style-type: none"> No improvement in current data 	<ul style="list-style-type: none"> Provide data to the study Reduce greenhouse gas leakage from refrigeration units
Consumer	<ul style="list-style-type: none"> Reduce food waste

One of the greatest opportunities for improvement is a reduction of food waste. An estimated 40 percent of all food produced in the United States is wasted, contributing to losses in efficiency across the entire food value chain. Food waste costs the average American family approximately \$2,500 annually. Although beef waste is about 20 percent of consumable product, it is still a significant burden and represents a major opportunity to improve the sustainability of the beef industry. By cutting beef waste in half, the full beef value chain would achieve an approximate 10 percent improvement in full-chain sustainability.

Conclusion

As the beef industry has improved over time, so too has the value chain's commitment to a more sustainable future. Farmers and ranchers recognize that the succession of multi-generation operations represents an important piece of sustainability's true meaning. However, they also understand that a complete look at beef sustainability requires a more holistic assessment of the industry. Today, the beef value chain has come to define sustainability as the industry's ability to meet growing global beef demand while balancing environmental responsibility, economic opportunity and social diligence.

Whether it is changing grazing patterns to increase weaning weights or the installation of a biogas recovery system at a packing plant, every stakeholder has a role to play in the effort to create a more sustainable beef industry. By uniting to complete the Beef Industry Sustainability Assessment, the U.S. beef value chain has taken a major step forward toward a more sustainable future. It also positions U.S. beef to be a leader in the increasingly important conversation among commodity groups, non-governmental organizations and consumers about how food will be produced in the future.



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HOW DO CURRENT MARKET INCENTIVES AFFECT GENETIC SELECTION DECISIONS?

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Introduction

The combination of historically tight beef cattle supplies, reduced feedstuffs prices, and stronger than perhaps expected beef demand have underpinned historically high prices and profit margins for many segments of the beef cattle industry. Expected cow-calf returns for 2015 exceed \$400/cow when previously returns over cash costs greater than \$100 characterized very favorable years (LMIC, 2015). How should \$400+/head cow-calf returns affect cow-calf producer decisions? The market signal is pretty clear—more calf production is needed and will be rewarded.

Producers should consider whether current market values should prompt management changes. The sharp jump in revenues this year (marginal benefits) implies that producers should consider a host of marginal changes in production and costs. This may mean producers doing more of something they have already done or beginning to do something they have not done in the past. Although not an all-inclusive list, some examples include pre-breeding exams, bolstering health programs, increasing the body condition of the cowherd, and putting more pressure on weaning weight through genetic selection or increasing feed substrates.

That said, it is important to keep in mind return on investment. Consider this question, for example: What is the optimal pregnancy rate for a cowherd? While we do not often think about it, the optimal level is not 100%. Could we achieve 100% pregnancy rate? Probably yes or something very close to it, but the last few pregnancies gained would likely require extreme measures such as drastically extending the breeding season, for which the costs exceed the benefits and thus is not optimal. However, the increase in calf values this year means that additional efforts to increase pregnancy rates are warranted compared to what was optimal in the past. This illustrates the economic principle that every producer should be examining now—adjust production activities until the marginal benefits equal the marginal costs.

For many producers, periods of profitability may be motivation for expanding the cow herd. However, it is future rather than current profit that should be of interest and, therefore, future costs and payments that must be considered along with the circumstances of today. Thus, a sound investment in expanding the cow herd will ultimately produce profitability over the entire investment period (i.e., initiation through end of useful life), whether short- or long-term. Selection and management decisions will affect the future productivity and profitability of an entire cowherd. Careful considerations of the economics of production and the reproductive status, breed type, and genetic make-up of the herd need to be considered.

This paper reviews some economic considerations related to beef cattle herd expansion and the relationship with management and genetic selection decisions, and outlines several important variations in individual ranch considerations.

Beef Cattle Herd Dynamics and Genetic Selection Decisions

Beef cattle production in the U.S. is a vertically connected system that spans from cow-calf operations producing feeder cattle for the nation's stocker and feedlot operations, which combine to feed cattle to heavier weights for eventual slaughter. Retail beef supplies are heavily

dependent on cow-calf production decisions, namely the retention of heifers as replacements and the holding of cows for further breeding service, as these decisions dictate the size of subsequent calf crops (Schmitz, 1997). As Melton (1980) states “probably no single aspect of modern beef herd management is as complicated, or has as potentially great an economic impact, as the cow culling and replacement decision.” Buhr and Kim (1997) illustrate how changes throughout the industry are associated with significant and vertically-connected adjustment costs. For instance, breeding herd expansion decisions directly influence the volume of transactions at auction markets and the number of calves available for feeding in commercial feedlots and processing by packing plants.

Beyond the volume of transactions and calves available, characteristics of cattle within a vertically connected system can ultimately impact the success of expansion. A survey of Iowa cow-calf producers and feedlot operators was conducted in February 2014 (Schulz, Gunn, and Loy, 2015a; 2015b). Some key findings include 77% of cow-calf respondents indicating genetic selection was important or very important for improving cost of production on their operation. This genetic merit was further buttressed by 70% of cow-calf respondents indicating that changing their genetic selection program would expand their marketing opportunities. However, only 29% of feedlot respondents indicate specific sire and/or genetic information was important or very important for the feeder cattle they buy. These responses signal a host of points, but perhaps most significant is the need for more transparency and enhanced information flow between the cow-calf and feeding sectors of the industry.

The U.S. is the world’s largest producer of beef and the world’s largest consumer of beef in terms of total pounds. In 2014, beef and beef variety meat exports amounted to 1.197 million metric tons worth \$7.135 billion. Approximately 14% of U.S. beef and variety meat production was exported in 2014 (USMEF, 2015). Over the next 10 years, global meat consumption is projected to grow by 1.6% annually, with exports of beef projected to rise even quicker at a rate of 2.7%/year (USDA ERS, 2015). This growth in beef demand results from an increasing human population, rising per capita incomes, changes in consumer preferences, and improvements in product characteristics such as convenience, tenderness, food safety, health, and nutrition, etc. (Schroeder et al., 2013). The projection of beef exports to grow faster than base consumption presents a favorable opportunity to major beef exporters. To capitalize on current and expected beef demand strength, many analysts indicate the U.S. needs to increase overall beef production, which is inherently initiated by expanding breeding herds.

It is useful to characterize the varied views on how much expansion may occur by comparing two different forecasts. The USDA Economic Research Service (2015) in February of 2015 released projections of 16.5% herd growth between 2015 and 2024 (33.7 million head in total by 2024). Conversely, the Food and Agricultural Policy Research Institute (2015) published projections in March of 2015 of the herd in 2024 only being 2.6% larger than in 2015 (30.3 million head in total by 2024). The difference in these economic projections, and the broader uncertainty of aggregate industry expansion, is only magnified at the individual level. That is, the list of possible reasons for expansion is extensive across a group as heterogeneous as the U.S. cow-calf sector.

Individual, Ranch-Level Considerations

As cattle producer interest in beef herd expansion grows, it is important to recognize what resources are available to guide these investment decisions and to appreciate key variables

that drive expected investment returns. Sensitivity analyses regularly highlight the critical role of production costs, investment returns being targeted, and expectations regarding future cattle prices. Producers are highly heterogeneous in these and other characteristics, which, in turn, magnify the range of interest in herd expansion and the varied approaches to accomplish expansion, etc. This situation is precisely the reason existing decision support tools regarding beef herd expansion have been developed and are regularly updated. For instance, available resources include partial budgets for assessing if an operation should buy or raise heifers and net present value analyses to estimate what price an operation can consider paying for a given targeted rate of return.

Raising Versus Buying Heifers for Beef Cow Replacement

Selecting the most economical source of replacement females may be one of the more important decisions confronting a cow-calf producer, as this decision has major implications for effectively using resources, controlling costs, and long-run business viability. As indicated by a BEEF survey (BEEF, 2014), producers utilize heifer retention and purchasing of external females to expand their breeding herd. USDA APHIS indicates that 83% of operations expand by retaining and raising their own heifers (USDA APHIS, 2008). Whether to use raised or purchased replacements can be a complex issue, because each alternative has both advantages and disadvantages. To assist producers in making the ‘raise vs. buy’ decision, Excel spreadsheets *Buying Heifers for Beef Cow Replacement* and *Raising Heifers for Beef Cow Replacement* can be used to determine which management strategy is best in any given year.¹

Although most producers raise herd replacements, purchasing replacements sometimes can be an attractive alternative. To illustrate this using the *Buying Heifers for Beef Cow Replacement* spreadsheet to analyze whether to continue raising replacements or purchase them, consider the following example. A cow-calf producer is considering selling raised heifer calves at weaning time and buying pregnant heifers at 22 months of age (2 months prior to calving). Heifer calves average 485 lbs. per head at 6 months of age and can be sold for \$2.60 per lb., net of selling costs. The interest rate is 4%, which is based on the returns realized from the investment of returns (or reduction in borrowing) from the sale of the heifer calves. The feed, non-feed, and fixed costs assumed for a heifer raised during the 16 month period between weaning and the arrival of a purchased heifer on the farm are \$499.00, \$289.82, and \$233.30 per head, respectively. It is assumed that a bred heifer at 22 months of age can be purchased for \$2,700 per head, net of purchase costs (e.g., transportation). Using this information, a producer can determine if buying replacement heifers will increase farm net income.

For added returns, the example cow-calf producer expects to realize \$1,328.25 if the heifer calf is sold and a replacement heifer is purchased 16 months later. Those returns stem from the sale of the heifer calf at weaning (\$1,261.00) and interest earned or saved on that amount (\$67.25), assuming an annual rate of 4% and a term of 16 months. The producer estimates there will be no increase in genetic improvement if heifers are purchased; if there were any multi-year gain in genetics, added returns would increase. For reduced costs, the producer eliminates the cost of raising a replacement heifer during the 16 month development period by purchasing a replacement. These cost reductions sum to \$1,022.12 per head. Included in the cost savings are feed, non-fed, and fixed costs. The total added returns from buying rather than raising replacements is the sum of the added returns and reduced costs, \$2,350.37 per head. Turning to the total added costs, the only added cost projected by the producer is the \$2,700

¹ These spreadsheets and video tutorial are available at: <http://www.iowabeefcenter.org/heiferdevelopment.html>.

purchase cost for the bred heifer. The producer estimates there will be no reduced returns (e.g., less genetic control, less control over disease). Subtracting total added costs (\$2,700) from total added returns (\$2,350.37) shows a net income decrease of -\$349.63 per replacement if the producer switches from raising to buying replacement heifers. However, if the heifer purchased for \$2,700 can garner \$350 in added genetic merit over females that would have been developed internally through increased weaning weight, improved heifer progeny pregnancy, or improved stayability, then purchasing replacements becomes a more competitive decision.

The above analysis assumes a market return on surplus home-grown forages, operating capital, operator labor and management, and no return on the existing investment in buildings, equipment, and facilities made available for use when heifers are no longer raised on the farm. To the extent these resources can be diverted to an alternative use (e.g., herd expansion) with returns exceeding these assumed levels, the analysis would understate the economic benefits (i.e., reduced costs) of buying heifers.

Net Present Value of Beef Replacement Females

Before decisions regarding purchasing or retaining replacement females are made, producers may want to consider the economic value of a replacement entering the herd. A cattleman's objective is to maximize the present value of the stream of residual earnings from cows in the herd (Melton, 1980; Melton and Colette, 1993). The *Net Present Value of Beef Replacement Females* Excel spreadsheet evaluates the economic situation presented by a given producer purchasing an available replacement female for their breeding herd.² When it comes to projecting the net present value (NPV) offered by purchasing or retaining a replacement female, a number of assumptions about the future must be made, providing key inputs into this process. These include: purchase price of replacement female (if any), number of calving opportunities, number of marketable calves, weaning weights of calves, sale prices of calves, annual cow costs, annual heifer development costs (if any), weight of cow when culled, sale price of cull cow, and discount rate.

To provide an example of this NPV analysis, a \$2,700 purchase price of a replacement female, long-run projected cattle prices guided by USDA's Economic Research Service 10-year projections, annual cow costs of \$750, and a discount interest rate of 5% are assumed. Using these default values, the NPV of replacement females expected to provide calves over the next seven years is \$49. The total of the discounted earnings is \$2,749, which is greater than the initial investment of \$2,700, thus this investment is profitable at this time. If a producer in this base situation paid more (less) than the max bid price of \$2,749, he or she effectively would be initiating an investment with an expected rate of return less (more) than 5%.

To illustrate the impact of production costs, reducing annual cow costs to \$600 from the base value of \$750 increases the NPV to \$916, consistent with the fact that each calf yields a greater net return per year, facilitating operations with lower annual costs to pay more for replacements. Conversely, adjusting the base case from a discount rate of 5% to 15% reduces the NPV to -\$754, highlighting how producers more concerned with increased volatility and uncertainty may be less aggressive in purchasing or retaining replacement females. Increasing expected output (calf and cull cow) prices by 5% increases the NPV to \$403, reflecting more optimistic future profitability expectations. Finally, increasing calf weaning weights by 4% increases the NPV to \$302, reflecting more optimistic future production expectations. These scenarios clearly illustrate how varied cost structures, heterogenous comfort with the risk

² This spreadsheet and video tutorial is available at: <http://www.iowabeefcenter.org/heiferdevelopment.html>.

environment, and diverse views on future cattle prices and output each notably impact NPV analyses.

Summary

The entire U.S. beef cattle industry is in the middle of several structural changes with herd expansion at the heart of each current and possible industry adjustment. The net impacts of these adjustments will dictate the collective make-up of the U.S. beef cattle industry for years to come. The future size and structure of the U.S. beef cow herd will be determined by the individual decisions of over 700,000 cattle owners (USDA NASS, 2014). These owners are very diverse, not only in their physical operational characteristics and lifestyles, but also in their perceptions and acceptance of the economic factors impacting herd expansion. Where individual operations fall on this varied continuum will drive individual interest in herd expansion and, hence, directly impact the future size and composition of the U.S. cow-calf industry. Similarly, the aggregate industry's ability to recognize and act upon the importance of ongoing beef demand growth is critical for the broader industry's ability to both expand in size and improve overall economic well-being.

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Profitability: Looking to the Future of Your Operation
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Introduction

The current cattle market has been one for the record books. The result has most beef producers' accounts out of the red and (finally) in the black as many have recorded positive profits. However, accounting profits and economic profits are not always on equal footing.

Even when considering the real price of cattle, the current market is recording prices that have never been experienced. Figure 1 illustrates both nominal and real prices of the feeder cattle futures contract. Figure 1 shows that, after adjusting for inflation, prices in the final quarter of 2014 were 85.9% higher than the average of all prices from 2003 through 2008.

The first objective of this article is to provide a distinction between accounting and economic profits. Second, economic profits are elaborated on more thoroughly. Finally, as the primary objective, a review of factors that impact profit for beef industry participants are discussed and ways to utilize profits to increase efficiency and long-term sustainability are outlined.

Accounting vs. Economic Profit

Accounting and economic principles are often incorrectly placed into the same conversation. While these disciplines do exhibit similarities, there are distinct differences when calculating profit. The most important difference is the economic principle of 'opportunity cost'. Accounting profit is the most commonly expressed profit equation. This is:

$$\text{Total Profit} = \text{Total Sales} - \text{Total Expenses} \quad (1)$$

Total sales, in the accounting sense, includes all income (or revenue) from the sale of goods, products, or services. Total expenses include all costs from the production of the products, including labor, materials, financing, and taxes. Economic profit has a similar construct, but includes 'opportunity costs' in the equation, as follows:

$$\text{Total Profit} = \text{Total Sales} - \text{Total Expenses} - \text{Opportunity Costs} \quad (2)$$

While similar to accounting profits, the economic profit equation (equation 2), considers the costs of other endeavors given up by the firm or individual in order to produce the specific good or service that generated revenue. Therefore, the opportunity to do something else was not acted on in order to produce the specific good or service.

An example in this case is often useful. Consider a beef cattle operation that utilizes 100 acres of pasture that is quite fertile. This ground could be used to grow high yielding crops. The costs of

not growing crops would be considered ‘opportunity costs’ from an economic standpoint but would not factor into accounting profits. In this case, the costs are actually lost revenues from not planting crops.

Another example is the costs of owning and using a tractor as opposed to (a) owning the tractor and leasing it to neighbors, or (b) owning the tractor, with financing, as opposed leasing the same tractor which may exclude financing costs and depreciation. In both cases, the ownership and use of the tractor involves costs that would be considered by accounting, however the lack of income or increased costs of not utilizing the asset (the tractor) in another way is not considered from an accounting perspective.

The reason for this slight variation in defining profit stems from the economic theory of zero profits in the long term. This implies that resources will flow from ‘best uses’ at one point in time to ‘best uses’ at another, where the best use of the resource is not always the same. Going back to the fertile acreage example, the land might switch from pasture to crop land as the accounting profits are positive to grow, say, corn. In this case the opportunity costs of not producing corn is realized and the land switches from a previous ‘best use’ (pasture for cattle) to an updated ‘best use’ (crop land).

Zero Economic Profits

Again, in the long term, economic profits are zero. This fine point is important within the principles of the field of economics. This provides the basis for perfect competition, rational markets, and asset allocation. As an asset’s ‘best use’ changes, the revenues and costs associated with that asset change. In the long term (say, 5 to 10 years) the difference between the revenues and costs equal zero, or:

$$\text{Total Revenue} = \text{Total Costs} \quad (3)$$

From equation (2), this leaves Profit equal to negative opportunity costs, but again, in the long term these are zero and therefore all profits are zero.

The emphasis on long term is that assets can be tied up in specific uses in the short term. Examples of this include (1) contracts or leases, (2) labor force skills or education, and (3) beef cattle herd genetics. Each of these prove difficult to deviate from in the short term. Contracts may have steep penalties if broken, increasing the skill set of the labor force requires time and effort, and changing herd genetics quickly is often costly.

Factors of Cattle Industry Profits

Cow-Calf

Dhuyvetter and Langemeier (2010) conducted a study of high, medium and low profit cow-calf producers. Using accounting profit measures, collected via the Kansas Farm Management

Association, the authors teased out the factors that influence profitability of Kansas cow-calf producers. They find that owning more cattle increase profits, but this phenomenon has a diminishing effect and as herd size continues to increase profits will eventually decline. For their Kansas Farm Management Association data, they show that 345 head is the point at which profits switch from increasing with each additional cow to declining.

Not surprisingly, selling calves at heavier weights increased profits as did selling at higher prices. However, these are offsetting since heavier weights typically fetch lower prices. As calf weight is increased by 10 pounds (the average weight of calves sold in their data was 583 pounds) profits increase by \$7.55 per cow. However, profits decline by \$5.12 per cow for every \$1 per hundredweight decrease in the price those calves receive (typically as calf weight increases, price decreases).

Dhuyvetter and Langemeier found that low cost producers are more profitable. In retrospect, this is obvious, but the finding is profound. Operations that dedicated a smaller amount of their costs to all other things except feed were more profitable. They found that as the percentage of total costs for feed increased 1% profit increased \$10.68 per cow.

While owing more head and selling at heavier weights are obvious ways to increase revenues (via more head sold and more pounds sold), there are costs associated with these (maintenance costs on cows and the costs of adding weight to cattle). Not surprisingly, producers that managed costs most effectively were high profit cow-calf producers.

Feedlot

Langemeier, Schroder and Mintert (1992) analyzed data from Kansas feedlots and found that the price cattle received, the price paid for cattle going into the feedlot and corn prices had the largest impact on feedlot profitability. Later in 1999, Lawrence, Wang, and Loy found similar results from data in Iowa. Feedlots operate on a much narrower range of output weights (fed cattle weights) and thus output price versus weight does not experience the same offsetting characteristics that cow-calf producers see.

Beyond output price, the largest two costs (feeder cattle and feed) impact feedlot profits the greatest. Once again, this is not surprising and is to be expected. However, it speaks to the importance of costs management in the cattle industry.

Summary and Implications

For the most part, cattle producers are “price takers.” This is due to the similarities in the cattle sold (i.e., homogeneity). As a result, minimizing costs is the best way for beef producers to increase profits since they have limited options to increase revenue. This implies it is very important for beef producers to strive to reduce cash outflows in their operation without sacrificing performance and productivity.

The interesting aspect of the current cattle market is that it has provided an opportunity for even high cost producers to be profitable. To maintain this momentum into the future, producers are encouraged to use these higher bottom lines to make improvements to their herd’s productivity

(primarily achieved through genetics, but also via improved forages and other production aspects) and their farm infrastructure (improve facilities, equipment, etc). These investments will most likely pay dividends in the long run and increase the likelihood of long term sustainability.

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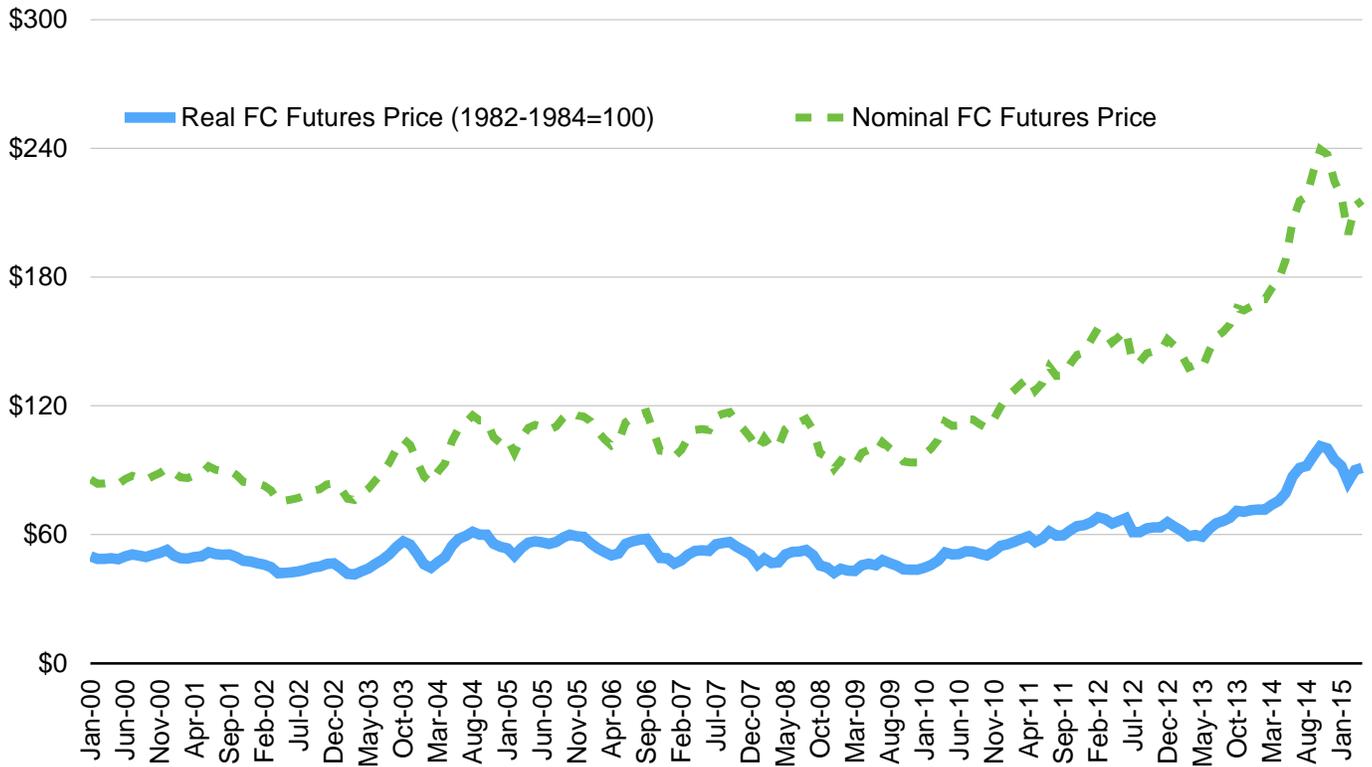


Figure 1. Nominal (dashed line) and Real (solid line) Feeder Cattle Futures Prices.

**PHENOTYPIC DATA COLLECTION FOR REPRODUCTIVE TRAITS
IN REPLACEMENT BEEF HEIFERS**

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BACKGROUND. Heifers that calve early during their first calving season have higher lifetime calf production than those that calve late (Lesmeister et al., 1973; Perry and Cushman, 2013). Because most calves are weaned at a particular time rather than on a weight-constant or age-constant basis, calves born late in the normal calving season are usually lighter than those born early. This tends to decrease the total lifetime productivity of their dams (Lesmeister et al., 1973). Furthermore, cows that calve late one year tend to calve late or fail to calve the subsequent year (Burriss and Priode, 1958). Therefore the age at which a heifer reaches puberty is highly correlated to the date at which conception occurs, and conception date during a heifer’s first breeding period is correlated to lifetime fertility and reproductive longevity. Improvements in procedures to assess the reproductive status of beef heifers prior to their first breeding period creates the opportunity to standardize procedures for phenotypic data collection among heifers selected as future herd replacements and utilization of more predictive indicator traits in national cattle evaluations of heifer pregnancy. This document provides an overview of the procedures that warrant consideration for evaluation of heifers prior to their first breeding period and suggestions for phenotypic data collection and reporting criteria for specific reproductive traits.

PREBREEDING EVALUATION. A prebreeding evaluation is recommended for all yearling-age heifers, and should include: animal identification, weight, pelvic area measurement and reproductive tract score. It is strongly encouraged that prebreeding exams be performed four to six weeks prior to breeding.

Reproductive tract scores. The reproductive tract scoring system (RTS, Table 1; Anderson et al., 1991) was developed to assist beef producers with selection of potential herd replacements and support timing of estrous synchronization programs (Patterson et al., 2013a). The reproductive tract scoring system is used to estimate pubertal status. Scores are subjective estimates of sexual maturity, based on ovarian follicular development and palpable size of the uterus. A RTS of 1 is assigned to heifers with infantile tracts, as indicated by small, toneless uterine horns and small ovaries devoid of significant structures. Heifers scored with a RTS of 1 are likely the furthest from puberty at the time of examination. Heifers assigned a RTS of 2 are thought to be closer to puberty than those scoring 1, due primarily to larger uterine horns and ovaries. Those heifers assigned a RTS of 3 are thought to be on the verge of estrous cyclicity based on uterine tone and palpable follicles. Heifers assigned a score of 4 are considered to be estrous cycling as indicated by uterine tone and size, coiling of the uterine horns, as well as presence of a preovulatory size follicle. Heifers assigned a score of 4 do not have an easily distinguished corpus luteum. Heifers with RTS of 5 are similar to those scoring 4, except for the presence of a palpable corpus luteum. Prebreeding examinations that include RTS furnish the opportunity to assess reproductive development, but further provide an appraisal of possible aberrant situations (freemartins, pregnancy, cystic conditions) that may detract from a heifer’s subsequent reproductive potential (Patterson et al. 1999; Lamb, 2013; Patterson et al., 2013b).

RTS	Reproductive status	Uterine horns	Ovarian length (mm)	Ovarian height (mm)	Ovarian width (mm)	Ovarian structures
1	Prepubertal, infantile tract	Immature, < 20 mm diameter, no tone	15	10	8	No palpable follicles
2	Prepubertal, > 30 days to puberty onset	20-25 mm diameter, no tone	18	12	10	8 mm follicles
3	Peripubertal, < 30 days to puberty onset	20-25 mm diameter, slight tone	22	15	10	8-10 mm follicles
4	Pubertal, follicular phase	30 mm diameter, good tone	30	16	12	10 mm follicles, CL possible
5	Pubertal, luteal phase	> 30 mm diameter	>32	20	15	CL present

Reproductive tract scoring is a repeatable (between and within veterinarians) and accurate (sensitivity = 82% and specificity = 69%) measure of pubertal status in heifers (Rosenkrans and Hardin, 2003). Holm et al. (2009), Pence et al. (2007), and Pence and BreDahl (1998) concluded that RTS is a predictor of heifer fertility, compares well with other traits used as predictors of production outcomes, and is likely to be a good predictor of lifetime production of the cow. Recently, RTS has been found to correlate with AI pregnancy rate following fixed-time AI (Thomas et al., 2013). But, RTS has not yet been implemented in national cattle evaluations. Figure 1 represents a modified interpretation of the conceptual model for puberty onset in the heifer presented by Day and Anderson (1998). This model combines the associated endocrine and ovarian changes that occur as heifers approach puberty, in addition to the corresponding RTS that would be assigned at respective points in development. A RTS of 1 corresponds to the point in time at which the pattern of luteinizing hormone (LH) release is characterized by low-frequency, high amplitude pulses. This is due to the fact that the hypothalamic-pituitary axis is highly responsive to negative feedback from estradiol. Reproductive tract scores of 2 and 3 are associated with the pre- and peri-pubertal phase, at which time responsiveness to estradiol negative feedback begins to decrease, causing increases in LH pulse frequency, follicular growth, and estradiol secretion. The decline in estradiol negative feedback and increase in LH secretion result in significant increases in follicular growth, and elevated concentrations of estradiol sufficient to induce estrus and the preovulatory LH surge. Reproductive tract scores of 4 and 5 are assigned to heifers that have reached puberty, but differ in stage of the estrous cycle at the time of the prebreeding exam (follicular phase = 4; luteal phase = 5).

While RTS can be effectively used in phenotypic selection to cull heifers that are abnormally delayed in achieving puberty, its greatest value would be inclusion into national cattle evaluations. This could be accomplished by developing heifer puberty EPDs that could be used in economic selection indexes, or as indicators of reproductive success in heifer pregnancy, sustained reproductive success, or stayability EPDs. Further research is needed in this area.

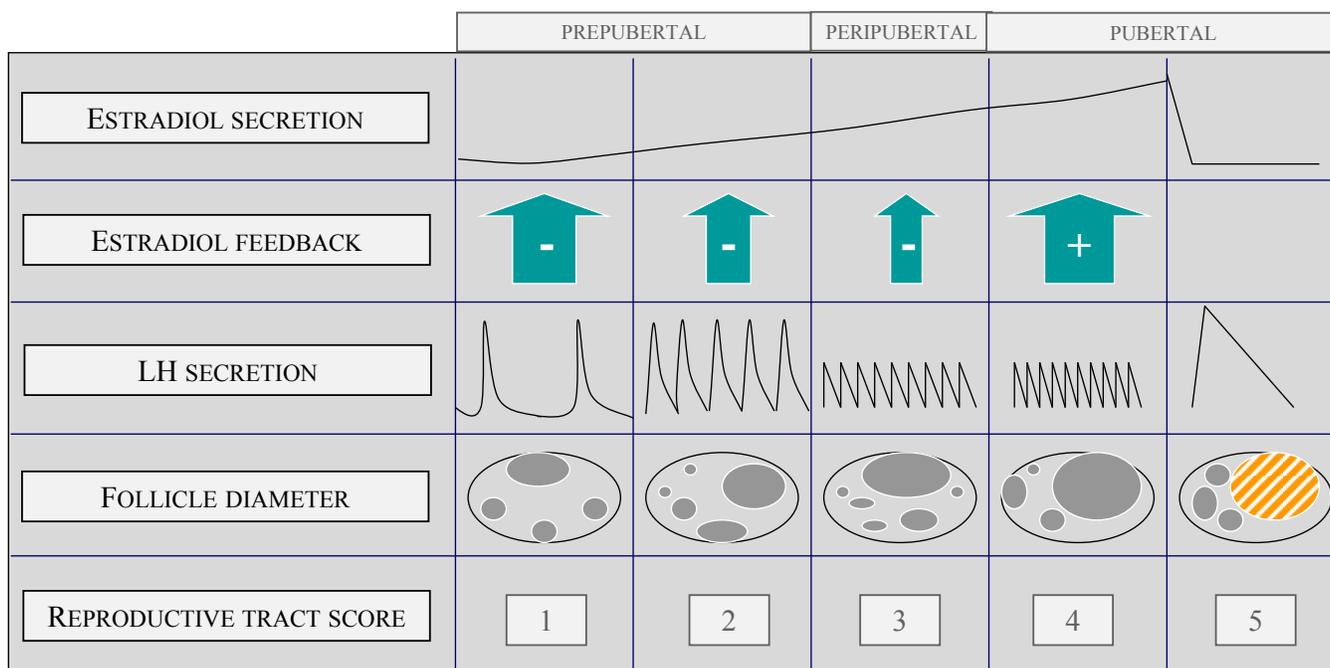
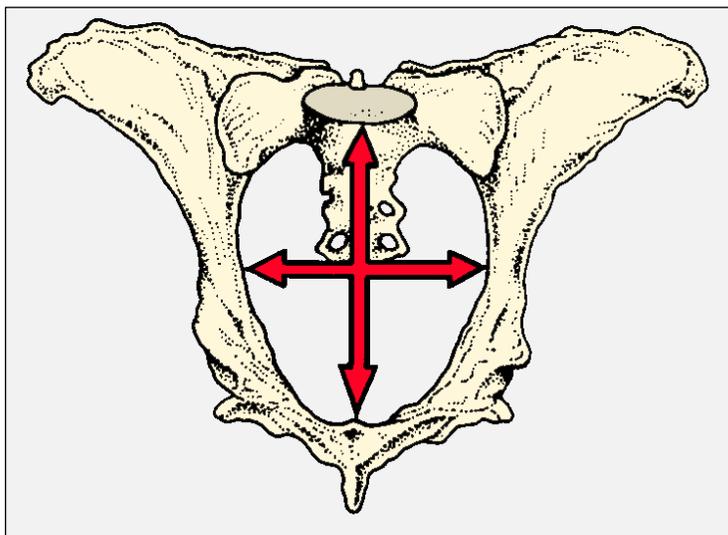


Figure 1. Endocrine and ovarian changes associated with puberty onset (adapted from Day and Anderson, 1998; Anderson et al., 1991).

Pelvic measurements. Pelvic measurements should be used in addition to, not in place of, selection for size, weight, and above all fertility (Bellows and Staigmiller, 1990). Producers should be aware that selection for pelvic area will not likely result in increased pelvic dimensions alone, but may result in increased size of the entire skeleton and animal (Morrison et al., 1986). This can be minimized in a multiple trait selection program with pressure to moderate mature size and improve direct calving ease. Pelvic measurements can be used successfully to identify abnormally small or abnormally shaped pelvises. These situations, left unidentified, often are associated with extreme dystocia, resulting in Cesarean delivery and even death of the calf or dam (Patterson et al., 1992).

Pelvic area is an effective indicator of maternal calving ease (Bellows and Staigmiller, 1990). Selection of sires with high CED EPD mated to heifers that are screened for pelvic area contribute to a decrease in the incidence and (or) severity of calving problems and minimize calf losses from dystocia. Bullock and Patterson (1995) reported that puberty exerts a positive influence on pelvic width and resulting pelvic area in yearling heifers; however, the preceding differences that were seen among heifers as yearlings did not carry through to calving as two-year-olds. Therefore pubertal status of the heifer at the time prebreeding examinations are performed should be considered in selection (culling) decisions based on pelvic measurements and contemporary grouping for genetic analysis of pelvic measurements. The data suggest that puberty plays a role in pelvic size as yearlings, but once heifers reach puberty the effects may no longer be present. An independent culling level for pelvic size in heifers that are at different stages in their reproductive development appears to be more restrictive for those heifers that are peripubertal at the time of the exam. Heifers with a pelvic area less than 150 cm² at the time a prebreeding exam is performed should be re-measured at the initial pregnancy exam within 90 days from the start of the breeding season. At this time the heifer is expected to have attained a minimum pelvic area of 180 cm². Growth of the pelvis at yearling age is based on BIF guidelines, suggesting an anticipated growth rate of 0.27 cm²/day. Due to the issues described above in using pelvic measurements in phenotypic selection, pelvic measurements would be best utilized in a national cattle evaluation setting.

While pelvic area can be used as an effective indicator trait of maternal calving ease, it may also be helpful to predict earlier maturing heifers. As previously discussed, earlier maturing heifers have greater lifetime production, and effective measures of fertility in beef cattle are sorely lacking.



Management considerations related to use and application of RTS. The reproductive tract scoring system can be used to select heifers that are “reproductively ready” for the breeding season and thus minimize carrying costs of heifers that will very likely fail to cycle and conceive. Reproductive tract scores, when timed appropriately, serve as a useful indicator in determining whether heifers are ready to be placed on an estrous synchronization protocol and are useful too, in

determining the most appropriate method of estrous synchronization to use. Reproductive tract scores (RTS) should be performed on heifers no more than two weeks before administering an estrous synchronization protocol; and are considered “ready” to be placed on a progestin-based estrous synchronization protocol when at least 50 percent of the heifers are assigned a RTS of 4 or 5 (Patterson et al., 1999).

Heifers that are retained for breeding should not have received growth promoting implants during the suckling period as calves (Bartol et al., 1995). Heifer calves administered implants beginning on or before postnatal day 45, experience developmental loss of adult uterine endometrial area and glandularity. These changes cannot be considered desirable effects, because both maternal uterine tissues and related uterine secretions affected by implant use are recognized to play critical roles in support of conceptus development (Bartol et al., 1995). The significance of these findings as they relate to RTS pertain to situations involving heifers in which the management history of the heifer is unknown at the time the prebreeding examination is performed. The changes that occur in uterine morphology as a result of implant administration are in many cases palpable per rectum at the time the RTS is performed.

PREGNANCY EXAMINATION. An initial pregnancy examination should be performed within 90 days from the start of the breeding season. Individual animal identification, pregnancy status and fetal age (in days) should be recorded. Herds utilizing artificial insemination should report breeding dates. Pregnancy determination at this point relative to the start of the breeding period enables the veterinarian to more accurately determine fetal age and success of the heifer’s first breeding period.

- In situations where artificial insemination is performed, heifers should not be exposed for natural service for a minimum of:
 - 14 days after AI.

National cattle evaluations have typically used a success/failure measurement of heifer pregnancy to calculate EPDs. But, the information content in measures of when in the breeding season a heifer conceives (days pregnant) is greater than a success/fail measurement. This is simply due to the greater information content in quantitative versus categorical measures (Kizikaya, Fernando, and Garrick, 2014). While not all producers will provide pregnancy examination reports, using the information from those that do would increase the reliability of heifer pregnancy EPDs.

HERITABLE VARIATION. Previous work by breed associations has shown that heifer fertility is a heritable trait. The American Angus Association reports a heritability of 0.14 for heifer pregnancy (<http://www.angus.org/nce/heritabilities.aspx>) and the American Hereford Association reports a heritability of 0.27 for heifer calving rate EPD (<http://hereford.org/content/heifer-calving-rate-epds>). Our RTS heritability estimate of 0.26 from 180 Angus sires and 1,556 heifers in the Show-Me-Select Replacement Heifer Program (SMS) closely matches previously published estimates of 0.32 (Anderson et al. 1991). Heritability estimates for pelvic width vary from 0.38 to 0.82 (Morrison, Williamson, and Humes 1986; Nelsen et al. 1986), and in our data we estimate a heritability of 0.45. Pelvic height heritabilities vary from 0.10 to 0.59 (Morrison, Williamson, and Humes 1986; Nelsen et al. 1986), and in the SMS data we estimate a heritability of 0.31. Clearly, there is ample genetic variation present for genetic evaluation of RTS, pelvic area, and days pregnant in cattle.

CONCLUSION. Reproductive biologists have spent the last three decades developing and refining measures of puberty and reproductive success in cattle. But, animal breeders and quantitative geneticists have not employed these methods in the prediction of beef cattle fertility. We now propose the standardization and reporting of reproductive tract scores (RTS), pelvic measurements, and pregnancy diagnosis within 90 days of the start of the breeding season to use in selecting replacement heifers and national cattle evaluation.

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PHENOTYPIC DATA COLLECTION FOR REPLACEMENT BEEF HEIFERS

PREBREEDING

- Farm/ranch name & address
 - Animal ID
 - Birth date
 - Breed or breed cross
 - Sire
 - Dam
 - Weight^a
 - Hip height^a
 - Reproductive tract score^a
 - Pelvic height^a
 - Pelvic width^a
 - Pelvic area^a
 - Hair or blood sample(s) for genomic testing
- ^aPrebreeding exams should be performed 4 to 6 weeks prior to breeding.

BREEDING

- Breeding method
 - AI
 - Natural service
 - AI followed by natural service clean-up
- Estrous synchronization method
 - No synchronization
 - PG
 - MGA-PG
 - 5-day CO-Synch + CIDR
 - 7-day CO-Synch + CIDR
 - 14-day CIDR-PG
 - Others as developed
- Estrous detection
 - No detection
 - Visual
 - Aids
 - Estroject
 - HeatWatch
 - Other
- AI breeding^b
 - Heat detection
 - Heat detection & TAI
 - Fixed-time AI
 - Split-time AI
- AI sire
 - Conventional semen
 - Sex-sorted
- AI technician
 - Lay
 - Professional

^bFollowing AI, heifers should not be exposed to clean-up bulls for 14 days to provide more accurate determination of AI versus natural-service sired pregnancies.

PREGNANCY DIAGNOSIS

- Examiner
- Method
 - Ultrasound
 - Palpation
- Pregnancy status
 - AI
 - Fetal age
 - Natural service
 - Fetal age
 - Open/short
- Fetal sex

Background for Guidelines to Facilitate Enhanced Genetic Potentials for Cow Efficiency

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Introduction

Efficiency is the ability to produce an output without wasting inputs. Quantifying efficiency must relate outputs to inputs and its units are those of the inputs and outputs. Study of efficiency has been an important topic of investigation for more than a century (Mumford *et al.*, 1917) and of fundamental interest to the Beef Improvement Federation at least since its 2002 meeting when virtually the entire program focused primarily on that topic in honor of the life's work of Dr. Gordon Dickerson. The papers published therein provide useful background for today's conversation. Dickerson (1969) defined *biological* objectives, in a manner consistent with these being a measure of efficiency, as "the relative *economic* importance of the major components of performance in terms of the approximate direct effect of each on cost per unit of production. This definition seems consistent with identification of what has since come to be termed "Economically Relevant Traits" (Golden *et al.*, 2000). Consider the mathematical definition of efficiency for animal production adapted similarly to Tess and Davis (2002) from the works of Dickerson (1970, 1976, 1982).

$$\frac{\text{Expense}}{\text{Product}} = \frac{\overbrace{R_d + I_d + F_{md} + F_{pd}}^{\text{per breeding female}} + \overbrace{N_o [D_o (I_o + F_{mo} + F_{po}) + S_o]}^{\text{per her offspring}}}{P_d V_d + N_o P_o V_o}$$

Where:

R_d = annualized replacement cost; I_d = annual non-feed cost; F_{md} = annual maintenance feed cost; F_{pd} = annual feed cost for performance (e.g., milk production); N_o = number of offspring marketed per breeding female (may be fractional); D_o = number of days from weaning to harvest for offspring; I_o = daily non-feed cost for progeny during the postweaning period; F_{mo} = daily feed cost for maintenance of offspring; F_{po} = daily feed cost for performance of offspring; S_o = annual non-feed cost per offspring marketed; P_d = annualized product marketed from a breeding female (i.e., a cull cow); V_d = unit value of

product marketed from a breeding female; P_o = annual product marketed from offspring; and V_o = unit value of product marketed from offspring.

It is anticipated that any evaluation for efficiency would be based on a corresponding breeding objective: one to be improved following transformation to linearity (Lin 1980; Gunsett, 1984). In context of genetic evaluation a key question is: how well does the current suite of genetic predictions indicate the merit of individuals with respect to components of efficiency? It must be recognized that, with exceptions, genetic evaluation for the offspring-related components of the objective is currently substantially more accurate than it is for the breeding female-related components of the objective. One notable exception is the lack of widespread evaluation of days to finish (Brigham et al., 2006; Speidel, 2011) However, this deficiency aside, the aim of this paper is to review aspects of current genetic evaluation systems for traits of the breeding female and to stimulate progress toward more effective systems of evaluation of her genetic potential as she contributes to efficiency of the production system.

Current tools

Conceptually, the number of offspring marketed per breeding female can be divided into two components: the probability of producing an offspring from each breeding season, and longevity. When non-pregnant females are consistently culled these components are at least somewhat intertwined. This interrelationship is obvious in the genetic evaluation of “stayability” developed by Snelling *et al.* (1995) following its formal definition as the probability of surviving to a specific age, given the opportunity to reach that age (Hudson and Van Vleck, 1981). As such, the observations are binary and observed late in life (6 years of age in most current evaluations), with static contemporary groups defined at the time each female is first exposed for breeding. Inefficient use of contemporary group information and partial records are two problems that may limit current genetic evaluations for stayability. For instance, a cow sold to another breeder may result in her observation not being included in genetic evaluation due to the resulting single-animal contemporary group. These problems can be addressed by using survival analysis to account for time-dependent contemporary groups and censored records (Ducrocq and Sölkner, 1994, 1998). However, implementation of survival analysis for animal models can be challenging (Ducrocq, 2001). Due to issues of timeliness of phenotypic observations and generally low heritability, achieving a desirable level of accuracy in evaluation of individual animals prior to making a “keep or cull” decision may also be difficult.

Replacement costs are in large part functionally related to an opportunity cost for weaning weight not marketed, postweaning growth, postweaning feed intake, and pregnancy (calving) and culling rates. Weaning weight and postweaning growth are long-time standard components of genetic evaluation in beef cattle. Multi-trait genetic evaluation of postweaning growth and feed intake was more recently developed (MacNeil et al., 2011). Genetic evaluation of heifer pregnancy rate was developed more than 15 years ago (Doyle et al., 2000), but implementation has been slow due in part to the inability to record proper contemporary groups and exposure

information. Heifer calving rate has been proposed as an alternative to heifer pregnancy rate in order to overcome issues with data recording (Callis, 2010; Venot et al., 2013). Impacts of pregnancy and culling rates may be understood from a stable age distribution modeled following Leslie (1945, 1948). Days to calving has also been proposed as a trait for genetic evaluation to improve fertility in beef cattle (Johnston and Bunter, 1996). However, the trait days to calving does not readily lend itself to quantifying either annualized replacement cost or number of offspring marketed.

Equations, of varying degrees of complexity, are readily available to predict feed requirements for beef females. In many cases, these equations contain cow weight and milk production as independent variables and explain upwards of 75% of the phenotypic variation in annual energy consumption (e.g., Anderson et al., 1983; Kirkpatrick et al., 1985). More complex predictions of intake are part of the National Research Council (1987) treatise on predicting feed intake. Genetic evaluation of preweaning gain or weaning weight is virtually universal and the genetic prediction of the maternal contribution to preweaning growth is widely available. The genetic correlation between milk production and maternal weaning weight may be sufficiently strong to indicate these are alternative measures of the same trait (Miller and Wilton, 1999; Meyer et al., 1994; MacNeil et al., 2006). Further, genetic evaluation for cow weight is somewhat commonplace (e.g., Northcutt and Wilson, 1993; Anonymous, 2014). To date, genetic prediction for energy intake by cows has been accomplished without reliance on direct measurement of the trait of interest (MacNeil and Mott, 2000; Evans, 2001), which is expected to be exceedingly costly and necessarily only recorded late in life. Whereas, forage consumption depends not only on characteristics of the animal, but also on characteristics of the forage (Van Soest, 1965; Allison, 1985) whether or not genetic prediction of intake is robust across environments remains a researchable question.

In summary, some components of efficiency, such as stayability and longevity, related to breeding females are measured late-in-life with evaluations that could be facilitated by early-in-life indicator traits including genotypes. Likewise, there are additional components of the objective that are exceedingly expensive to measure directly and whose evaluation would also be facilitated by highly correlated indicator traits and accurate genomic predictions. Finally, evaluation of these traits depends on them being accurately recorded and perhaps even more so on the appropriate grouping of contemporaries. This should be a goal of “whole-herd” reporting systems.

Implementation

Successful evaluation of “efficiency” requires capturing the full range of variation in its underlying components. Making data capture too onerous is likely to dissuade producers from participating in national cattle evaluation systems focused on efficiency. Thus, while whole herd reporting is essential and must include information about females that “fail” and leave the system, specific data to be captured should be carefully thought out.

More accurate description of variation in probability of producing an offspring from each breeding season and measurement of longevity could be enhanced by culling codes that are both limited in number and focused on the economically relevant traits. It is recommended that disposal date be routinely reported and coupled with coded descriptors (e.g., age, open, bred late, or unsoundness: teats, udder, feet, legs, mouth, sold for breeding use).

Survival analysis offers a number of opportunities to accommodate unique characteristics of time-to-event reproductive data from beef cattle. First, modeling non-genetic effects, particularly on traits expressed as a time-to-event (reproductive failure, culling) can be somewhat different than similar modeling for traits expressed once early-in-life. For the latter class of traits the individuals that are most directly compared make up a single static contemporary group. However, for the former class of traits the non-genetic effects change over time as do the animals that are directly compared one to another. For instance, consider a hypothetical breeding group of females exposed for breeding together in a given year. Some of them will not become pregnant thus experience reproductive failure (an event) while others will become pregnant and thus do not experience the same event. Those not becoming pregnant will be culled and replaced by heifers that calved at two years of age. This changes the competitive structure within the group of females exposed the following year. Further, as environmental conditions fluctuate over years those experiencing reproductive failure after the second year have been exposed to different effects than those exhibiting the same event after the first year. This leads to a recommendation for modeling time-dependent contemporary groups. A second complication for some traits that are expressed late-in-life is the difficulty of including contemporary animals in an evaluation as they have not yet expressed the relevant phenotype. This missing data problem is referred to as censoring. The analysis of censored data is accommodated by survival analysis (Miller et al., 1981). Survival analysis can also accommodate time-to-event data that are categorical in nature (Prentice and Gloeckler, 1978); a cow calves at 2, 3, 4, years of age, but fails to become pregnant after her third calf and hence does not calve at 5. Further, Giolo and Demétrio (2011) show the concept of frailty may provide a useful extension to survival analysis in order to account for unobserved within group heterogeneity (e.g., accounting for relationships among daughters of sires) in the context of genetic evaluation. Results from survival analysis correspond with predictions derived from matrix models of stable age distributions. This correspondence can be exploited in the development of breeding objectives.

Some components of efficiency may be geographically dependent and thus require different emphases depending on the region where the germplasm is intended for use. For example, given an EPD for heat tolerance, the economic weight placed on it is appropriately far greater in selection of cattle for use in Texas than those for use in Montana. Similar regionally specific emphases would include traits like fescue endophyte tolerance and disease resistance. This concept may even extend to dystocia as evidenced by Hereford cows of comparable genetic

make-up moved from Miles City, Montana, to Brooksville, Florida, and vice versa. Ten years after this switch was made, birth weights in the Montana herd that had been moved to Florida had declined from 81 pounds to 64 pounds. Conversely, birth weights in the Florida herd that had been moved to Montana had increased from 66 pounds to 77 pounds. Other studies have yielded similar results, indicating that calves of comparable genotype will be born lighter in the south than in the north (Ritchie and Anderson, 2001).

It should be noted that any index of “cow efficiency”, while generally in keeping with Dickerson’s description of efficiency is incomplete, due to the omission of some traits, with respect to the efficiency of beef production. This circumstance requires the economic values be adjusted to account for the incomplete recording and limits the opportunity to break genetic antagonisms (Amer et al., 2014). Thus, there is no guarantee that improvement in cow efficiency leads to generally more efficient beef production. Efficiency cannot be quantified, and therefore useful in genetic selection, without recording the economically relevant inputs and outputs. Past experimental evaluations of cow efficiency have focused on indexes of weaning weight of the calf divided by energy consumption by its dam (Marshall et al., 1976; Davis et al., 1983) and on weaning weight of the calf divided by body weight of its dam (e.g., Kress et al., 2001; MacNeil, 2005) or weaning weight of the calf divided by Large Stock Unit (Mokolobate, 2015). In all of these cases, the denominator is considered as a proxy for energy consumption by the cow. Use of these indexes as a selection criterion to improve efficiency seems debatable; certainly they fail to account for differences in reproduction and the latter indexes may not explain much variation in energy consumed. Furthermore, selection for ratio traits places inconsistent emphasis on the component traits, resulting in variable responses to selection (MacNeil, 2007).

It is envisioned that any evaluation of efficiency would proceed from components evaluated via direct measurement and indicators to a multiple-trait index. Economic weights for such indexes could be restricted (e.g., Eisen, 1977) so as to not allow improvement in efficiency to result from increased resource utilization. Smith et al (1986) extended this principle to focus weighting selection criteria in a way that facilitates genetic change that can be achieved by a resource-constant enterprise. Estimating economic weights by procedures adapted from microeconomic production theory may also be viable in accomplishing genetic improvement in efficiency (Amer and Fox, 1992). Currently, the greatest impediment to genetic evaluation of efficiency is having data to allow evaluation of the components. Successful implementation of EPD or EBV for “efficiency” rests on the twin pillars of “whole-herd” and “complete” reporting. Compromising either pillar results in a reduced ability to evaluate and thus improve efficiency.

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Genetic evaluation using single-step genomic BLUP in American Angus

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Introduction

Genomic selection in beef cattle has currently been performed with multistep methods, which uses deregressed EBV to estimate SNP effects and then direct genomic value (DGV) for selection candidates based on their genotypes (Meuwissen et al., 2001; Garrick et al., 2009). The main advantage of this approach is that the traditional BLUP evaluation is kept unchanged and genomic selection can be carried out by a separate entity owning genotypes but not phenotypes. Also new animals are easily evaluated if DGV is computed as a sum of marker effects, but not if selection indexes including DGV and parent average (PA) are used.

When both phenotypes and genotypes are available jointly, single-step genomic BLUP (ssGBLUP) (Aguilar et al., 2010) is a simple alternative. This method does not rely on deregressed proofs, properly weighs information from genotyped sires and cows, thus avoiding double-counting of contributions due to relationships and records, and accounts for pre-selection bias of genomically selected parents without phenotypes (Legarra et al., 2014). In ssGBLUP it is also possible to quickly evaluate young genotyped animals without running a complete evaluation that requires several hours to converge. Quick predictions can be calculated indirectly, where genomic predictions for young animals are obtained from SNP effects. It was shown by Wang et al. (2012) that SNP effects can be derived from GEBV solutions from the main ssGBLUP evaluation.

In its current implementation, ssGBLUP uses direct inversion of genomic matrices (Aguilar et al., 2011), which has a cubic cost and a limit of 150,000 animals (Aguilar et al., 2013). Several methods were proposed to overcome that limit (Legarra and Ducrocq, 2012; Fernando et al., 2014; Liu et al., 2014), but none was successful. Recently Misztal et al. (2014) presented a method which uses an approximate inversion of genomic relationships based on recursions on a fraction of the total population; which can be suitable and inexpensive.

The goal of this paper is to discuss the feasibility of ssGBLUP for genomic evaluation in Angus cattle with reference populations of different composition. Additional goals were to evaluate the ability to predictive GEBV with genomic recursions and with indirect prediction for young animals.

Single-step genomic BLUP (ssGBLUP)

The difference between BLUP and ssGBLUP can be observed in the mixed model equations, where the inverse of pedigree-based relationship matrix (\mathbf{A}) is replaced by the inverse of the realized relationship matrix (\mathbf{H}). The \mathbf{H} matrix blends \mathbf{A} with the genomic relationship matrix constructed based on SNP genotypes (\mathbf{G}) and a pedigree-based relationship matrix for genotyped animals only (\mathbf{A}_{22}):

$$\mathbf{H}^{-1} = \mathbf{A}^{-1} + \begin{bmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{G}^{-1} - \mathbf{A}_{22}^{-1} \end{bmatrix}$$

Contrary to genomic BLUP (GBLUP), ssGBLUP accounts not only for genotyped animals, but also for ungenotyped ones. In \mathbf{H} matrix, genomic relationships can influence nongenotyped animals if they are related to genotyped animals in \mathbf{A} . Even if two animals are unrelated in \mathbf{A} , they will be related in \mathbf{H} if they have genotyped descendants that are related in \mathbf{G} . This is possible because \mathbf{G} is usually identical by state, which means the genomic relationships are based on allele sharing independently of the origin.

Composition of genomic EBV (GEBV) from ssGBLUP

From traditional BLUP evaluations, EBV for an animal i can be expressed as (VanRaden and Wiggans, 1991):

$$u_i = w_1 PA + w_2 YD + w_3 PC$$

where PA is Parent Average, YD is Yield Deviation (phenotypes adjusted for the model effects' solutions other than additive genetic and error), PC is Progeny Contribution. When both parents are known, phenotype is available, and each progeny has a known mate, the weights w_1 to w_3 sum to 1. The decomposition of EBV can be derived from analyzing a row of mixed model equations for a given animal. In particular, YD is due to own phenotypic information, PA is the average of parental EBV for animal i , and PC is the sum of the differences between any progeny EBV of animal i minus one half the EBV of its dam (or the mate of animal i).

On the other hand, EBV for an animal i when genomic information is available (GEBV) is (VanRaden and Wright, 2013):

$$u_i = w_1 PA + w_2 YD + w_3 PC + w_4 GI$$

where GI contains information from animal's genotype and all weights sum to 1. According to VanRaden and Wright (VanRaden and Wright, 2013), the weight for GI is:

$$w_4 = \frac{g^{ii} - a_{22}^{ii}}{den}, \text{ with } den = 2 + n_r/\alpha + n_p/2 + g^{ii} - a_{22}^{ii}$$

Aguilar et al. (Aguilar et al., 2010) showed that in ssGBLUP, GI corresponds to two components:

$$GI = w_{4_1} DGV - w_{4_2} PP$$

with values for DGV and PP equal to:

$$DGV_i = \frac{-\sum_{j,j \neq i} g^{ij} u^j}{g^{ii}}; PP_i = \frac{-\sum_{j,j \neq i} a_{22}^{ij} u^j}{a_{22}^{ii}}$$

where DGV is the portion of prediction due to the genomic information, which comes from \mathbf{G} , and PP is pedigree prediction that comes from \mathbf{A}_{22} . The weights w_1, w_2, w_3, w_{4_1} , and w_{4_2} sum to 1.

In general, PP accounts for part of PA explained by DGV; when $\mathbf{A}=\mathbf{A}_{22}$, PA and PP cancel out and DGV explains a larger fraction of GEBV; when a genotyped animal is unrelated to the genotyped population, $PP=0$ and DGV explains a smaller fraction of GEBV; when two parents are genotyped, PP will include a large fraction of PA. Subsequently, accuracy of DGV will vary on an animal basis depending on how many ancestors of that animal are genotyped, as found by Mulder et al. (Mulder et al., 2012). When a genotyped animal has many progeny, $w_3 \approx 1$ and its GEBV is mainly driven by PC; however, genotyping those animals is useful as they are usually part of the reference population. When an animal is not genotyped, $w_4=0$ and predictions can be improved due to improved PA and PC if its relatives are genotyped. When an animal is not genotyped and has no phenotypes and no progeny, the genetic prediction is driven by PA and in most cases improvements in predictions are small (Legarra et al., 2009; Aguilar et al., 2010; Christensen and Lund, 2010).

Dataset

Datasets from American Angus Association (AAA) were available that included growth traits and calving ease (CE). Growth traits included birth weight (BW), weaning weight (WW), and post-weaning gain (PWG). Table 1 shows general statistics for all traits. The animals were genotyped for 54,609 SNP from the BovineSNP50k v2 BeadChip (Illumina Inc., San Diego, CA). Currently, no genotyping strategy is applied by AAA; therefore, the members can choose which animals are being genotyped.

Table1. Heritability (h^2) and general statistics for growth traits and CE

Trait ¹	h^2	Number of records	Average (kg)	SD (kg)	Number of genotyped animals with records
BW	0.41	6,189,661	36.47	4.45	50,784
WW	0.20	6,890,625	263.13	44.63	51,830
PWG	0.20	3,387,252	162.25	67.00	36,196
CE	0.12	1,310,684	-	-	10,558
easy	-	1,215,571	-	-	10,228
difficult	-	95,113	-	-	330

¹ BW = birth weight; WW = weaning weight; PWG = post-weaning gain; CE = calving ease.

ssGBLUP with different reference populations

The current trend in livestock genomics is to genotype young animals; however, more important animals in the reference population may give more information to the evaluations. For growth traits (CE), the first reference population tested was composed of 1,628 (1,541) top bulls with EBV accuracy (based on prediction error variance - PEV) for $BW \geq 0.85$; which we will refer hereinafter as “ref_bulls”. In this case, the **G** matrix was composed of animals in the reference population and also animals in the validation population; the last had 18,721 animals for growth traits and 13,166 for CE. The second reference population was composed of the top bulls and also top cows that had an EBV accuracy for $BW \geq 0.85$; which we will refer as ref_2k. The number of top cows was small and only 268 were added for the growth trait analysis and 323 for CE. The third reference population was composed of top bulls, top cows, and all other genotyped animals born from 1977 to 2012 (we will refer as ref_33k). This group had a total of 33,162 animals for growth and 27,380 for CE, with an average EBV accuracy for BW of 0.77 (\pm 0.05). For the latter analysis, the **G** matrix was composed of the maximum number of 51,883 genotyped animals for growth analysis and 40,546 for analysis of CE.

Method for Validation

The ability to predict future phenotypes was the validation method chosen. This method is based on Legarra et al. (2008), and predictive ability for traditional and genomic evaluations for animals born in 2013 was calculated as the correlation between (G)EBV and phenotypes corrected for fixed effects ($y-Xb$):

$$r = \text{cor}[(G)EBV, y-Xb]$$

The predictive ability or predictivity is used as an approach to compare the methods applied in this paper. For all analyses, the validation groups were kept the same to make comparisons easier. Validations involved 18,721 animals for growth traits and 16,133 animals for CE.

Results

Predictive ability on young animal when using several reference populations is shown in Figure 1. Using only top bulls as a reference population (ref_bulls) increased predictivity relative to BLUP by 0.05 for BW, 0.01 for WW, 0.04 for PWG, and 0.01 for CE. Addition of top cows to the reference population (ref_2k) did not increase the predictivity for any trait. This could be due to the small number of animals added and also because daughters of those cows already contributed through the inclusion of bulls. Addition of around 31,000 animals to the reference population provided an additional increase in predictivity of 0.05 for BW, of 0.03 for WW and of 0.02 for PWG. However, no additional increase was observed for CE by adding extra 27,000 genotyped animals, of which about 7,000 had phenotypes for that trait.

The addition of 31,000 animals with few or no progeny led to the same increase of predictivity as using only the top bulls for BW, led to an increase of 3 times for WW and an increase of 0.5 times for PWG. Among the 31,000 extra animals, almost all had phenotypes for BW and WW, but only 24,000 had phenotypes for PWG. Evidently, the composition of reference

population is also a factor that influences predictivity of GEBV besides the reference population size. Thus, genotyping strategy should take into account genotyping more important and maybe older animals with more information (higher EBV accuracy) along with genotyping large amounts of young animals.

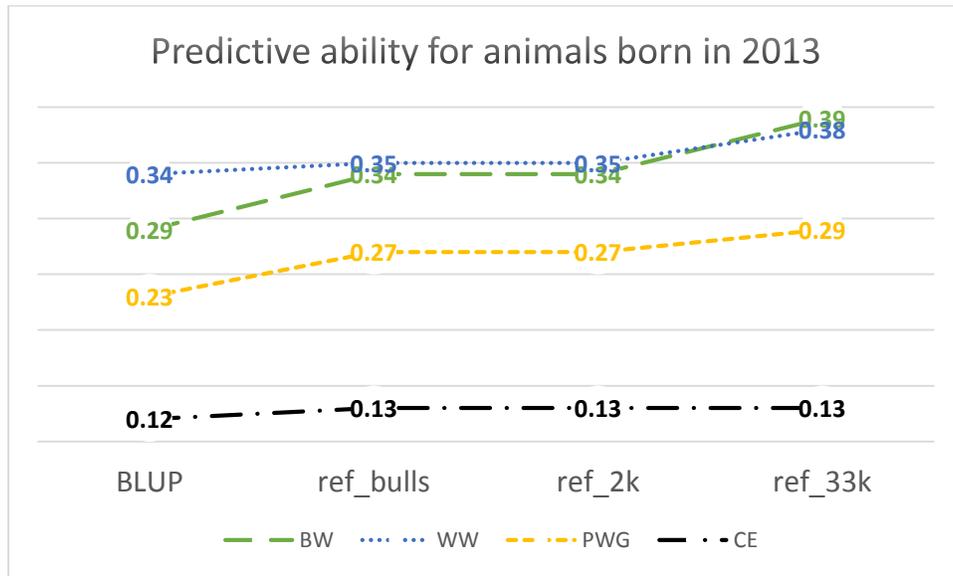


Figure 1. Predictive ability of future phenotypes for young genotyped animals born in 2013. *BW* = birth weight; *WW* = weaning weight; *PWG* = post-weaning gain; *CE* = calving ease. Predictive ability was calculated as correlation between corrected phenotypes and genomic EBV; *ref_bulls* is a reference populations that contains top bulls, *ref_2k* contains top bulls and top cows, and *ref_33k* contains all genotyped animals born up to 2012.

ssGBLUP with indirect predictions for young animals

With the increasing number of genotyped heifers and steers in beef cattle populations, the genomic methods should be able to provide predictions for young animals without phenotypes in a quick run, externally to the official evaluations. This concept is introduced here as indirect ssGBLUP, and basically mimics the mixed model equations. It would be advantageous from different perspectives: to evaluate young animals mainly for traits that are measured later in life, after the selection decisions are made; and to reduce computing costs

because the dimension of \mathbf{G} would not increase in the same proportion as the number of genotyped animals.

For ssGBLUP with indirect predictions, SNP effects can be calculated using the current run of ssGBLUP with all but young animals, and genomic predictions for young animals are obtained by multiplying the SNP content by SNP effect to obtain DGV; a more complete GEBV can also be available through a selection index that combines DGV and PA. In order to explain how it works, consider the equation for the GEBV of a single individual in ssGBLUP as a combination of equations in Aguilar et al. (2010) and VanRaden and Wright (2013):

$$\text{GEBV} = w_1\text{PA} + w_2\text{YD} + w_3\text{PC} + w_{4_1}\text{DGV} - w_{4_2}\text{PP}$$

The flow for indirect predictions in ssGBLUP is:

- 1) Run ssGBLUP with a reference population to obtain GEBV. In this step, 3 reference populations were tested:
 - a) ref_2k: reference population with top bulls and top cows (n=1,896);
 - b) ref_8k: reference population with all parents that were genotyped (n=8,285), this includes ref_2k;
 - c) ref_33k: reference population with all genotyped animals born up to 2012 (n=33,162), this includes ref_8k;
- 2) Split GEBV into all the components shown before, where DGV for an animal i in the reference population is calculated as below (Aguilar et al. (2010): $\text{DGV}_i = \frac{\sum_{j \neq i} g^{ij} \text{GEBV}^j}{g^{ii}}$ with all elements previously defined.
- 3) Calculate SNP effects using DGV from the reference population: $\hat{\mathbf{u}} = \mathbf{DZ}'\mathbf{G}^{-1}(\mathbf{DGV})$ where $\hat{\mathbf{u}}$ is a vector of estimated SNP effects, \mathbf{D} is a diagonal matrix of weights (standardized variances) for SNP (identity matrix in this case), and \mathbf{Z} is a matrix of centered genotypes for each

animal (VanRaden, 2008). A similar approach that uses GEBV instead of DGV to calculate SNP effects was proposed by Wang et al. (2012). However, for numerical purposes this involves approximations as \mathbf{G} matrix is formed as $\mathbf{G}=0.95\mathbf{ZDZ}'+0.05\mathbf{A}_{22}$ (Aguilar et al., 2010). This is done as a default approach to avoid singularity problems and may result in negligible error as shown later.

4) Calculate DGV for young genotyped animals (\mathbf{DGV}_y): $\mathbf{DGV}_y=\mathbf{Z}_y\hat{\mathbf{u}}$

where \mathbf{DGV}_y and \mathbf{Z}_y are direct genomic values and a matrix of centered genotypes for young animals not included in ssGBLUP evaluation, respectively.

5) Combine \mathbf{DGV}_y with PA for young genotyped animals: $\text{GEBV}_y \approx w_1\text{PA} + w_4\mathbf{DGV}_y$

where GEBV_y is GEBV obtained via indirect predictions for young animals, w_1 and w_4 are weights identical for all animals and calculated based on selection index.

Results

Predictive ability for indirect prediction via conversion of DGV into SNP effects is shown in Figure 2. When the reference population included top bulls and top cows (ref_2k), the predictivity of indirect \mathbf{DGV}_y was lower than predictivity for traditional EBV for the three traits (0.23 vs. 0.29 for BW; 0.28 vs. 0.34 for WW; 0.19 vs. 0.23 for PWG). Predictivity for GEBV_y calculated as an index of indirect \mathbf{DGV}_y with PA was higher than those for EBV for the three traits (0.31 vs. 0.29 for BW; 0.36 vs. 0.34 for WW; 0.24 vs. 0.23 for PWG), however, this predictivity was lower than the ones from full ssGBLUP (except for WW). With larger reference population (ref_8k), all indirect \mathbf{DGV}_y were similar or more accurate than EBV, and the index had similar predictivity as the full ssGBLUP. With the largest reference population (ref_33k), all indirect \mathbf{DGV}_y were almost as accurate as GEBV from full ssGBLUP, with the index marginally improving predictivity for WW. This marginal improvement for WW may be caused by the use

of less than optimal genetic parameters, e.g., zero covariance between direct and maternal effects (to reduce computing costs). The DGV_y obtained with ref_33k reference population were more accurate than GEBV from full ssGBLUP obtained with ref_8k reference population.

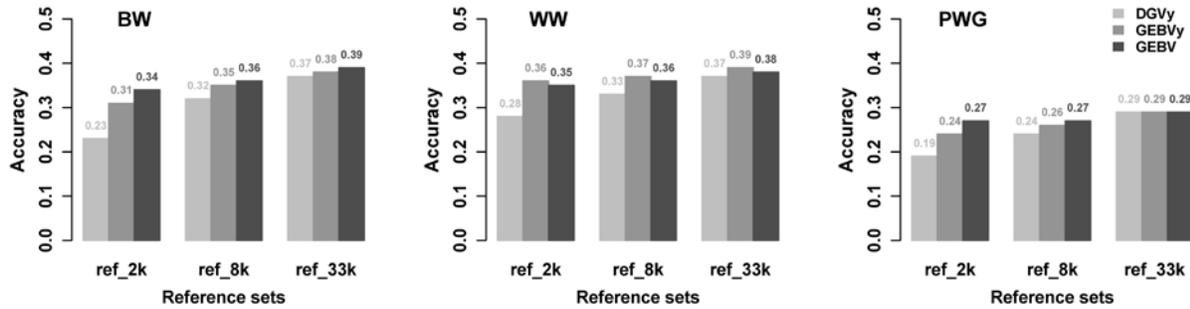


Figure 2. Predictive ability of indirect predictions on 18,721 young genotyped animals when using reference populations ref_2k, ref_8k, and ref_33k animals to run single-step genomic BLUP (ssGBLUP) and derivate SNP effects. *ref_2k* is a reference populations that contains top bulls and top cows, *ref_8k* contains all parents that were genotyped, and *ref_33k* contains all genotyped animals born up to 2012. DGV_y is direct genomic value; $GEBV_y$ is the indirect genomic EBV obtained by an index combining parent average and DGV_y ; $GEBV$ is genomic predictions obtained directly from ssGBLUP when genotypes on reference and validation animals were considered together in evaluations.

For young animals, indirect predictions via SNP effects from ssGBLUP seems a viable alternative as it can be done separately from the full evaluation. As SNP effects are calculated based on trait GEBV or DGV, indirect predictions are easily obtained for multi-trait models, as done in this study; multi-breed and crossbred evaluations are possible when the G matrix is able to account for information on all breeds. However, if young animals and particularly full-sibs are intensively selected, selection on the Mendelian sampling will not be accounted for, leading to pre-selection bias (Patry and Ducrocq, 2011). Analyses by ssGBLUP with all genotypes subject to selection are expected to account for pre-selection (VanRaden and Wright, 2013), because selection is accounted for when all information used for selection is included in the model (Henderson, 1975).

ssGBLUP with \mathbf{G} inverted by a recursive algorithm

When the number of genotyped animals is large and there is a desire for using all of them in ssGBLUP evaluations to get direct predictions for all, including young animals, an algorithm that splits genotypes into proven and young animals and uses recursion to approximate the inverse of the \mathbf{G} matrix was proposed by Misztal et al. (2014). This algorithm is known as APY, and \mathbf{G}^{-1} containing all genotyped animals can be expressed as:

$$\mathbf{G}^{-1} = \begin{bmatrix} \mathbf{G}_{pp}^{-1} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} \end{bmatrix} + \begin{bmatrix} -\mathbf{G}_{pp}^{-1} \mathbf{G}_{py} \\ \mathbf{I} \end{bmatrix} \mathbf{M}_g^{-1} \begin{bmatrix} -\mathbf{G}_{yp} \mathbf{G}_{pp}^{-1} & \mathbf{I} \end{bmatrix}$$

where the subscript pp stands for proven animals and py for the covariance between proven and young animals; each element of \mathbf{M}_g is obtained (for the i^{th} young animal) as $m_{g,i} = g_{ii} -$

$\mathbf{G}_{ip} \mathbf{G}_{pp}^{-1} \mathbf{G}_{pi}$ and is called genomic Mendelian sampling. In APY, the only direct inversion needed is for part of \mathbf{G} that contains relationships among proven animals (\mathbf{G}_{pp}), whereas all other coefficients are obtained through recursions.

For this analysis, four definitions of proven animals were tested that included the 3 definitions used for indirect predictions (ref_2k, ref_8k, and ref_33k), plus one more definition where 3,872 genotyped parents of genotyped animals were considered as proven (ref_4k). This last group was added to test if proven animals would have strong links with the young genotyped population.

The greatest advantages of this algorithm are the reduction of computing cost, which is still cubic for proven animals, but can be linear for young animals; and the possibility of using large amounts of genotyped animals in ssGBLUP evaluations. The secondary advantage is numerical stability as the regular \mathbf{G} matrix is singular when the number of animals is greater than the number of SNP markers and cannot be inverted without blending with \mathbf{A}_{22} .

Results

Predictive ability of GEBV when the inverse of \mathbf{G} is computed with APY is shown in Figure 3. When the recursions were conditioned on ref_2k, ref_4k, ref_8k, and ref_33k, the procedure accounted for 67%, 88%, 97%, and 100% of predictivity gains of ssGBLUP over BLUP, respectively. Therefore, in ssGBLUP, using genomic recursion to invert \mathbf{G} while conditioning on enough number of animals, in this case about 8,000, has the same prediction power as \mathbf{G} using direct inversion. The amount of memory necessary for APY \mathbf{G}^{-1} using ref_2k, ref_4k, ref_8k, and ref_33k was approximately 0.8, 1.6, 3.2, and 13.7 Gbytes, respectively, whereas the amount of memory for the regular \mathbf{G}^{-1} is 21.6 Gbytes. Therefore, using APY \mathbf{G}^{-1} makes computations less costly and faster.

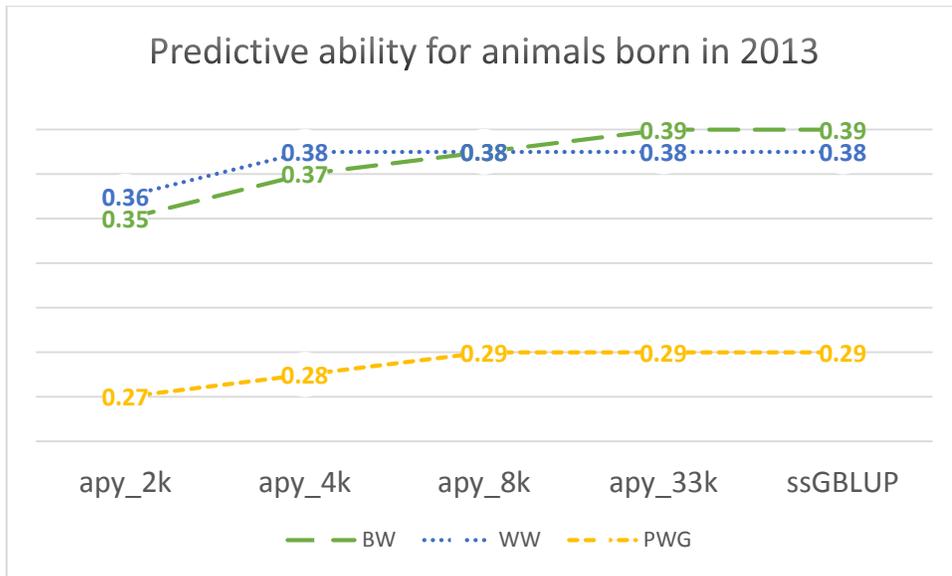


Figure 3. Predictive ability of GEBV for 18,721 young genotyped animals when using APY (algorithm for proven and young animals) to invert \mathbf{G} matrix (genomic-based relationship matrix) with different definitions of proven animals: ref_2k, ref_4k, ref_8k, and ref_33k. *ref_2k is a reference populations that contains top bulls and top cows, ref_4k contains genotyped parents of genotyped animals, ref_8k contains all parents that were genotyped, and ref_33k contains all genotyped animals born up to 2012.*

The main advantages of APY are low computing costs and numerical stability. With conditioning on 8,000 animals, for example, the only inverse required is for a block of \mathbf{G} for 8,000 animals, and additional genotypes require only linear storage and computations. Subsequently, computations with a large number of genotyped animals may be feasible with similar predictivity as in the regular inversion. APY would be the algorithm of choice for regular evaluations with very large number of genotyped animals.

Conclusions

Genomic evaluation in beef cattle using single-step genomic BLUP is feasible for either linear or categorical traits. Gains in predictive ability over BLUP are dependent on the composition of the reference population, and are greater for growth traits and small for CE. With a sufficient number of animals in the reference population, indirect prediction for young animals via SNP effects provides similar predictivity to full single-step genomic BLUP, allowing for quick genomic predictions without running a complete evaluation. Use of the algorithm for proven and young animals in single-step genomic BLUP allows for incorporation of large number of genotyped animals at low cost without compromising the predictive ability.

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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 24 breeds are presented in this report. Mean EPDs for growth traits are shown in Table 1 (24 breeds), for other production traits in Table 2 (19 breeds), and for carcass and composition traits in Table 3 (20 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 American Akaushi, Blonde d'Aquitaine, North American Piedmontese, American Pinzgauer, and American Waygu breeds but have not found summaries containing current breed averages. 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 2013 average EPDs from 2015 evaluations for growth traits

Breed	Birth Weight (lb)	Weaning Weight (lb)	Yearling Weight (lb)	Maternal Milk (lb)	Total Maternal (lb)
Angus	1.7	50	88	23	
Hereford	3.3	47	77	19	43
Murray Grey	3.7	23	35	4	15
Red Angus	-1.2	56	87	20	
Red Poll	1.6	15	24	6	
Shorthorn	2.2	48	52.7	19.7	41.6
South Devon	2.5	43.2	80.8	24.5	46.2
Beefmaster	0.3	10	14	2	
Braford	1.0	11	17	3	9
Brahman	1.8	16	25.5	5.6	
Brangus	1.1	24.7	46.2	9.5	21.8
Red Brangus	1.5	12.6	19.8	5.0	11.3
Santa Gertrudis	0.2	3.6	5.2	0.3	
Senepol	1.2	12.1	16.5	4.5	9.6
Simbrah	3.9	62.9	85.2	20.7	52.1
Braunvieh	2.9	44.5	69.2	34.3	56.6
Charolais	0.5	26.1	47.5	8.5	21.6
Chianina	2.4	43.3	62.2	16.8	38.3
Gelbvieh	1.0	67.5	97.5	28.3	61.9
Limousin	1.9	64.3	90.6	25.4	
Maine-Anjou	1.2	45.3	59.8	17.1	39.6
Salers	1.5	42	80	19	40
Simmental	2	62.9	91	21.9	53.4
Tarentaise	1.3	17.5	30.8	.7	9.4

Table 2. Birth year 2013 average EPDs from 2015 evaluations for other production traits

Breed	Calving Ease Direct (%)	Calving Ease Maternal (%)	Scrotal Circ (cm)	Docility Score	Mature Weight (lb)	Heifer Pregnancy (%)	Stayability (%)
Angus	4	8	0.82	13	30	10.1	
Hereford	0.9	1.2	0.8		87		
Murray Grey	-0.6	-0.1	0.2		53		
Red Angus	4	5				10	11
Shorthorn	4.0	1.4					
South Devon			0.1				
Beefmaster			0.2				
Brahman				0.0			
Brangus	4.6	3.7	0.48				
Simbrah	2.5	6.4		6.8			
Braunvieh	5.4	0.7	-0.12				
Charolais	3.1	3.5	0.72				
Chianina	5.5	-2.5					
Gelbvieh	10.2	7.2					6.6
Limousin	6.9	5.5	0.14	21.6			19.4
Maine Anjou	7.8	2.4					
Salers	0.4	0.4	0.3	9			23
Simmental	8.6	9.4		9.6			20.6
Tarentaise	-0.1	0.7					

Table 3. Birth year 2013 average EPDs from 2015 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	32			0.54	0.51	0.012		
Hereford				0.07	0.30	0.003		
Murray Grey	31	0.4		0.0 ^a	0.10 ^a	0.00 ^a	0.00 ^a	
Red Angus	20		0.01	0.44	0.10	-0.001		
Shorthorn	0.2			0.05	-0.06	-0.030		
South Devon	27.4	0.8		0.4	0.22	0.01		
Beefmaster				0.00 ^a	0.03 ^a	0.01 ^a	0.01 ^a	
Braford	6			0.01	0.06	0.012		
Brahman	1.2	0.00		0.01	0.01	-0.001		0.02
Brangus	23.5			0.00 ^a	0.31 ^a	-0.043 ^a	-0.008 ^a	
Santa Gertrudis	3.3			-0.01	0.03	0.002		
Simbrah	25.6		-0.23	-0.08	0.46	-0.060		-0.03
Braunvieh	20.3			0.57 ^a	0.33 ^a	-0.43 ^a	-0.057 ^a	
Charolais	15.9			0.03	0.28	0.003		
Chianina	10.5	0.33		0.15	0.19	-0.04		
Gelbvieh	28.8		-0.19	0.06	0.45	-0.05		
Limousin	25.9		-0.18	-0.07	0.50			
Maine-Anjou	7.0	0.43		0.04	0.19	-0.051		
Salers	22	0.1		0	0.04	0.00		
Simmental	26.8		-0.32	0.12	0.77	-0.05		-0.32

^aDerived using ultrasound measures and reported on an ultrasound scale (IMF% instead of marbling score)

Table 4. Birth year 2013 average EPDs from 2015 evaluations for other traits unique to individual breeds

Angus	Residual		Cow		Weaned		Grid Value (\$)	Beef Value (\$)	
	Average Daily Gain (lb)	Mature Height (in)	Yearling Height (in)	Energy Value (\$)	Calf Value (\$)	Feedlot Value (\$)			
	0.18	0.3	0.5	-6.98	35.94	34.67	30.24	84.8	
Hereford	Baldy Maternal Index (\$)	Brahman Influence Index (\$)	Certified Hereford Beef Index (\$)	Calving Ease Index (\$)	Udder Score	Teat Score			
	17	15	22	15			1.13	1.13	
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 (\$)		
	0.8	0.008	-0.002	-0.007	69.59	100.82	69.40		
Limousin	Mainstream Terminal Index (\$)								
	47.7								
Simmental	All Purpose Index (\$)	Terminal Index (\$)	Simbrah	All Purpose Index (\$)	Terminal Index (\$)				
	119.4	66.7		69.8	52.4				
Shorthorn	\$ British Maternal								
	\$ Calving Ease	\$ Feedlot	Index						
	21.72	47.81	108.67						
Murray Grey	600-d wt (lb)	Gestational length (d)	Days to calving (d)						
	51	-0.2	-0.8						

ACROSS-BREED EPD TABLES FOR THE YEAR 2015 ADJUSTED TO BREED DIFFERENCES FOR BIRTH YEAR OF 2013

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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 2015 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 of each breed born in year 2013. 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 2013) 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 2015 update of estimates of sire breed means from data of the Germplasm Evaluation (GPE) project at USMARC adjusted to a year 2013 basis using EPD from the most recent national cattle evaluations. The 2013 basis year is chosen because yearling records for weight and carcass traits should have been accounted for in EPDs for progeny born in 2013 in the Spring 2015 EPD national genetic evaluations. Factors to adjust Spring 2015 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, 2015)

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 2014 (Kuehn and Thallman, 2014):

This year we are reporting breed differences and adjustment factors for carcass weight for the first time (Table 8). Like other carcass traits in this report, these carcass weight differences are derived by accounting for age (rather than weight or fat). The differences and factors are reported for all breeds in the program that report a carcass weight EPD.

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 and carcass traits) and Santa Gertrudis and Chiangus (especially for maternal milk). However, all of the breeds will 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 (2012-2014). 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 F₁ 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 (255), 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 (265) 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 2015 EPD for breed i for animals born in the base year (YY, which is two years before the update; e.g., YY = 2013 for the 2015 update),

EPD(i)_{USMARC} is the weighted (by total relationship of descendants with records at USMARC) average of 2015 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 2015: 1.17, 0.80, 0.98, and 1.11 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 1.71 lb, 14.59 lb, 23.73 lb, -0.03 marbling score units (i.e. $4.00 = S1^{00}$, $5.00 = S_m^{00}$), 0.28 in², 0.033, and 30.39 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 F₁ is expected to exceed that of its parental breeds. The estimate of maternal heterosis for WWT was 8.32 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 2013 birth year basis. The column labeled 6 of each table corresponds to the Across-breed EPD Adjustment Factor for that trait. Table 4 summarizes the analysis of MILK. Tables 5, 6, and 7 summarize data from the carcass traits (MAR, REA, FAT). Because of the accuracy of sire carcass EPDs and the greatest percentage of data being added to carcass traits, sire effects and adjustment factors are more likely to change for carcass traits in the future.

Column 5 of each table represents the best estimates of sire breed differences for calves born in 2013 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 2013) 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 2010 through 2014 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 2013 average of 97.5 for Gelbvieh) and for a Simmental bull is +89.0 (which is below the birth year 2013 average of 91.0 for Simmental). The across-breed adjustment factors in the last column of Table 3 are -30.4 for Gelbvieh and -9.5 for Simmental. Then the adjusted EPD for the Gelbvieh bull is $98.0 + (-30.4) = 67.6$ and for the Simmental bull is $89.0 + (-9.5) = 79.5$. The expected yearling weight difference when both are mated to another breed of cow, e.g., Hereford, would be $67.6 - 79.5 = -11.9$ 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 0.5 lb for Red Angus to 7.4 lb for Charolais and 11.0 lb for Brahman. Angus continued to have the lowest estimated sire effect for birth weight (Table 1, column 5). The relatively heavy birth weights of Brahman-sired progeny would be expected to be offset by favorable maternal effects reducing birth weight if progeny were from Brahman or Brahman cross dams which would be an important consideration in crossbreeding programs involving Brahman cross females. Changes in breed of sire effects were generally small, less than 1.0 lb for all breeds relative to last year's update (Kuehn and Thallman, 2014).

Weaning Weight

All of the 17 breed differences (Table 2, column 5) were within 5 lb of the values reported by Kuehn and Thallman. (2014) except for Shorthorn. Shorthorn did have a change of base in their last evaluation, which may be part of the cause; the mean EPD of sires sampled at USMARC changed relative to this new base. Otherwise, changes in breed effects for all 18 breeds seem to be stabilizing since continuous sampling started in 2007.

Yearling Weight

Breed of sire effects for yearling weight were also similar to Kuehn and Thallman (2014) in general. Again, Shorthorn changed more relative to other breeds also likely because of a base change in their yearling weight EPD. Angus continued to have the greatest rate of genetic change for yearling weight, 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 7 lb difference from those reported in 2014. 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 just begun to have progeny in this update; however, 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. The Salers breed average for marbling decreased (Table 5, column 1) 0.20 marbling score units while average EPD of USMARC sampled bulls (Table 5, column 2) had little change relative to last year's update. Hence, their marbling score difference decreased by approximately 0.20 compared to Kuehn and Thallman (2014). Carcass weight differences and factors are reported for the first time in this update.

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 0.56, 0.17, 0.44, and 0.16, respectively. Heritability estimates for MAR, REA, FAT, and CWT were 0.46, 0.49, 0.41, and 0.51 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, 0.80 for WWT, and 0.98 for YWT were used to adjust breed of sire solutions to the base year of 2013. 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 1.11 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 2013 base and factors to adjust within breed EPD to an Angus equivalent – BIRTH WEIGHT (lb)

Breed	Number		Ave. Base EPD		Breed Soln at USMARC (vs Ang) (3)	BY 2013 Sire Breed Average (4)	BY 2013 Sire Breed Difference ^a (5)	Factor to adjust EPD To Angus (6)
	AI Sires	Direct Progeny	Breed 2013 (1)	USMARC Bulls (2)				
Angus	162	2095	1.7	1.9	0.0	86.6	0.0	0.0
Hereford	160	2449	3.3	2.3	3.6	90.9	4.3	2.7
Red Angus	57	749	-1.2	-1.9	-0.3	87.2	0.5	3.4
Shorthorn	60	557	2.2	2.6	6.8	92.3	5.6	5.1
South Devon	28	213	2.5	2.1	4.5	91.0	4.4	3.6
Beefmaster	56	509	0.3	0.9	5.5	90.9	4.3	5.7
Brahman	57	706	1.8	0.6	11.3	97.7	11.0	10.9
Brangus	57	518	1.1	1.0	3.5	89.9	3.3	3.9
Santa Gertrudis	24	311	0.2	0.6	6.6	92.1	5.4	6.9
Braunvieh	33	480	2.9	4.1	5.6	90.4	3.7	2.5
Charolais	111	1205	0.5	0.2	8.1	94.0	7.4	8.6
Chiangus	26	326	2.4	2.2	4.5	90.9	4.2	3.5
Gelbvieh	82	1091	1.0	2.8	4.2	88.6	2.0	2.7
Limousin	76	1171	1.9	1.5	3.1	89.9	3.2	3.0
Maine Anjou	51	547	1.2	2.2	6.2	91.2	4.5	5.0
Salers	52	497	1.5	2.4	3.3	88.7	2.0	2.2
Simmental	90	1216	2.0	3.2	5.8	90.6	3.9	3.6
Tarentaise	17	265	1.3	2.0	3.8	89.3	2.7	3.1

Calculations:

$$(4) = (3) / b + [(1) - (2)] + (\text{Recent Raw Angus Mean: } 86.8 \text{ lb}) \text{ with } b = 1.17$$

$$(5) = (4) - (4, \text{Angus})$$

$$(6) = (5) - (5, \text{Angus}) - [(1) - (1, \text{Angus})]$$

^aThe 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 2013 base and factors to adjust within breed EPD to an Angus equivalent – WEANING WEIGHT (lb)

Breed	Number		Ave. Base EPD		Breed Soln	BY 2013	BY 2013	Factor to adjust EPD To Angus (6)
	AI Sires	Direct Progeny	Breed 2013 (1)	USMARC Bulls (2)	at USMARC (vs Ang) (3)	Sire Breed Average (4)	Sire Breed Difference ^a (5)	
Angus	162	1935	50.0	29.0	0.0	570.2	0.0	0.0
Hereford	158	2263	47.0	28.4	-4.0	562.8	-7.4	-4.4
Red Angus	57	717	56.0	50.5	-3.4	550.5	-19.7	-25.7
Shorthorn	60	526	48.0	53.8	-4.7	537.5	-32.7	-30.7
South Devon	28	194	43.2	27.2	-7.9	555.4	-14.8	-8.0
Beefmaster	56	481	10.0	11.9	15.2	566.3	-3.9	36.1
Brahman	56	613	16.0	6.4	19.9	583.7	13.5	47.5
Brangus	57	494	24.7	22.3	5.7	558.7	-11.4	13.9
Santa Gertrudis	24	294	3.6	6.5	15.1	565.2	-5.0	41.4
Braunvieh	33	445	44.5	46.3	-3.9	542.5	-27.6	-22.1
Charolais	110	1096	26.1	14.6	20.2	585.9	15.7	39.6
Chiangus	26	291	43.3	46.3	-7.8	536.6	-33.6	-26.9
Gelbvieh	82	1023	67.5	60.9	8.3	566.2	-4.0	-21.5
Limousin	76	1076	64.3	46.2	0.2	567.5	-2.7	-17.0
Maine Anjou	51	509	45.3	46.1	-6.0	541.0	-29.2	-24.5
Salers	52	472	42.0	34.5	1.1	558.1	-12.1	-4.1
Simmental	88	1112	62.9	56.3	18.0	578.3	8.1	-4.8
Tarentaise	17	257	17.5	-1.9	-2.2	565.9	-4.2	28.3

Calculations:

(4) = (3) / b + [(1) – (2)] + (Raw Angus Mean: 549.2 lb) with b = 0.80

(5) = (4) – (4, Angus)

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

^aThe 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 2013 base and factors to adjust within breed EPD to an Angus equivalent – YEARLING WEIGHT (lb)

Breed	AI	Number		Ave. Base EPD		Breed Soln	BY 2013	BY 2013	Factor to adjust EPD To Angus
		Direct	Progeny	Breed 2013	USMARC Bulls	at USMARC (vs Ang)	Sire Breed Average	Sire Breed Difference ^a	
	Sires			(1)	(2)	(3)	(4)	(5)	(6)
Angus	153		1699	88.0	50.3	0.0	1041.9	0.0	0.0
Hereford	147		2074	77.0	47.3	-29.1	1004.2	-37.6	-26.6
Red Angus	49		643	87.0	73.1	-8.0	1009.9	-31.9	-30.9
Shorthorn	55		475	52.7	60.4	-2.1	994.3	-47.6	-12.3
South Devon	25		176	80.8	55.0	-20.8	1008.7	-33.1	-25.9
Beefmaster	53		386	14.0	18.1	0.1	1000.2	-41.7	32.3
Brahman	56		541	25.5	11.0	-29.5	988.5	-53.3	9.2
Brangus	53		399	46.2	40.8	-4.4	1005.1	-36.7	5.1
Santa Gertrudis	21		261	5.2	10.1	1.9	1001.2	-40.6	42.2
Braunvieh	30		420	69.2	72.0	-27.0	973.8	-68.1	-49.3
Charolais	105		993	47.5	28.4	18.5	1042.2	0.3	40.8
Chiangus	24		254	62.2	62.9	-25.8	977.2	-64.6	-38.8
Gelbvieh	79		970	97.5	79.4	-1.3	1020.9	-20.9	-30.4
Limousin	66		992	90.6	61.5	-30.2	1002.5	-39.4	-42.0
Maine Anjou	48		472	59.8	62.1	-22.8	978.6	-63.2	-35.0
Salers	50		438	80.0	65.8	-10.6	1007.6	-34.3	-26.3
Simmental	84		961	91.0	81.7	21.4	1035.3	-6.5	-9.5
Tarentaise	17		234	30.8	1.1	-38.8	994.3	-47.6	9.6

Calculations:

(4) = (3) / b + [(1) – (2)] + (Raw Angus Mean: 1004.2 lb) with b = 0.98

(5) = (4) – (4, Angus)

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

^aThe 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 2013 base and factors to adjust within breed EPD to an Angus equivalent – MILK (lb)

Breed	AI Sires	Number		Ave. Base EPD		Breed Soln at USMARC (vs Ang) (3)	BY 2013 Sire Breed Average (4)	BY 2013 Sire Breed Difference ^a (5)	Factor to adjust EPD To Angus (6)
		Direct Gpr	Direct Progeny	Breed 2013 (1)	USMARC Bulls (2)				
Angus	133	2999	709	23.0	14.0	0.0	558.2	0.0	0.0
Hereford	134	3677	895	19.0	10.6	-23.6	536.4	-21.8	-17.8
Red Angus	46	906	257	20.0	16.6	5.5	557.6	-0.6	2.4
Shorthorn	47	457	172	19.7	20.8	12.6	559.5	1.3	4.6
South Devon	24	368	90	24.5	20.1	9.4	562.1	3.9	2.4
Beefmaster	41	374	120	2.0	0.0	-2.4	549.1	-9.1	11.9
Brahman	55	836	249	5.6	7.1	18.5	564.4	6.2	23.6
Brangus	41	358	111	9.5	5.6	-4.2	549.3	-8.9	4.6
Santa Gertrudis	21	207	102	0.3	-1.8	-1.8	549.7	-8.5	14.2
Braunvieh	28	674	174	34.3	33.7	21.4	569.1	10.9	-0.4
Charolais	92	1628	413	8.5	5.9	-0.9	551.0	-7.2	7.3
Chiangus	24	203	99	16.8	13.5	-0.4	552.2	-6.0	0.2
Gelbvieh	73	1548	379	28.3	31.8	21.6	565.1	6.9	1.6
Limousin	63	1770	423	25.4	22.6	-0.3	551.8	-6.4	-8.8
Maine Anjou	41	676	184	17.1	16.1	-1.6	548.7	-9.5	-3.6
Salers	46	554	184	19.0	19.7	11.8	559.1	0.9	4.9
Simmental	71	1745	427	21.9	25.7	16.9	560.7	2.5	3.6
Tarentaise	14	363	100	0.7	4.0	14.8	559.3	1.1	23.4

Calculations:

(4) = (3) / b + [(1) – (2)] + (Raw Angus Mean: 549.2 lb) with b = 1.11

(5) = (4) – (4, Angus)

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

^aThe 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 2013 base and factors to adjust within breed EPD to an Angus equivalent – MARBLING (marbling score units^a)

Breed	Number		Ave. Base EPD		Breed Soln	BY 2013	BY 2013	Factor to adjust EPD To Angus
	AI Sires	Direct Progeny	Breed 2013 (1)	USMARC Bulls (2)	at USMARC (vs Ang) (3)	Sire Breed Average (4)	Sire Breed Difference ^b (5)	
Angus	130	765	0.54	0.20	0.00	6.14	0.00	0.00
Hereford	144	972	0.07	0.00	-0.52	5.36	-0.79	-0.32
Red Angus	47	242	0.44	0.47	-0.06	5.72	-0.42	-0.32
Shorthorn	54	248	0.05	0.09	-0.35	5.41	-0.73	-0.24
South Devon	22	68	0.40	-0.07	-0.36	5.92	-0.23	-0.09
Brahman	55	227	0.01	-0.01	-1.04	4.79	-1.36	-0.83
Santa Gertrudis	21	126	-0.01	-0.02	-0.84	4.97	-1.17	-0.62
Charolais	52	274	0.03	-0.04	-0.63	5.25	-0.90	-0.39
Chiangus	24	123	0.15	0.15	-0.45	5.36	-0.79	-0.40
Gelbvieh	77	426	0.06	-0.24	-0.77	5.34	-0.81	-0.33
Limousin	62	404	-0.07	-0.15	-0.95	4.94	-1.21	-0.60
Maine Anjou	48	237	0.04	0.03	-0.78	5.04	-1.10	-0.60
Salers	46	213	0.00	-0.36	-0.70	5.46	-0.68	-0.14
Simmental	80	454	0.12	-0.02	-0.60	5.35	-0.80	-0.38

Calculations:

$$(4) = (3) / b + [(1) - (2)] + (\text{Raw Angus Mean: } 5.81) \text{ with } b = 1.00$$

$$(5) = (4) - (4, \text{Angus})$$

$$(6) = (5) - (5, \text{Angus}) - [(1) - (1, \text{Angus})]$$

$$^a 4.00 = S1^{00}, 5.00 = S m^{00}$$

^bThe 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 2013 base and factors to adjust within breed EPD to an Angus equivalent – RIBEYE AREA (in²)

Breed	Number		Ave. Base EPD		Breed Soln	BY 2013	BY 2013	Factor to adjust EPD To Angus (6)
	AI Sires	Direct Progeny	Breed 2013 (1)	USMARC Bulls (2)	at USMARC (vs Ang) (3)	Sire Breed Average (4)	Sire Breed Difference ^a (5)	
Angus	130	766	0.51	0.09	0.00	13.24	0.00	0.00
Hereford	144	972	0.30	-0.04	-0.22	12.93	-0.31	-0.10
Red Angus	47	242	0.10	-0.12	-0.18	12.86	-0.38	0.03
Shorthorn	54	248	-0.06	-0.07	0.16	12.98	-0.26	0.31
South Devon	22	68	0.22	0.21	0.33	13.16	-0.08	0.21
Brahman	55	232	0.01	0.05	-0.14	12.63	-0.61	-0.11
Santa Gertrudis	21	127	-0.01	0.02	-0.13	12.66	-0.58	-0.06
Charolais	52	275	0.28	0.12	1.01	13.99	0.75	0.98
Chiangus	24	124	0.19	0.18	0.43	13.26	0.02	0.34
Gelbvieh	77	428	0.45	0.36	0.92	13.83	0.59	0.65
Limousin	62	405	0.50	0.37	1.26	14.21	0.97	0.98
Maine Anjou	48	237	0.19	0.21	0.90	13.70	0.46	0.78
Salers	46	214	0.04	0.03	0.79	13.62	0.38	0.85
Simmental	80	455	0.77	0.55	0.89	13.93	0.69	0.43

Calculations:

(4) = (3) / b + [(1) – (2)] + (Raw Angus Mean: 12.82 in²) with b = 1.00

(5) = (4) – (4, Angus)

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

^aThe 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 2013 base and factors to adjust within breed EPD to an Angus equivalent – FAT THICKNESS (in)

Breed	Number		Ave. Base EPD		Breed Soln	BY 2013	BY 2013	Factor to adjust EPD To Angus (6)
	AI Sires	Direct Progeny	Breed 2013 (1)	USMARC Bulls (2)	at USMARC (vs Ang) (3)	Sire Breed Average (4)	Sire Breed Difference ^a (5)	
Angus	130	766	0.012	0.002	0.000	0.668	0.000	0.000
Hereford	144	971	0.003	-0.003	-0.058	0.606	-0.062	-0.053
Red Angus	47	241	-0.001	-0.009	-0.034	0.632	-0.036	-0.023
Shorthorn	54	248	-0.030	-0.031	-0.140	0.519	-0.149	-0.107
South Devon	22	68	0.010	0.008	-0.123	0.537	-0.131	-0.129
Brahman	55	232	-0.001	-0.002	-0.150	0.509	-0.159	-0.146
Santa Gertrudis	21	127	0.002	0.002	-0.097	0.561	-0.107	-0.097
Charolais	52	274	0.003	0.005	-0.205	0.452	-0.216	-0.207
Chiangus	24	123	-0.040	-0.025	-0.141	0.502	-0.166	-0.114
Gelbvieh	77	426	-0.050	-0.083	-0.202	0.490	-0.179	-0.117
Maine Anjou	48	237	-0.050	-0.029	-0.223	0.414	-0.254	-0.192
Salers	46	214	0.000	-0.007	-0.212	0.453	-0.215	-0.203
Simmental	80	455	-0.050	-0.052	-0.192	0.469	-0.199	-0.137

Calculations:

(4) = (3) / b + [(1) – (2)] + (Raw Angus Mean: 0. 658 in) with b = 1.00

(5) = (4) – (4, Angus)

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

^aThe 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 2013 base and factors to adjust within breed EPD to an Angus equivalent – CARCASS WEIGHT (lb)

Breed	AI Sires	Number Direct Progeny	Ave. Base EPD		Breed Soln at USMARC (vs Ang) (3)	BY 2013 Sire Breed Average (4)	BY 2013 Sire Breed Difference ^a (5)	Factor to adjust EPD To Angus (6)
			Breed 2013 (1)	USMARC Bulls (2)				
Angus	130	766	32	12.4	0.0	904.9	0.0	0.0
Red Angus	47	242	20	10.6	-8.0	886.6	-18.2	-6.2
Shorthorn	54	248	0.22	8.6	-15.5	861.4	-43.4	-11.6
South Devon	22	68	27.4	15.2	-19.6	877.9	-26.9	-22.3
Brahman	55	233	1.2	-0.5	-41.4	845.5	-59.3	-28.5
Brangus	50	242	23.5	18.6	-6.3	883.9	-21.0	-12.5
Santa Gertrudis	21	127	3.3	6.0	-11.8	870.8	-34.1	-5.4
Braunvieh	30	196	20.3	14.4	-42.9	848.3	-56.6	-44.9
Charolais	52	275	15.9	11.1	4.1	894.2	-10.7	5.4
Chiangus	24	124	10.5	9.5	-23.8	862.4	-42.4	-20.9
Gelbvieh	77	428	28.8	19.0	-16.0	879.1	-25.8	-22.6
Limousin	62	405	25.9	5.8	-20.0	885.4	-19.5	-13.4
Maine Anjou	48	237	7	10.4	-25.6	856.3	-48.6	-23.6
Salers	46	215	22	14.9	-27.2	865.2	-39.7	-29.7
Simmental	80	455	26.8	20.6	12.0	903.4	-1.4	3.8

Calculations:

(4) = (3) / b + [(1) – (2)] + (Raw Angus Mean: 885.3 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	0.81	0.78	0.73	0.74	0.54	0.53	0.51	0.51
Hereford	0.67	0.63	0.63	0.60	0.29	0.41	0.33	
Red Angus	0.92	0.92	0.91	0.89	0.68	0.66	0.68	0.60
Shorthorn	0.82	0.81	0.80	0.80	0.45	0.43	0.45	0.57
South Devon	0.44	0.47	0.42	0.49	0.06	0.09	0.10	0.33
Beefmaster	0.88	0.90	0.86	0.75				
Brahman	0.52	0.49	0.43	0.33	0.09	0.11	0.09	0.26
Brangus	0.88	0.82	0.71	0.71				0.68
Santa Gertrudis	0.73	0.67	0.58	0.54	0.40	0.49	0.50	0.45
Braunvieh	0.62	0.55	0.31	0.49				0.26
Charolais	0.81	0.75	0.68	0.70	0.49	0.52	0.46	0.47
Chiangus	0.81	0.78	0.78	0.74	0.24	0.21	0.33	0.56
Gelbvieh	0.85	0.83	0.83	0.81	0.62	0.57	0.59	0.55
Limousin	0.93	0.93	0.93	0.92	0.66	0.65		0.60
Maine Anjou	0.80	0.79	0.79	0.79	0.31	0.30	0.34	0.56
Salers	0.83	0.82	0.76	0.80	0.27	0.30	0.35	0.61
Simmental	0.94	0.94	0.94	0.93	0.73	0.71	0.71	0.60
Tarentaise	0.93	0.92	0.92	0.88				

^aWeighted by relationship to phenotyped animals at USMARC for BWT, WWT, YWT, MAR, REA, and FAT and by relationship to daughters with phenotyped progeny MILK.

Table 10. Estimates of variance components (lb²) for birth weight (BWT), weaning weight (WWT), yearling weight (YWT), and maternal weaning weight (MWWT) and for marbling (MAR; marbling score units²), ribeye area (REA; in⁴), fat thickness (FAT; in²), and carcass weight (CWT; lb) from mixed model analyses

Analysis	BWT	WWT ^a	YWT	
Animal within breed (18 breeds)	69.40	483.34	3612.43	
Maternal genetic within breed (18 breeds)		444.29		
Maternal permanent environment		719.55		
Residual	55.63	1263.93	4551.99	

Carcass Direct	MAR	REA	FAT	CWT
Animal within breed (13-16 breeds)	0.269	0.644	0.0102	2335.22
Residual	0.281	0.768	0.0145	2252.06

^aDirect maternal covariance for weaning weight was -54.15 lb²

Table 11. Pooled and within-breed regression coefficients (lb/lb) for weights at birth (BWT), 205 days (WWT), and 365 days (YWT) of F₁ progeny and for calf weights (205 d) of F₁ dams (MILK) on sire expected progeny difference and by sire breed

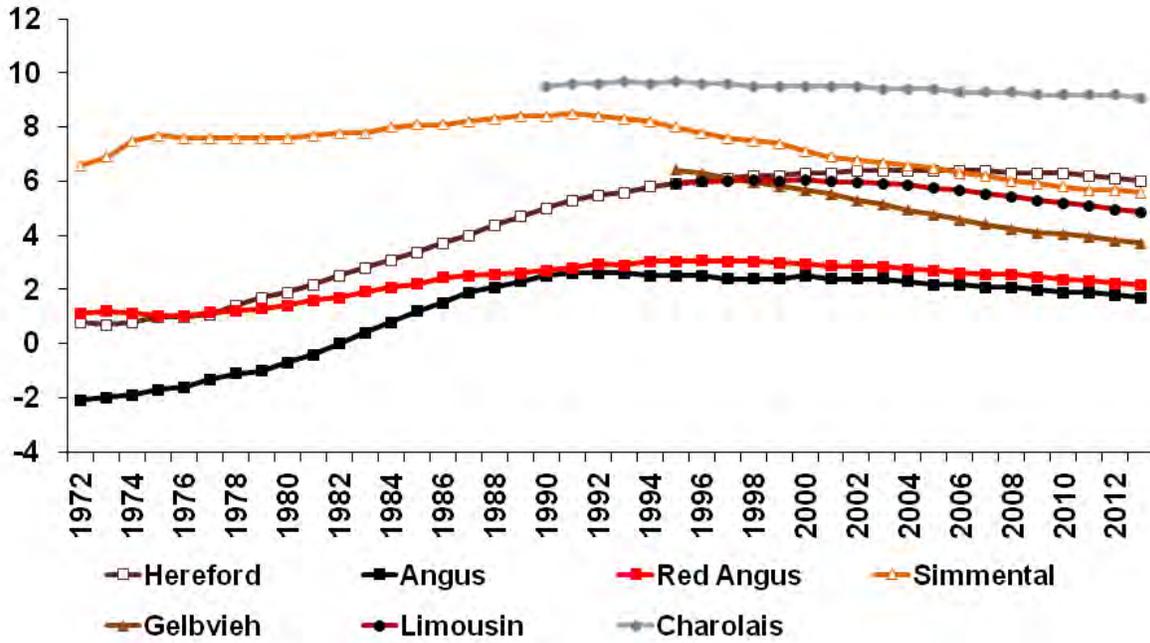
	BWT	WWT	YWT	MILK
Pooled	1.17 ± 0.04	0.80 ± 0.03	0.98 ± 0.04	1.11 ± 0.07
Sire breed				
Angus	1.06 ± 0.09	0.83 ± 0.06	1.18 ± 0.07	1.08 ± 0.15
Hereford	1.16 ± 0.07	0.71 ± 0.05	1.00 ± 0.06	1.03 ± 0.15
Red Angus	1.01 ± 0.14	0.74 ± 0.13	0.61 ± 0.15	1.34 ± 0.26
Shorthorn	0.75 ± 0.21	0.52 ± 0.14	0.55 ± 0.17	1.00 ± 0.43
South Devon	-0.24 ± 0.53	0.80 ± 0.29	0.50 ± 0.32	1.08 ± 1.06
Beefmaster	2.08 ± 0.33	0.98 ± 0.21	0.76 ± 0.31	3.41 ± 0.67
Brahman	1.93 ± 0.21	1.08 ± 0.18	1.36 ± 0.22	0.09 ± 0.62
Brangus	1.49 ± 0.23	0.74 ± 0.20	0.81 ± 0.18	0.28 ± 0.58
Santa Gertrudis	3.75 ± 0.71	1.31 ± 0.25	1.15 ± 0.29	0.78 ± 1.00
Braunvieh	0.88 ± 0.26	0.63 ± 0.28	0.31 ± 0.27	1.54 ± 0.65
Charolais	1.14 ± 0.12	0.96 ± 0.11	0.86 ± 0.12	1.06 ± 0.22
Chiangus	1.44 ± 0.30	0.13 ± 0.24	0.35 ± 0.28	0.19 ± 0.41
Gelbvieh	1.05 ± 0.14	0.81 ± 0.11	1.15 ± 0.12	0.84 ± 0.25
Limousin	1.11 ± 0.11	0.80 ± 0.07	0.86 ± 0.09	1.42 ± 0.21
Maine Anjou	1.40 ± 0.18	0.97 ± 0.19	0.83 ± 0.24	2.02 ± 0.39
Salers	1.26 ± 0.23	0.82 ± 0.25	0.60 ± 0.24	1.70 ± 0.38
Simmental	1.16 ± 0.14	1.44 ± 0.12	1.33 ± 0.12	0.95 ± 0.30
Tarentaise	0.70 ± 0.59	1.07 ± 0.24	1.55 ± 0.37	1.49 ± 0.81

Table 12. Pooled and within-breed regression coefficients marbling (MAR; score/score), ribeye area (REA; in²/in²), fat thickness (FAT; in/in), and carcass weight (CWT; lb) of F₁ progeny on sire expected progeny difference and by sire breed

	MAR	REA	FAT	CWT
Pooled	0.55 ± 0.04	0.80 ± 0.06	0.96 ± 0.08	0.90 ± 0.06
Sire breed				
Angus	0.84 ± 0.08	0.78 ± 0.13	1.05 ± 0.14	0.99 ± 0.11
Hereford	0.68 ± 0.14	0.64 ± 0.13	0.99 ± 0.17	
Red Angus	0.75 ± 0.15	1.17 ± 0.20	0.67 ± 0.36	1.20 ± 0.24
Shorthorn	1.52 ± 0.29	0.58 ± 0.35	1.44 ± 0.46	0.55 ± 0.28
South Devon	-0.08 ± 0.18	2.08 ± 2.36	4.24 ± 2.54	-0.66 ± 0.88
Brahman	1.97 ± 0.94	1.13 ± 0.36	1.25 ± 0.57	0.53 ± 0.27
Brangus				0.78 ± 0.24
Santa Gertrudis	1.07 ± 0.62	0.85 ± 0.48	1.31 ± 0.88	1.37 ± 0.49
Braunvieh				0.18 ± 0.23
Charolais	1.11 ± 0.20	0.80 ± 0.18	1.33 ± 0.38	0.54 ± 0.30
Chiangus	0.55 ± 0.20	0.22 ± 0.44	0.53 ± 0.39	0.75 ± 0.46
Gelbvieh	1.23 ± 0.19	1.33 ± 0.16	1.98 ± 0.30	1.46 ± 0.20
Limousin	0.86 ± 0.27	0.74 ± 0.14		0.75 ± 0.15
Maine Anjou	-0.12 ± 0.65	-0.79 ± 0.47	-0.84 ± 0.53	1.41 ± 0.33
Salers	0.05 ± 0.07	1.14 ± 0.55	0.90 ± 0.58	0.41 ± 0.47
Simmental	0.83 ± 0.16	0.63 ± 0.15	0.07 ± 0.29	1.59 ± 0.23

Figure 1. Relative genetic trends for birth weight (lb) of the seven most highly used beef breeds (1a) and all breeds that submitted 2015 trends (1b) adjusted for birth year 2013 using the 2015 across-breed EPD adjustment factors.

1a.



1b.

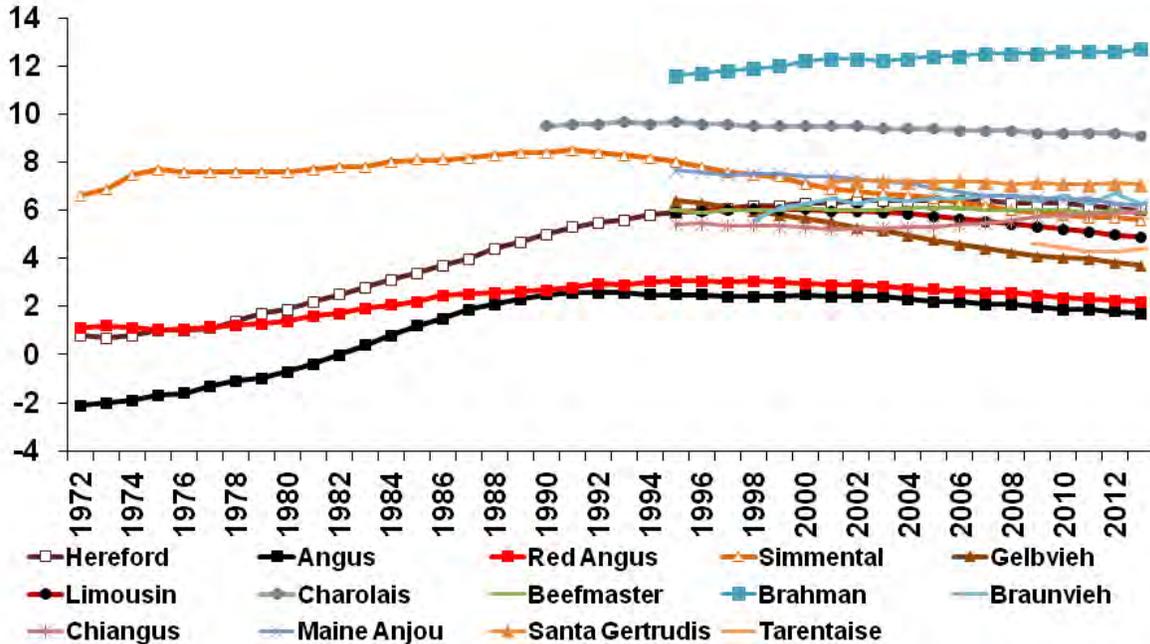
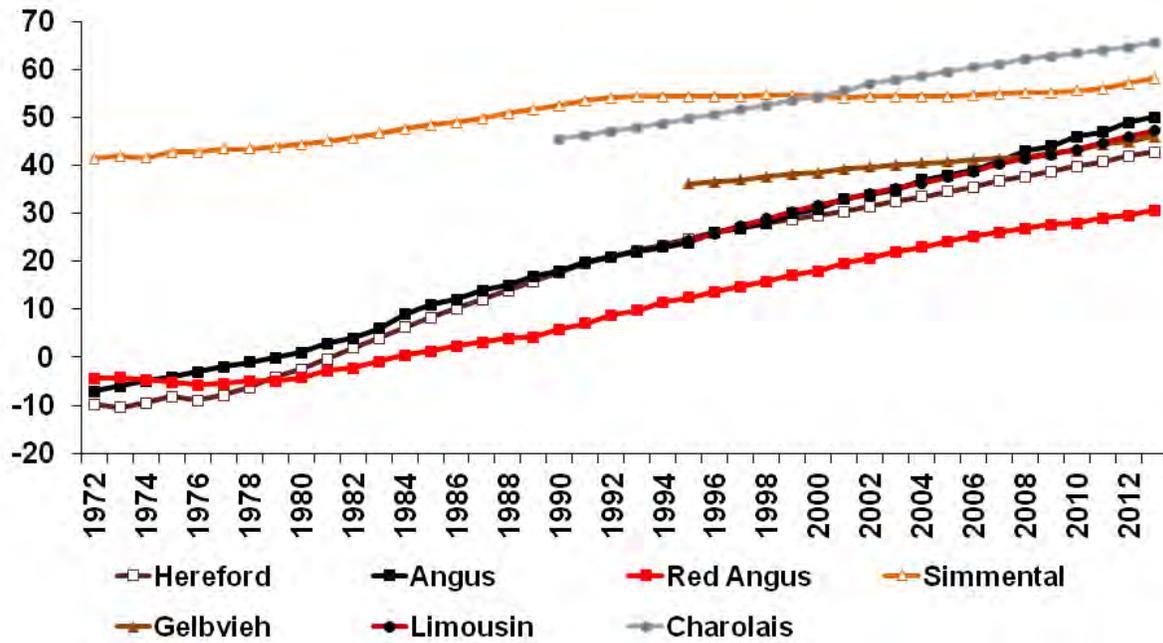


Figure 2. Relative genetic trends for weaning weight (lb) of the seven most highly used beef breeds (2a) and all breeds that submitted 2015 trends (2b) adjusted for birth year 2013 using the 2015 across-breed EPD adjustment factors.

2a.



2b.

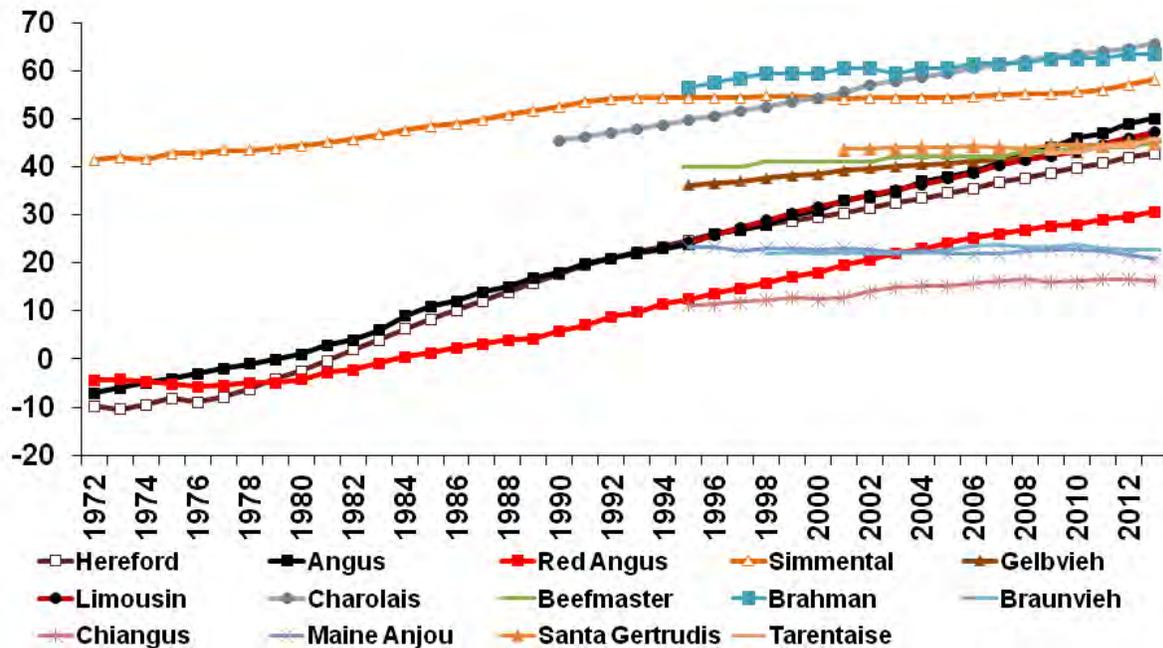
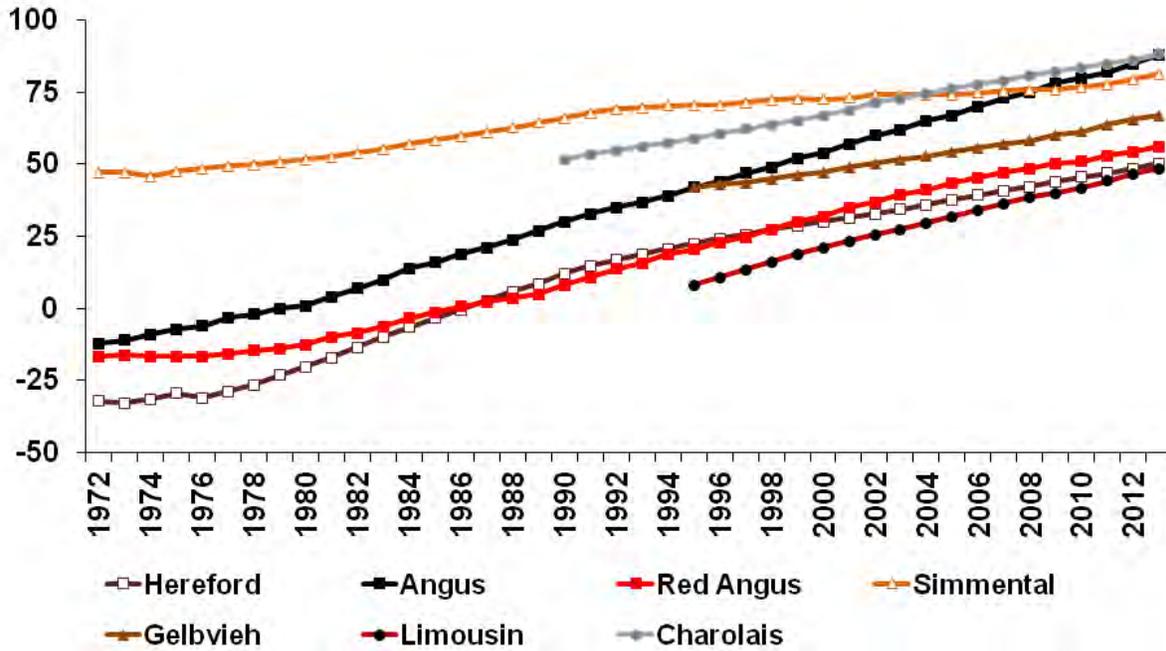


Figure 3. Relative genetic trends for yearling weight (lb) of the seven most highly used beef breeds (3a) and all breeds that submitted 2015 trends (3b) adjusted for birth year 2013 using the 2015 across-breed EPD adjustment factors.

3a.



3b.

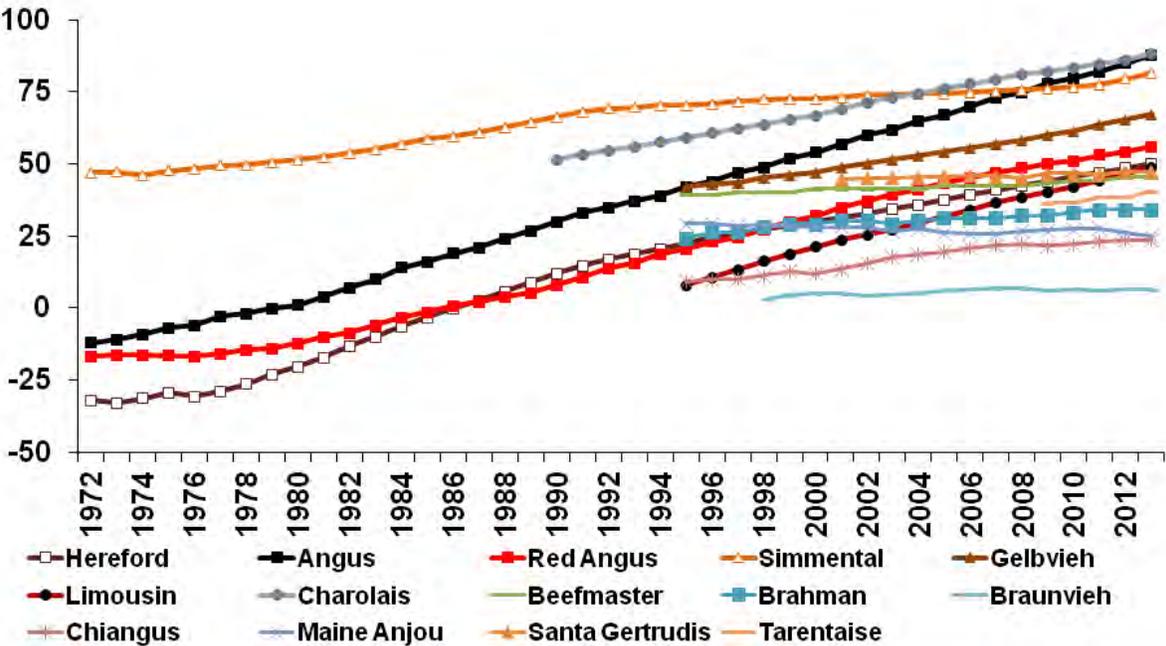
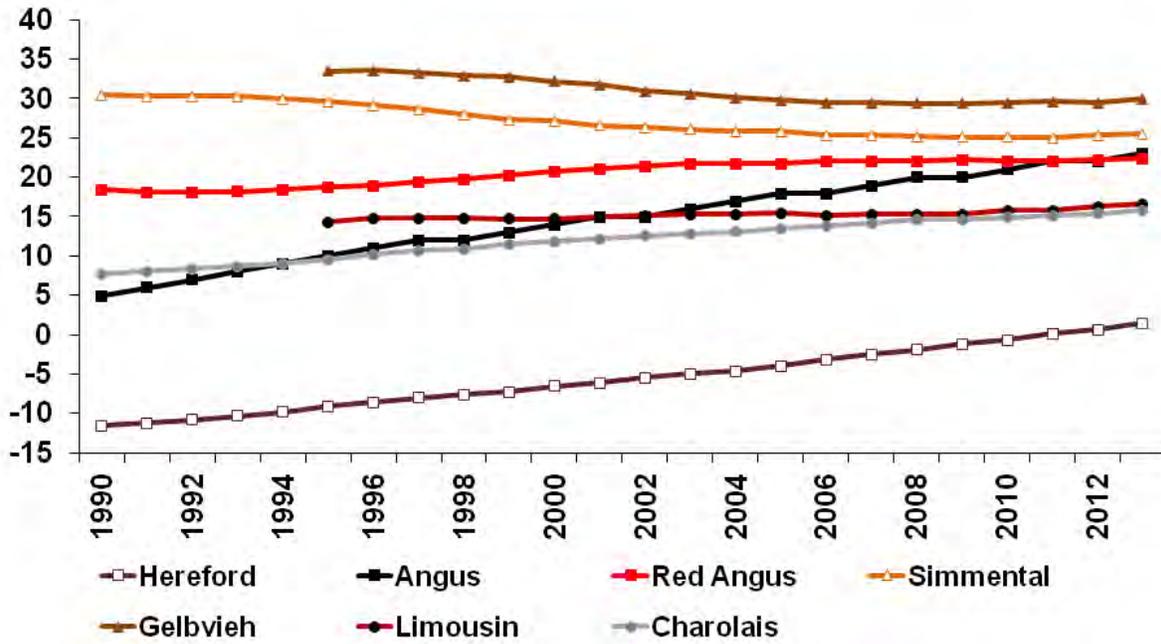
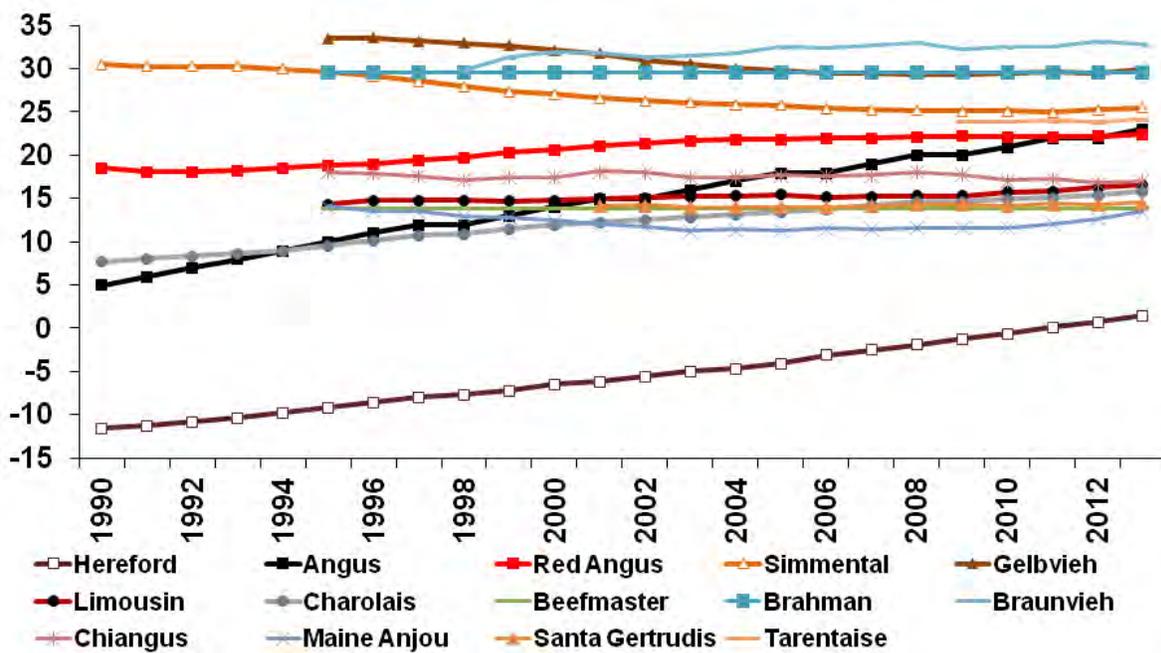


Figure 4. Relative genetic trends for maternal milk (lb) of the seven most highly used beef breeds (4a) and all breeds that submitted 2015 trends (4b) adjusted for birth year 2013 using the 2015 across-breed EPD adjustment factors.

4a.



4b.



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2015 COMMERCIAL PRODUCER AWARD NOMINEES

Goose Creek Valley Farms
(a division of Daltons on the Sycamore)
Owners: Douglas and Beverley Dalton
Manager: Jess Herbers
Lynchburg, Virginia



Goose Creek Valley Farms, located in central Virginia, is a progressive and diversified commercial cattle operation. In 2004, the Doug Dalton family made a significant acquisition of land along with that entity's 40 head of commercial cows. This acquisition led to the commercial operation known today as Goose Creek. From 1850 to the 1970s, Dalton farmland produced tobacco. In 1977, Aubrey Dalton and his son, Doug, purchased 25 commercial pairs. Over the next several decades the farm evolved into the progressive Angus seedstock operation known as "Daltons on the Sycamore." Today the sixth generation of Daltons manages registered and commercial cows on 3,200 acres. The family's 520 commercial cows compliment the 200-head seedstock operation plus 200-400 stockers yearly. Sons-in-law Jess Herbers (married to Wynn) and Tad Melton, (married to Whitney) offer a wide breadth and depth of experience, providing valuable advice and oversight, making essential contributions to this program. Jess manages Goose Creek and utilizes Hereford and Angus genetics to meet his production goals. Calving in the spring and fall, ownership of commercial calves is retained through harvest. The calves are weaned and backgrounded, then shipped to western Kansas to be fed and sold on the U.S. Premium Beef grid. Jess focuses on carcass merit while balancing all the production traits. This cattle operation maintains diversity operating in each of the beef industry's production segments utilizing DNA technology, embryo transfer, in vitro fertilization (IVF), fetal sexing and carcass analysis. The American Hereford Association is proud to nominate Goose Creek Valley Farms.

Winslow Farms
Owners: Ricky and Karen Tucker
Manager: Ricky Tucker
Autaugaville, Alabama



Winslow Farms, owned and operated by Ricky and Karen Tucker, is located in southwest Autauga County, Alabama. Having begun in the 1950s, Winslow Farms is a third generation commercial cow/calf operation with 150 breeding females at present. The original cow herd consisted of Angus and Hereford crosses; however, Winslow Farms presently operates with a cow herd base of Angus and Simmental genetics. Hybrid Simmental Angus herd sires are used to maintain heterosis and provide both growth and maternal performance. Performance records for all cows, sires and calves are maintained through the Alabama BCIA commercial record keeping program. Whole herd record keeping has been maintained through Alabama BCIA since 1986. However, farm performance records have been collected and maintained since the early 1980s. Performance data such as adjusted 205 day weights and ratios and cow MPPA are used to evaluate individual calf, sire, and cow performance. Winslow Farms has been annually honored with numerous BCIA Gold Star Cow Awards for over 10 years. A 90 day fall calving season, beginning in October, is planned to allow for marketing of preconditioned feeder calves in early August. The majority of calves are born within the first 30 days of the calving season. Preconditioned feeder calves are marketed in early August through the Producers Feeder Calf Sale, a cooperative tele-auction. Goals of Winslow Farms are to continue to increase weaning weights through genetic selection, while striving to decrease input costs and increase pasture productivity. Winslow Farms is proudly nominated by the Alabama Beef Cattle Improvement Association.

2015 COMMERCIAL PRODUCER AWARD NOMINEES

Woodbury Farms

Owner: Fred H. Woodbury Family

Managers: Howard Woodbury and John Woodbury

Quenemo, Kansas



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, KS. 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 cowherd 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, KS. 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.

The Kansas Livestock Association is proud to nominate Woodbury Farms.

Woodward Hi-Altitude Cattle

Owners: John and Beth Woodward

Manager: John Woodward

Bailey, Colorado

The ranch is located in the NE corner of Park County at an elevation of 8500 feet. John took over the family ranch in 1980 after graduating from Colorado State University. He graduated with a BS degree in Animal Science. Currently, the ranch runs cattle and puts up hay on approximately 4400 acres. Most of that acreage is grazing land, and irrigated hay ground is about 100 acres. Currently, they run 80 mother cows and feed out approximately 20 steers each year for private treaty sales. Thirty-five years ago, their base herd was Hereford, and was bred to Angus bulls. Today all of the cows are Angus cross, with about 30% of them being black baldies. A unique aspect of the operation is how they have gone about reducing the occurrence of high altitude disease, also known as brisket disease. They started PAP testing their bulls 20 years ago, and then later realized they also needed to start PAP testing all of their replacement heifers. Today, every breeding animal on the ranch has been PAP tested by Dr. Tim Holt. Running cattle at over 8500 feet year-round is an extraordinary challenge. Woodward Hi-Altitude Cattle is proudly nominated by the Colorado Cattlemen's Association and Colorado State University.





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BIF COMMERCIAL PRODUCER OF THE YEAR

Name	State	Year
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

2015 SEEDSTOCK PRODUCER AWARD NOMINEES

CK Cattle

Owners: Chuck and Katie Madaris

**Managers: Chuck & Katie Madaris, Charlie & Carrie Madaris,
Bradfield & Kathleen Evans**

Hope Hull, Alabama



CK Cattle is a multi-generational, family owned Chiangus, Angus, and SimAngus seedstock and commercial cattle operation located near Hope Hull, Alabama. The CK Cattle family involves Chuck and Katie Madaris, Charlie and Carrie Madaris, Bradfield and Kathleen Evans, and their children Ellis Ann and Shep. CK Cattle began in 1979, with the purchase of 4 Angus pairs. Today, CK Cattle consists of 650 breeding females. The American Simmental Association's Multi Breed Evaluation and Total Herd Enrollment program and the American Angus Association's AHIR program are all used for performance evaluation. All performance and carcass ultrasound measurements, as well as, DNA data are collected. Artificial insemination is a key genetic tool within the breeding program. Proven AI sires and CK herd sires are used for predictability and environmental adaptability. Alabama BCIA has had a significant influence in the development of the CK bull market. The goal to market 2 year old bulls has been successful, providing customers with older bulls ready for large cow herds. Currently, 140 bulls are marketed in the Alabama BCIA Fall Round Up Bull Sale, the It's All Black and White Bull Sale, and also by private treaty. Plans are being made for the first annual bull sale to be held this fall. CK Cattle also annually markets 100 bred heifers and 50 cows, plus three loads of feeder calves. With 3 family generations, CK Cattle is just beginning to reach its' potential of enhancing genetics of the beef cattle industry in the region. CK Cattle strives to market high value cattle and operate very efficiently to ensure continued profitability into the future. CK Cattle is proudly nominated by the Alabama Beef Cattle Improvement Association.

Diamond Peak Cattle Company (DPCC)

**Owners/Managers: John, George & Angelo Raftopoulos
Craig, Colorado**



Diamond Peak Cattle Company is one of the largest ranching operations in Colorado. The original outfit was established as a sheep operation in the 1920's and was expanded to include a cattle operation after John graduated from the Colorado State University College of Veterinary Medicine in 1978. John Raftopoulos is an innovator, risk taker, entrepreneur, cowman, and a steward of the land, but the description he most closely associates with, the one he is most proud of, is father and husband. It is his family that he cherishes the most and they are his most valuable asset. John and his two sons, George and Angelo, own and operate Diamond Peak Cattle Company; an operation that encompasses some 50,000 acres of deeded land and another 250,000 to 300,000 acres of BLM and state and private leases, making the ranch one of the larger holders of grazing rights on public lands. They run 2800 head of spring-calving, Angus and Angus cross cows. The cattle operation is located in the high desert, sage brush environment west of Craig, Colorado in the northwest corner of Moffat County; and extends into southern Wyoming and northeastern Utah. The breeding program is unique in that only a few (high-accuracy, moderate-framed, deep-bodied, big-spread, easy-calving) AI sires that are positive for carcass traits are selected. Milk, fertility, disposition, and the ability to travel are all critically important. Consistency and uniformity is the main goal through the production of large numbers of 31/32 and 63/64 brothers and sisters for commercial producers. Diamond Peak Cattle Co. is building a niche market for bulls suited for high altitude. PAP tested bulls are offered in the spring at their annual sales in Loma, Colorado and Riverton, Wyoming. Bulls are also offered by private treaty. Today, their registered cow herd stands at 1050 head. The Colorado Cattlemen's Association and Colorado State University are proud to nominate Diamond Peak Cattle Company.

2015 SEEDSTOCK PRODUCER AWARD NOMINEES

Journagan Ranch/Missouri State University

Owner: Missouri State University

Manager: Marty Lueck

Mountain Grove, Missouri



With the focus and commitment to provide the best Hereford genetics it can produce, Journagan Ranch has grown to be the largest Hereford seedstock producer in Missouri and the 15th largest in the U.S. Located in the beautiful Ozarks of south central Missouri, the Journagan Ranch in its 40th year of seedstock production is home to more than 400 Hereford females. Leo Journagan purchased his first Hereford heifers while serving in World War II. After the war, he rented property until the mid-60s when he bought his first piece of land. Continuing to add ground to that original parcel, the ranch has grown to 3,800-plus acres. In 1975 Leo purchased his first registered polled Herefords and Marty Lueck joined Journagan Ranch as manager in 1981. To complement the seedstock herd, the ranch also maintains 160 commercial females, which has remained a closed herd for 32 years. A majority of the registered herd and all the commercial cows calve in the spring. Since 1985, LJR genetics have been marketed in a production sale the first Saturday of October. Also 50-60 yearling bulls are sold private treaty off the farm. Today, Journagan Ranch also serves as an outdoor classroom and demonstration farm for Missouri State University (MSU) students. In 2010, Leo and his family gifted the ranch and cattle to MSU to preserve the program and continue Leo's legacy. Recently a ranch-to-plate beef program has been initiated with the beef marketed in local stores in Springfield, Mo. Journagan Ranch/Missouri State University is proudly nominated by the American Hereford Association.

McCurry Angus Ranch

Owners: Andy & Mary McCurry

John & Melody McCurry

Manager: John McCurry

Burton, Kansas



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.

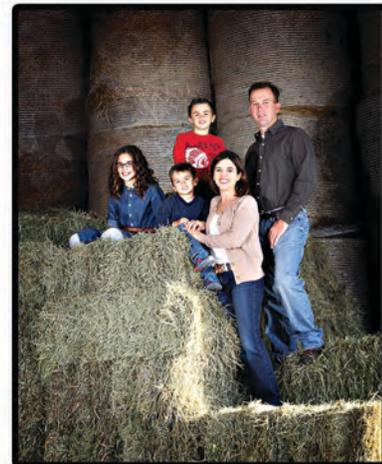
McCurry Angus Ranch is proudly nominated by the Kansas Livestock Association.

2015 SEEDSTOCK PRODUCER AWARD NOMINEES

Prairie View Farms

**Owners/Managers: Alan and Theresa Miller and Family
Gridley, Illinois**

Prairie View Farms is located in the heart of central Illinois corn country near Gridley and owned by Alan and Theresa Miller. The commitment to raising Angus cattle has ebbed and flowed for more than three generations of Alan's family. His grandfather, Adam Schlipf, started the herd in the 1940s and was active in the purebred cattle business through the 1960s, until the focus became centered on the crop side of the farm. The cow herd was revitalized in the 1990s as a 4-H project for Alan and his siblings, and has grown from 25 cows to 175 head today. A desire to return to the production agriculture lifestyle after a 15-year career in academia led Alan to diversify his family's operation and start raising Angus cattle full-time. He turned corn fields into lush green pastures, remodeled the weathered barn into a polished show cattle facility and built a working barn equipped with a lab to handle the latest reproductive technologies, and set out to make Prairie View Farms one of the nation's leading Angus seedstock operations. Each year, Prairie View Farms markets around 200 animals with more than one-third being show heifers at a spring production sale held on the farm, an online sale hosted in December, private treaty sales, and through state consignment sales. The operation markets bulls in a partnership with a ranch in Kansas and owns 10 bulls leased by AI studs. Alan's lifelong ambition has been to build a cow herd that makes a difference in the industry and he is a great example of someone who grew his love of showing cattle into a profitable business with little to no startup or family background. Alan has worked hard to find a niche in the beef business that would pay off for his family's livelihood and for the dozens of high-quality Angus female buyers Prairie View Farms attracts every year. The University of Illinois Extension is proud to nominate Prairie View Farms.



BIF SEEDSTOCK PRODUCER OF THE YEAR

Name	State	Year
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 Borrer	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



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BIF AMBASSADOR AWARD RECIPIENTS

Name	Publication	State	Year
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



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BIF PIONEER AWARD

2014	Merlyn Nielsen, NE Gary Bennett, NE Steve Radakovich, IA	2000	Harlan Ritchie, MI Robert R. Schalles, KS	1985	Mel Kirkiede ND
2013	Keith Bertrand, GA Ignacy Misztal, GA Glenn Selk, OK	1999	Joseph Graham, VA John Pollak, NY Richard Quaas, NY	1984	Bill Graham GA Max Hammond FL Thomas J. Marlowe VA
2012	Sally Buxkemper, TX Donald Franke, LA Leo McDonnell, MT	1998	John Crouch, MO Bob Dickinson, KS Douglas MacKenzie Fraser, CAN	1983	Jim Elings, CA W. Dean Frischknecht OR Ben Kettle, CO
2011	Mike Tess, MT Mike MacNeil, MT Jerry Lipsey, MT	1997	Larry V. Cundiff, NE Henry Gardiner, KS Jim Leachman, MT	1983	Jim Sanders NV Carroll O. Schoonover, WY
2010	Richard McClung, VA John & Bettie Rotert, MO Daryl Strohhahn, LA Glen Klippenstein, MO	1996	A.L. "Ike" Eller, VA Glynn Debter, AL	1982	Gordon Dickerson NE Mr. & Mrs. Percy Powers, TX
2009	Bruce Golden, CA Bruce Orvis, CA Roy McPhee (<i>posthumously</i>), CA	1995	James S. Brinks, CO Robert E. Taylor, CO	1981	F.R. "Ferry" Carpenter, CO Otha Grimes, OK Milton England, TX L.A. Maddox, Jr., TX Charles Pratt, OK Clyde Reed, OK
2008	Donald Vaniman, MT Louis Latimer, CAN Harry Haney, CAN Bob Church, CAN	1994	Tom Chrystal, IA Robert C. DeBaca, IA Roy A. Wallace, OH	1980	Richard T. "Scotty" Clark, CO Bryon L. Southwell, GA
2007	Rob Brown, TX David & Emma Danciger, CO Jim Gosey, NE	1993	James D. Bennett, VA M.K. "Curly" Cook, GA O'Dell G. Daniel, GA Hayes Gregory, NC Dixon Hubbard, VA James W. "Pete" Patterson, ND Richard Willham, IA	1979	Robert Koch, NE Mr. & Mrs. Carl Roubicek, AZ Joseph J. Urick, MT
2006	John Brethour, KS Harlan & Dorotheann Rogers, MS Dave Pingrey, MS	1992	Frank Baker, AR Ron Baker, OR Bill Borrer, CA Walter Rowden, AR	1978	James B. Lingle, MD R. Henry Mathiessen, VA Bob Priode VA
2005	Jack and Gini Chase, WY Jack Cooper, MT Dale Davis, MT Les Holden, MT Don Kress, MT	1991	Bill Long, TX Bill Turner, TX	1977	Ralph Bogart, OR Henry Holsman, SD Marvin Koger, FL John Lasley, MO W. L. McCormick, GA Paul Orcutt, MT J.P. Smith, MO H.H. Stonaker, CO
2004	Frank Felton, MO Tom Jenkins, NE Joe Minyard, SD	1990	Donn & Sylvia Mitchell, CAN Hoon Song, CAN Jim Wilton, CAN	1976	Forrest Bassford CO Doyle Chambers LA Mrs. Waldo Emerson Forbes, WY C. Curtis Mast, VA
2003	George Chiga, OK Burke Healey, OK Keith Zoellner, KS	1989	Roy Beeby, OK Will Butts, TN John W. Massey, MO	1975	Glenn Butts, MO Keith Gregory, NE Braford Knapp, Jr. MT
2002	H.H. "Hop" Dickenson, KS Martin & Mary Jorgensen, SD L. Dale Van Vleck, NE	1988	Christian A. Dinkle, SD George F. & Mattie Ellis, NM A.F. "Frankie" Flint, NM	1974	Reuben Albaugh, CA Charles E. Bell, Jr. VA John H. Knox, NM Paul Pattengale, CO Fred Wilson, MT Ray Woodward, MT
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47TH BEEF IMPROVEMENT FEDERATION ANNUAL MEETING AND RESEARCH SYMPOSIUM

BIF CONTINUING SERVICE AWARD

Name	Affiliation / State	Year	Name	State	Year
Larry Kuehn	US MARC	2014	Burke Healey	Oklahoma	1998
Wade Shafer	American Simmental Assn.	2014	Glenn Brinkman	Texas	1997
Warren Snelling	US MARC	2014	Russell Danielson	North Dakota	1997
Susan Willmon	American Gelbvieh Assn.	2014	Gene Rouse	Iowa	1997
Ben Eggers	Sydenstricker Genetics	2013	Doug L. Hixon	Wyoming	1996
Brian House	Select Sires	2013	Harlan D. Ritchie	Michigan	1996
Lauren Hyde	American Simmental Assn.	2013	Paul Bennett	Virginia	1995
Jerry Taylor	University of Missouri	2013	Pat Goggins	Montana	1995
Jack Ward	American Hereford Assn.	2013	Brian Pogue	Canada	1995
Tom Field	Nebraska	2012	Bruce E. Cunningham	Montana	1994
Stephen Hammack	Texas	2012	Loren Jackson	Texas	1994
Brian McCulloh	Wisconsin	2012	Marvin D. Nichols	Iowa	1994
Larry Olson	South Carolina	2012	Steve Radakovich	Iowa	1994
Tommy Brown	Alabama	2011	Doyle Wilson	Iowa	1994
Mark Enns	Colorado	2011	Robert McGuire	Alabama	1993
Joe Paschal	Texas	2011	Charles McPeake	Georgia	1993
Marty Ropp	Montana	2011	Henry W. Webster	South Carolina	1993
Bob Weaber	Missouri	2011	Jack Chase	Wyoming	1992
Bill Bowman	Missouri	2010	Leonard Wulf	Minnesota	1992
Twig Marston	Nebraska	2010	John Crouch	Missouri	1991
David Patterson	Missouri	2010	Robert Dickinson	Kansas	1990
Mike Tess	Montana	2010	Roger McCraw	North Carolina	1989
Darrh Bullock	Kentucky	2009	Bruce Howard	Canada	1988
Dave Daley	California	2009	Bill Borrer	California	1987
Renee Lloyd	Iowa	2009	Jim Gibb	Missouri	1987
Mark Thallman	Nebraska	2009	Daryl Strohbehn	Iowa	1987
Doug Fee	Canada	2008	Larry Benyshek	Georgia	1986
Dale Kelly	Canada	2008	Ken W. Ellis	California	1986
Duncan Porteous	Canada	2008	Earl Peterson	Montana	1986
Craig Huffhines	Missouri	2007	Jim Glenn	IBIA	1985
Sally Northcutt	Missouri	2007	Dick Spader	Missouri	1985
Jimmy Holliman	Alabama	2006	Roy Wallace	Ohio	1985
Lisa Kriese-Anderson	Alabama	2006	James Bennett	Virginia	1984
Dave Notter	Ohio	2006	M.K. Cook	Georgia	1984
Jerry Lipsey	Montana	2005	Craig Ludwig	Missouri	1984
Micheal MacNeil	Montana	2005	Art Linton	Montana	1983
Terry O'Neill	Montana	2005	J.D. Mankin	Idaho	1982
Robert Williams	Missouri	2005	Mark Keffeler	South Dakota	1981
Chris Christensen	South Dakota	2004	Glenn Butts	PRI	1980
Robert "Bob" Hough	Texas	2004	Jim Gosey	Nebraska	1980
Steven M. Kappes	Nebraska	2004	C.K. Allen	Missouri	1979
Richard McClung	Virginia	2004	William Durfey	NAAB	1979
Sherry Doubet	Colorado	2003	James S. Brinks	Colorado	1978
Ronnie Green	Virginia	2003	Martin Jorgensen	South Dakota	1978
Connee Quinn	Nebraska	2003	Paul D. Miller	Wisconsin	1978
Ronnie Silcox	Georgia	2003	Lloyd Schmitt	Montana	1977
S.R. Evans	Mississippi	2002	Don Vaniman	Montana	1977
Galen Fink	Kansas	2002	A.L. Eller, Jr.	Virginia	1976
Bill Hohenboken	Virginia	2002	Ray Meyer	South Dakota	1976
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Kent Andersen	Colorado	2001	Dixon D. Hubbard	Washington, DC	1975
Don Boggs	South Dakota	2001	J. David Nichols	Iowa	1975
Ron Bolze	Kansas	2000	Frank H. Baker	Oklahoma	1974
Jed Dillard	Florida	2000	D.D. Bennett	Oregon	1974
Bruce Golden	Colorado	1999	Richard Willham	Iowa	1974
John Hough	Georgia	1999	F. R. Carpenter	Colorado	1973
Gary Johnson	Kansas	1999	Robert DeBaca	Iowa	1973
Norman Vincil	Virginia	1999	E.J. Warwick	Washington, DC	1973
Keith Bertrand	Georgia	1998	Clarence Burch	Oklahoma	1972
Richard Gilbert	Texas	1998			

FRANK H. BAKER MEMORIAL SCHOLARSHIP

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 2½ 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.

2015 RECIPEINTS

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The effect of discovery bias on genomic selection and why it can no longer be ignored

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Introduction

In the past, traditional breeding methods have concentrated mainly on genetic improvement by artificial selection and have contributed in large amount to the advancement of animal productivity over the past 50 years (Dekkers and Hospital, 2002). However, this traditional approach is based on the knowledge of genetic parameters such as heritabilities, genetic variances and correlations for an entire population, all of which can be estimated using statistical analysis of pedigree data (Dekkers and Hospital, 2002), but does not take advantage of an animal's genomic information.

Recent advancements in the field of molecular genetics have led to the identification of multiple genes and markers associated with economically relevant traits in livestock species (Dekkers, 2004). This discovery provides opportunities to further enhance response to selection, particularly in traits that are difficult to measure, have low heritabilities, are measured late in life, or are sex-limited (Dekkers, 2004; Garrick, 2009). The idea of genomic selection was first introduced by Meuwissen et al. (2001), who used dense marker maps to estimate the effects of ~50,000 haplotypes simultaneously using a limited number of phenotypic records. Meuwissen et al. (2001) suggested that by using a large number of markers, it becomes possible to estimate breeding values without having knowledge of their location on the genome. This is because dense marker maps are believed to have genetic markers covering the entire genome, and therefore all quantitative trait loci (QTL) are thought to be in linkage disequilibrium (LD) with at least one marker (Goddard and Hayes, 2007).

There are numerous advantages to utilizing an animal's genomic data to enhance selection decisions. Overall, genomic selection has given animal breeders the ability to enhance genetic improvement programs in livestock populations by direct selection on genes and genomic regions (Dekkers and Hospital, 2002). Perhaps the biggest advantage of genomic selection is the obvious possibility to increase the rate of genetic gain within a population.

Because genomic data, unlike phenotypes, can be collected early in an animal's life (Eggen, 2012), selection decisions can be made sooner. It then follows that bulls who can be bred at one year of age largely reduce generation intervals within a herd (Eggen, 2012; Goddard and Hayes, 2007; Schaeffer, 2006) causing an increase in selection intensity (Eggen, 2012). This is essential to the rate of genetic gain in the population.

Genomic selection can also reduce the cost of bull testing in cattle. The purpose of progeny testing a bull is to quantitatively measure how his offspring will perform to estimate his breeding value. In the context of carcass traits in beef cattle, progeny performance data is the only way to estimate a bull's performance. Utilization of genomic data will provide breeders with estimated values sooner as well as possibly reduce the cost.

Finally, the use of genomic selection is not sex limited (Eggen, 2012). It becomes possible to shift the emphasis of selection to the dam side of the pedigree (Schaeffer, 2006). New technologies such as flushing and embryo transfer allow animal breeders to take advantage and propagate the genetics of superior dams for an even further increase in genetic gain.

Although genomic selection seems very promising, the accuracy of the calculated molecular breeding values (MBV) will be the deciding factor in their successful implementation. The higher the accuracy of the MBV, the more successful the breeding program and the faster the rate of genetic change within a population.

The most important aspect of any experiment or trial is the ability to replicate the results. One of the main issues occurring in genomic studies is the inability to observe the same outcomes between populations (Goddard et al., 2009; Xaio and Boehnke, 2009; Xu et al., 2011). Calus (2010) suggests that the accuracy of the estimated marker effects depends heavily on the characteristics and size of the training population, how those animals are sampled, and the heritability of the trait being selected.

In genome wide association studies (GWAS), the goal is to test SNP for associations with a trait or phenotype (Goddard et al., 2009). However, the common occurrence seems to be the overestimation of the SNP effects, which tend to be larger in magnitude than the true effects (Goddard et al., 2009; Xiao and Boehnke, 2009). This causes the accuracy of MBV to be overestimated as well. This overestimation, or upward bias, causes any follow up study to fail (Xiao and Boehnke, 2009). It is believed that this type of discovery bias occurs because the

predictions are applied to the same animals, or data, from which model selection and parameter estimation were calculated (Xu et al., 2011).

This consistent over estimation of marker effects has been termed the “winner’s curse” or “Beavis effect” in most of today’s literature (Goddard et al., 2009; Xiao and Boehnke, 2009; Xu et al., 2011), but was perhaps first introduced by Göring et al. (2001). They believed that a sampling bias in reported test statistics of an analysis caused a sampling bias in the reported parameter estimates. This was based on the observation that follow-up studies give lower estimates of effect size. Because all tests of linkage or association are conceptualized mathematically, the estimation of any relationship between marker genotypes and trait phenotypes are subject to genome wide sampling bias.

The best explanation of the winner’s curse is perhaps given by Bazerman and Samuelson (1983), who explain the occurrence in terms of an auction. For example, if an item is up for auction, participants who have no concept of the item’s actual value place unbiased bids. However, these are imprecise estimates of the item’s true value causing the final selling price to be higher than its actual value. This upward bias occurs because the winning bid is contingent on being the highest of the unbiased bids. This carries over into GWAS because an initial positive finding is based on a SNP having a higher effect than the rest, resulting in estimates of its effect size being upwardly biased (Xiao and Boehnke, 2009). But where exactly does this occur in beef cattle genomic selection? It is possible that the cause comes in part from the use of “training” and “validation” populations.

Literature Review

Genomic information was first introduced into the National Cattle Evaluation (NCE) by the American Angus Association (AAA) in 2009. Upon this initial incorporation, the identification of animals in training populations was unknown, causing the relationship between them and the target populations to be unknown (Spangler, 2013). It was discovered that the use of a known training population, in conjunction with a validation population was the most efficient way to calculate MBV. According to Garrick and Saatchi (2013), the development of MBV requires a group of historic animals that have both genomic data and information related to their true breeding values, known as a training population. Phenotypes and genotypes from the training population are used to develop MBV prediction equations using the individual SNP

additive effects of loci that show the strongest association with the trait of interest (Van Eenennaam et al., 2009). Using various statistical approaches to this procedure, an MBV is calculated for each animal within the population. Once the MBV prediction equations are created, they are then the focus of a validation study (Van Eenennaam et al., 2009). Another group of representative animals are selected and genotyped and the resulting MBV are compared to their phenotypes to assess their accuracy (Goddard and Hayes, 2007). As expected, prediction equations perform “best” when used in discovery populations in which the SNP associations were discovered or where the SNP effects were estimated (Van Eenennaam et al., 2009). Because the SNP effects are optimized to fit the data in the training populations, their estimated accuracies are higher, but not necessarily representative of the actual accuracy.

Methods of molecular breeding value calculation

One of the first methods used to estimate an animal’s MBV is termed genomic best linear unbiased prediction (GBLUP) and is described by Meuwissen et al. (2001) at the same time genomic selection was introduced. This GBLUP follows the assumption that each locus explains variance equal to V_g/n where V_g is the total genetic variance and n is the number of loci (i.e. an equal amount of variance), making the process unweighted. The main difference between using GBLUP over pedigree BLUP is instead of a numerator relationship matrix (**A**), the relationship matrix becomes the genomic relationship matrix (or realized relationship matrix, **G**) derived from the markers (Meuwissen et al., 2011; Erbe et al., 2012). An alternative to this method is weighted GBLUP, where the markers are weighted by their effects (Zhou et al., 2014).

A second method of calculating MBV is the use of Markov Chain Monte Carlo (MCMC) algorithms to implement Bayesian models. Unlike GBLUP, in Bayesian models the variance explained by the i th locus, V_{gi} , is assumed to be drawn from a prior distribution, meaning the variance can differ across loci (Meuwissen et al., 2001). This idea is more realistic than BLUP, which assumes the variance is fixed. Bayesian models include BayesA, BayesB, BayesC, BayesC π , BayesR, and BayesRC. While all of these Bayesian models are slight variations of each other, their most important aspect is that they assume the variance accounted for by each locus is different.

The final method of calculating MBV is the use of heterogeneous variance with restricted maximum likelihood. This requires the use of Expectation-Maximization (EM) algorithms instead of MCMC estimation, which are common in Bayesian Regression techniques, to speed

up computation time (Sun et al., 2012). Sun et al. (2012) termed this EM algorithm “fastBayesA”, as it follows a BayesA method but uses EM algorithms in place of MCMC. The fastBayesA approach predicts random SNP effects and estimates SNP variances by restricted maximum likelihood (REML), whereas BayesA bases predictions on posterior means of effects. In each EM iteration, BLUP estimates of SNP effects are predicted from a mixed linear model that incorporates a weighted marker-based realized relationship matrix.

Once MBV have been calculated they must be combined with EBV to produce a genome enhanced estimated breeding value (GE-EBV). The MBV do not include any information from phenotypes collected, and the inclusion of the EBV will help to increase the accuracy of the GE-EBV (Garrick and Saatchi, 2013). There are various ways in which this is done, including blending, the correlated trait method, one-step GBLUP, one-step random regression, and treating the MBV as an external EPD with corresponding accuracy.

Using the blending method, the American Hereford Association (AHA) released their first GE-EBV in the fall of 2012 (Ward, 2013). This method only impacts the genotyped animals because it is done post genetic evaluation (Spangler, 2013). Using selection index principles, the variance-covariance structure among the selection criteria, P , and the covariance between the same criteria and objective, g , are blended with the MBV (Garrick and Saatchi, 2013). Straightforward matrix calculation can be used to determine the weighting factors, b , once P and g are defined by solving $Pb = g$. The GE-EBV, along with a relationship matrix, can be used to derive a pedigree-imputed direct genomic value (DGV) for relatives of genotyped animals. This DGV is then blended with EPD to produce separate GE-EBV.

The American Angus Association (AAA) utilizes the correlated trait method to incorporate calculated MBV into EBV (Northcutt, 2013). This method was proposed by Kachman (2008) and used by MacNeil et al. (2010). It assumes that the calculated MBV could be fitted as a correlated indicator trait in already existing multiple-trait models and also allows for genomic information to influence the predictions of animals in a pedigree without genotypes (Spangler, 2013). Because marker scores are based on marker genotypes, their residual variances are expected to be small relative to their genetic variance (Kachman, 2008).

Another variation of incorporating MBV into NCE is considering the MBV as an external source of information following the approach of Quaas and Zhang (2006). The benefit of this concept is that it allows for varying accuracy of MBV, unlike blending and the correlated trait

method (Spangler, 2013). This follows the idea that MBV do not predict the genetic merit of every animal within a population with the same degree of accuracy, mainly due to their relationship with the training population.

A single step implementation of GBLUP (SS-BLUP) has been proposed based on linear mixed models and pedigree relationship matrices combined with genomic information (Vitezica et al., 2011). The SS-BLUP method modifies the numerator relationship matrix \mathbf{A} to $\mathbf{H} = \mathbf{A} + \mathbf{A}_\Delta$, where \mathbf{A}_Δ includes deviations from expected relationships (Miszta et al., 2009). Creation of \mathbf{H} can be interpreted as a projection of marker phenotypes from genotyped to non-genotyped animals using their pedigree relationships (Vitezica et al., 2011). However, using MME, it is necessary to calculate \mathbf{H}^{-1} which may prove to be more difficult for larger pedigrees (Miztal et al., 2009).

In similar fashion to SS-BLUP, single-step Bayesian Regression (SSBR) combines phenotype, genotype and pedigree information (Fernando et al., 2014). Unlike SS-BLUP, where the \mathbf{H} matrix is difficult to invert in large data sets, SSBR does not require computing \mathbf{H} or its inverse. Single-step Bayesian Regression is also not limited to normally distributed marker effects and can be implemented using the BayesB or BayesC π models.

How to calculate accuracy

The reliability of an MBV can be defined as the squared correlation between an animal's true breeding value and their calculated MBV (Kachman, 2013). The reliability is then a function of the variance of the true breeding value, the variance of the MBV, and the covariance between them. The reliability of an MBV is important because it impacts both an animal's EBV and the GE-EBV; the greater the reliability of an MBV, the greater the weight and the greater the resulting increase in reliability of the GE-EBV. Habier et al. (2010) discovered that the reliability of an MBV suffers as the genetic relationship between the training population and the animals under evaluation decreases.

There has been a progression of methods used to evaluate genomic tests. Van Eenennaam et al. (2007) described application of the "validation" concept based on independent confirmation of associations to various genomic tests. However, Thallman et al. (2009) shifted the emphasis to quantifying "how well" a genomic test works through estimation of the (co)variances used to incorporate MBV into NCE. Thallman et al. (2009) showed that the proportion of additive genetic variation accounted for by a genetic test is the square of the REML

estimate of the genetic correlation in a two-trait animal model including the target trait and the MBV as the second trait. It was suggested by Kachman (2008) that the proportion of additive genetic variation due to MBV is directly related to the (co)variances required for incorporation of MBV into NCE.

Accuracy Results

Habier et al. (2007) discovered that the presence of genetic relationships captured by markers have an effect on the accuracy of MBV calculations, causing the MBV of individuals with progeny in the training population to have higher accuracy. Genomic relationships cause the accuracy of prediction of MBV both across and within different families or lines to be different. Habier et al. (2010) showed that the accuracy of MBV is not constant, but can vary depending on the number of relatives in training and the degree of additive-genetic relationships. Overall, discovery bias caused by related animals may explain the variation in accuracies being observed.

There are many published studies documenting the increase in accuracy when using a weighted GBLUP compared to unweighted (Snelling et al, 2011; Su et al., 2014; Tiezzi and Maltecca, 2014; Zhang et al., 2014). Snelling et al. (2011) brings up the point that although increased accuracy occurs within the population being studied, this accuracy may not carry over to predictions of unrelated animals. Banos and Coffey (2010) determined that LD patterns are not consistent between selected lines of the same breed, meaning the weights given to SNP of one population may not be optimal when attempting to predict in an unrelated population. The weighting of selected SNP for use in GBLUP leads to bias in the estimated accuracy. The animals more closely related to the training population are more likely to have the LD patterns used to weight the SNP. This may be the cause of the increased accuracy.

When genomic selection was first suggested by Meuwissen et al. (2001), BLUP, BayesA and BayesB were used to calculate MBV and their accuracies were compared. These methods were selected to compare the effects of variance component estimation. Both BayesA and BayesB calculate variance at each locus separately, whereas BLUP assumes that all variances are equal across the genome. The main difference between BayesA and BayesB is that BayesB assumes some loci have no genetic variance. Results showed that while BLUP had reasonable accuracy, BayesA resulted in ~9% more accuracy and BayesB resulted in ~16% more accuracy, suggesting that BayesB was the superior method. Another study by Meuwissen and Goddard (2010) supports this hypothesis, stating that BLUP estimation does not take full advantage of the

high-density marker data, giving BayesB the higher accuracy. Because BayesB gives separate variances to each locus, it (as well as Bayes A) is able to put more weight on causative SNP, resulting in a higher accuracy (Meuwissen et al., 2001; Meuwissen and Goddard, 2010).

Comparisons of GBLUP to Bayesian regression report similar results. The GBLUP method is preferred by some because of its simplicity and low computational requirements (Gao et al., 2013), but its estimates are not as accurate as Bayesian regression. Gao et al. (2013) found that a Bayesian mixture model, most similar to BayesB, increased the reliabilities of MBV by anywhere from 2 to 6.2 percentage points, depending on the training and validation populations used. The increase in accuracy between Bayesian models over GBLUP increased as the relationship between the training and validation populations decreased. Although GBLUP has been proven to exploit LD, additive-genetic relationships and cosegregation to capture relationships of QTL, it does not capture the short-range LD as well as Bayesian regression (Habier et al., 2011; Habier et al., 2013; Gao et al., 2013). However, unweighted GBLUP avoids marker selection and marker weighting, leading to less bias (an accuracy that is closer to the true accuracy). A study by Erbe et al. (2012) found that BayesR outperformed GBLUP as well, with an average increase in accuracy across three traits of 5%. Because of this, Bayesian methods are expected to perform better than GBLUP (Habier et al., 2011; Habier et al., 2013). What has yet to be determined, however, is whether this increase in accuracy is due to the statistical method, or the presence of discovery bias within the analysis.

In comparing SS-BLUP to GBLUP, Aguilar et al. (2010) found similar accuracies, but stated that advantages of SS-BLUP over GBLUP were its simplicity and automatic weights for the various sources of information used to calculate MBV. One of the largest disadvantages of GBLUP as well as SS-BLUP is the necessity to calculate the dense inverse of the \mathbf{G} matrix (Koivula et al., 2012). A study by Koivula et al. (2012) found that SS-BLUP had slightly higher accuracies of validation populations over that of GBLUP. However, SS-BLUP includes information of non-genotyped animals in the genomic predictions of related animals with genotypes.

Using SS-BLUP methodology, Fernando and Garrick (2013) proposed a single step Bayesian Regression procedure (SSBR). They believed that the limitations of SS-BLUP could be overcome using SSBR to accommodate those animals without genotypes. Because the computational burden of Bayesian regression methods increases linearly with the number of

genotyped animals, SSBR has a computational advantage over SS-BLUP. Another computational advantage of SSBR over SS-BLUP is that dense matrix inversion is not required; but this comes at the expense of having to use MCMC methods instead (Fernando et al., 2014). Furthermore, unlike SS-BLUP, SSBR marker effects do not have to be normally distributed (Fernando and Garrick, 2013; Fernando et al., 2014). The Bayesian regression allows use of t -distributed marker effects as in BayesA, as well as mixture models such as BayesB and BayesC π (Fernando et al., 2014). An innovative aspect of SSBR is that it uses a marker model for genotyped animals and an animal model for ungenotyped animals, drawing upon the advantages of each model for the animals to which it is applied.

A step in the right direction

Perhaps the first step in addressing discovery bias can be seen in the form of K-fold validation. K-means clustering is used to split the animals used in an analysis into equal groups while attempting to maximize relatedness within each group and minimize relatedness between groups (Saatchi et al., 2012). Once the groups are established, analyses exclude one group and train on the others to estimate marker effects which are in turn used to predict the MBV of animals in the excluded group (validation population) (Saatchi et al., 2011). This process is repeated until every animal has a predicted MBV obtained without using its own DEBV.

Using the predicted MBV a bivariate model is used with the DEBV as the second trait (Garrick and Saatchi, 2013). Fitting this model allows for the estimation of the genetic correlation between the trait and its respective MBV (Saatchi et al., 2012). The \mathbf{G} matrix consists of non-zero elements of \mathbf{A} among individuals in the same group, but sets the covariances between individuals in different groups as zero. This method leads to predictions of accuracy that are pooled predictions from each fold (Garrick and Saatchi, 2013). The resulting variance components should show an MBV heritability near one as proposed by Kachman (2008), a DEBV heritability near the trait heritability and the genetic correlation between the two whose square represents the average proportion of genetic variance accounted for by the MBV (Garrick and Saatchi, 2013). K-fold validation has been used to assess the accuracy of MBV for the Angus, Simmental and Limousin breeds (Saatchi et al., 2011; Saatchi et al., 2012).

Conclusion

Finding ways to reduce the effects of discovery bias on the accuracy of GE-EBV is critical to the advancement of genomic prediction. While current methods of prediction that include genomic information are superior to traditional breeding methods, consistent accuracies have not been found. Ways in which to close the gap between true and calculated accuracy have been discussed with emphasis being placed on training and validation populations and minimizing the amount of relatedness between the two. Most importantly, discovery bias and the “winner’s curse” are pivotal issues that must be addressed if true accuracy is to be calculated. This increase in true accuracy will help increase the accuracy of selection, decrease generation interval, and increase selection intensity (Miller, 2010), all of which are critical to increasing the rate of genetic gain. While this issue is important for all breeds who compute GE-EBV to consider, it is even more crucial for smaller breed associations, in which all animals must be used for both training and validation. The ideal solution is to statistically adjust predictions for discovery bias.

The relationship between discovery bias and accuracy can be confusing. The GBLUP method has appeal because it does not seem to be subject to discovery bias, but that appeal comes at the cost of giving up some accuracy. Methods that use the data to improve the model (e.g. select or weight markers) are subject to the winners curse. The consequences are 1) accuracy is improved and 2) accuracy is estimated to be improved by even more than it really is. The latter is discovery bias. The cost of discovery bias is that genomics gets more weight relative to pedigree and phenotypes than it truly deserves. Nonetheless, the improved accuracy of the genomic part of GE-EBV that comes from weighting markers optimally is probably better than unweighted GBLUP. But, accounting for the discovery bias and weighting optimal genomic predictions more appropriately with pedigree and phenotype should yield still better GE-EBV.

The ultimate goal of any genetic evaluation or selection decision is to positively impact a population of animals, beef cattle or otherwise. The bottom line is always the impact that it has on the industry as a whole. Genomics provides new insights into the growth, nutrition, and overall health of animals while enabling a better understanding of traits of interest (Eggen, 2012). It provides breeders, breeding organizations, and members of the livestock industry the opportunity to increase efficiency and productivity of animal breeding (Eggen, 2012). Since first suggested by Meuwissen et al. (2001), the idea that a large number of SNP can give a reasonable

amount of information about the genomic make up of an animal has led to substantial progress in genomic selection (Miller, 2010). This is true especially for traits that are difficult to measure, have low heritabilities, are measured late in life or are sex limited (Dekkers, 2004; Garrick, 2009). However, in order to further this advancement, discovery bias can no longer be ignored. It is critical that new statistical methods be derived to address the issue so that unbiased estimates of accuracy can be calculated. Should this be accomplished, a profound increase as well as possible consistency in MBV could be observed.

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Frank Baker Memorial Scholarship

**FACTORS AFFECTING THE FATTY ACID PROFILE OF BEEF: SUMMARY AND
PROSPECTS FOR COMPLEX TRAIT ANALYSIS**

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Introduction

Beef is a nutritious product that provides an excellent source of protein, vitamins, minerals, and lipids in the human diet. The lipid profile of beef contributes to the overall healthfulness and palatability of the final beef product, which indicates it is an economic trait of interest for consumers. Previous studies have characterized the lipid profile in various beef cattle tissues under different dietary conditions, in different breeds, and at various age points. This published collection of fatty acid phenotype data indicates that lipid storage in beef cattle is a dynamic process with individual lipids exhibiting a wide range of phenotypic and genetic variance estimates under different environmental conditions and across many breeds. This range in observed variance can be partially explained by genetic differences among animals for lipid synthesis, desaturation, and deposition, as well as by the environmental interaction of specific lipids and lipid classes in the biological environment of muscle and fat tissues.

The two major lipid depots in beef cattle tissue are represented by the triacylglycerol and phospholipid fractions of the total lipid isolated from both muscle and adipose tissue. The triacylglycerol lipid fraction captures the lipids stored as triglycerides in adipose cells. The phospholipid fraction captures lipids contained in the more diverse phospholipid cellular membrane of both myocytes and adipocytes. The triacylglycerol and phospholipid fractions exhibit the characteristics of quantitative traits. These traits are controlled by many individual genes with many correlated individual lipids composing larger lipid classes such as saturated (SFA), monounsaturated (MUFA), and polyunsaturated (PUFA) fatty acids. There is also a significant environmental component that influences the fatty acid profile. Currently, there is an effort to combine high throughput “omics” data with data from multiple complex phenotypes and systems biology methodology in order to identify the biological drivers behind complex traits of interest. Given these factors, the triacylglycerol and phospholipid fatty acid fractions present an excellent opportunity for an analysis of genetic parameters, the identification of candidate genes, and the application of modern systems biology to analyze overall lipid profile in beef cattle tissues.

The Fatty Acid Profile of Beef Tissues

A wide range of studies have characterized the total fatty acid profile of various beef cattle tissues (Wood et al., 2008; Daley et al., 2010; Hoehne et al., 2012; Pavan and Duckett,

2013; Duckett et al., 2014). The total fatty acid fraction represents the distribution of all lipids present in a biological sample including those derived from the lipid membranes of multiple cell types other than adipocytes. Depending on factors such as diet, age, and tissue, the total fatty acid profile of beef is generally composed of approximately 40-50% of SFA, 40-60% of MUFA, and 5-15% of PUFA (Wood et al., 2008). Two important factors affecting fatty acid profile are maturity of the animal and location of the tissue sampled. Muscle type and adipose location have a significant effect on the fatty acid profile (Pavan and Duckett, 2013; Liu et al., 2015b). Also, as an animal matures and a larger proportion of excess energy is used for fatty acid synthesis there tends to be an increase in the accumulation of SFA in relation to PUFA (Warren et al., 2008). This is likely due to a shift towards lipogenesis and a shift away from adipogenesis as an animal reaches maturity and subsequent the need for more adipocytes is reduced. During lipogenesis the primary fatty acids being produced are saturated in nature. The primary product from the major protein complex driving lipogenesis, which is fatty acid synthase (FASN), is C16:0, which explains this shift in the SFA:PUFA ratio. It is known that this shift occurs as fatty acids are stored as triglycerides in adipocytes, but it is not clear how this shift affects the phospholipid membrane in a maturing animal. This membrane is a dynamic lipid depot and seems to undergo changes in fluidity and composition as adipogenesis proceeds in a maturing tissue (Pietilainen et al., 2011). More research is needed to understand the differences between these two lipid depots and how they change under various conditions and maturity points.

A method developed by Hartman (1967) allowed the separation of polar and non-polar lipids prior to gas chromatography that yields the neutral lipid and phospholipid fatty acid fractions in separate components. The non-polar neutral lipid fraction contains the triacylglycerol, diacylglycerol, ester, and cholesterol components of the tissue. The polar fraction contains the phospholipid bilayer fatty acids which are composed of four major phospholipids in mammals: phosphatidylethanolamine, phosphatidylserine, phosphatidylcholine, and sphingomyelin (Alberts, 2002). Each of these four major phospholipids contain two nonpolar fatty acid chains which compose the individual fatty acids identified as being associated with the phospholipid fatty acid fraction through gas chromatography analysis. Separating the total fatty acid fraction allows for a more detailed analysis of the genes and biological pathways affecting adipogenesis and lipid synthesis when compared to the total fatty acid fraction. When the two fractions are combined it cannot be determined if the fatty acids in the analysis come from the

triacylglycerol or the phospholipid which likely have distinct biological origins and configurations in various cell types.

To date, there have been few studies that have presented a comprehensive separate analysis of the triacylglycerol and phospholipid fatty acid fractions in beef cattle species. Kazala et al. (1999) presented an analysis of the intramuscular fatty acid composition in crossbred Wagyu cattle in which the triacylglycerol fraction was separated from and compared to the total lipid fraction. In this study the triacylglycerol fraction was found to be very similar in composition to the total lipid with no significant difference detected in the MUFA/SFA ratio in *longissimus*. Dannenberger et al. (2007) presented a comprehensive analysis of the fatty acids distributed in multiple phospholipid classes in beef muscle including the phosphatidylethanolamines, phosphatidylcholines, phosphatidylinositols, cardiolipins, sphingomyolins, and lysophosphatidylethanolamines using high performance thin layer chromatography. Analysis of these individual phospholipid classes revealed that pasture feeding to finishing leads to a significant accumulation of omega-3 fatty acids in all classes when compared to finishing on a concentrate diet. The phospholipid membrane is a dynamic lipid depot and is known to undergo changes in fluidity and composition as adipogenesis proceeds in a maturing tissue (Pietilainen et al., 2011). Smith et al. (1998) presented a comprehensive analysis of distribution and saturation of triacylglycerol species in beef cattle in response to different dietary formulas. This study concluded that diet had significant effects on the distribution of saturation and the composition of triacylglycerol species. The previous studies added important data sets for fatty acid analysis, but a future research on the triacylglycerol and phospholipid fractions is needed.

Margetak et al. (2012) presented a complete comparison of the triacylglycerol and phospholipid fatty acid fractions from the *pars costalis* diaphragmatic muscle and subcutaneous fat in beef cattle undergoing different dietary supplementations containing sunflower and flax oils. This study found the triacylglycerol fraction of muscle tissue to contain significantly higher amounts of C14:0 and C16:0. The phospholipid fraction of muscle tissue contained higher amounts of C18:0, C16:1c9, and C18:1c9. The phospholipid fraction of subcutaneous fat was found to contain higher amounts of C14:0, C16:0, C18:0, C16:1c9, and C18:1c9. The study also concluded that oil supplementation increased the absolute amounts of elongated unsaturated fatty acids in both the triacylglycerol and phospholipid fractions. There were no other studies

identified that presented a direct comparison of the triacylglycerol and phospholipid fractions in beef. Future research is needed to determine the effects of breed, maturity, muscle type, and lipid depot on the triacylglycerol and phospholipid fatty acid profiles.

Genetic Parameter Estimates of Fatty Acid Traits

Genetic parameter estimates for individual lipids and lipid classes in beef cattle tissues are available for the total fatty acid fraction. However, there are currently no studies available analyzing genetic parameters in triacylglycerol and phospholipid fractions. Heritability estimates for individual lipids and lipid classes range from 0 to a moderate heritability of approximately 0.6. These heritability estimates indicate the certain lipids would respond well to selection programs. Ekine-Dzivenu et al. (2014) estimated genetic parameters for fatty acids traits in 223 Angus and Charolais crossbred commercial steers. In this study heritability estimates for individual lipids ranged from approximately 0 to 0.51. Heritability estimates for most fatty acids were low, with SFA, MUFA, and PUFA fatty acid classes having a heritabilities less than 0.15. The highest heritability estimates were found for C14:1 and C18:1 with estimates of 0.51 and 0.43, respectively. The relatively low population size likely led to an underestimation of heritability estimates for fatty acid traits in this study.

Inoue et al. (2011) also estimated heritabilities for fatty acid traits in a population of 863 Japanese Black steers. Heritability estimates in this study ranged from approximately 0 to 0.86. Traits with the highest heritability estimates included C14:1 and C14:0 with heritability estimates of 0.86 and 0.82, respectively. Total MUFA also exhibited a high heritability estimate of 0.66. The authors of this study note that the heritability estimates obtained seem high when compared to other breeds and other studies. The authors also note that this difference might be present due to differences in fatty acid synthesis and desaturation enzyme activity in Japanese Black cattle compared to other breeds. Nogi et al. (2011) presented the results of a similar study in a population of 2,275 Japanese Black cattle. Heritability estimates in this study were similar and ranged from approximately 0 to 0.78. The highest heritability estimates were obtained for C14:0 and C18:1 with heritabilities of 0.70 and 0.78, respectively. The lipid classes SFA, MUFA, and PUFA had heritability estimates of 0.66, 0.68, and 0.47, respectively. These studies represent the best examples currently present in the literature for fatty acid heritability estimates in a single

breed of cattle due to the large population size, complete reporting of individual lipid heritability estimates, and uniform genetic background of the animals the study.

Pitchford et al. (2002) obtained heritability estimates for fatty acid traits in a population of 1,215 animals with 7 distinct sire breeds. This study also used the percentage of the total lipid as the measurement. Heritability estimates in this population range from approximately 0 to a moderate heritability of 0.27. Fatty classes SFA and MUFA had heritabilities of 0.27 and 0.17, respectively. The fatty acid C16:0 had one of the highest heritability estimates of all individual lipids at 0.21. In contrast to the study by Inoue et al. (2011), this study found relatively lower heritability estimates across all individual lipids and lipid classes. It is possible that using cattle from a variety of genetic backgrounds as opposed to a single breed results in lower heritability estimates.

Ahlberg et al. (2014) obtained posterior mean genomic heritability estimates for various fatty acid classes as a proportion of phenotypic variation explained by a genomic marker panel in a population of 236 crossbred steers and heifers. Heritability estimates for fatty acid classes PUFA and MUFA were 0.7 and 0.4, respectively, when measured on a percentage of total lipid basis. Heritability estimates of PUFA and MUFA were 0.7 and 0.85, respectively, when measured on the basis of mg/100 g of wet tissue.

Heritability estimates for fatty acid traits appear to be variable across the studies estimating these parameters in beef cattle. Genetic background of the animals in the study as well as the measurement system used to determine the fatty acid measurement seem to be the two factors causing the most variation in heritability estimates. In general, studies using a single breed with the percentage of total lipid measurement system yield the highest estimates of heritability for fatty acid traits. The classes SFA and MUFA as well as the individual lipids making up those classes appear to have moderate to high heritabilities. The more unsaturated lipids composing the PUFA class appear to have low to moderate heritabilities. The data gathered in these studies indicates that overall the fatty acid profile has a moderate heritability and certain fatty acids would respond to a marker assisted selection program.

Genetic Correlations Involving Fatty Acid Traits

Genetic correlation estimates have also been well characterized among individual lipids, lipid classes, and carcass traits for the total fatty acid fraction. Fatty acid synthesis and

desaturation occurs through a pathway of related enzyme complexes to produce the many lipids and lipid classes found in mammalian tissues. The central driver of lipid synthesis in mammalian tissues is a large protein complex known as fatty acid synthase (FASN) (Alberts, 2002). The primary products of FASN synthesis are C14:0 and C16:0, which are derived by the addition of 2 carbon acetyl CoA to a growing carbon chain until the final product reaches either 14 or 16 carbons in length. Many other enzymes in addition to FASN work to lengthen individual lipids and add features such as desaturations and isomerizations after the final C14:0 or C16:0 are produced. These include the desaturase class of enzymes, such as steroyl CoA desaturase, and elongation enzymes. It is reasonable to conclude that certain fatty acids would exhibit moderate to high genetic correlations since genetic variation in these biological pathways and networks would affect all lipid products in the assembly line. It also follows that individual lipids and lipid classes should be genetically correlated to carcass traits since the fatty acid profile is known to vary at different levels of tissue maturity (Warren et al., 2008).

Both direction and strength of phenotypic and genetic correlations among fatty acids appear to be highly dependent upon the measurement system used (percent of total lipid vs. mg/100 g tissue). Using percent of total lipid calculation appears to give higher heritability estimates for the majority of lipids and lipid classes (Saatchi et al., 2013; Ahlberg et al., 2014). Phenotypic correlations between SFA and the unsaturated lipid classes MUFA and PUFA are generally negative. SFA is the primary product of *de novo* lipid synthesis, and the newly synthesized saturated fatty acids are then used as precursors for unsaturated fatty acid products derived from that synthesis. Maturity of the animal is also known to drive this association, as fatter animals typically have higher amounts of SFA compared to unsaturated fatty acids (Warren et al., 2008). Multiple studies have identified this phenotypic association (Pitchford et al., 2002; Inoue et al., 2011; Ekine-Dzivenu et al., 2014).

Genetic correlations among fatty acids tend to be less predictable across multiple studies, but the general trend of SFA exhibiting a negative genetic correlation with other fatty acids seems to be a common association. This is likely a reflection of the general pathway of lipid elongation and desaturation that occurs as lipid synthesis and incorporation into various depots proceeds in the adipocyte. Ekine-Dzivenu et al. (2014) found SFA have a negative genetic correlation with MUFA and PUFA, with genetic correlation estimates of -0.99 and -0.41, respectively. MUFA and PUFA were found to have a weak but positive genetic correlation of

0.2. Similarly, Pitchford et al. (2002) found a negative genetic correlation between SFA and other unsaturated fatty acids. The fatty acid C14:0 had negative genetic correlations of -0.61 and -0.27 with MUFA and UFA, respectively. Inoue et al. (2011) also observed the C14:0 to have a negative genetic correlation with MUFA and UFA of -0.74 and -0.81, respectively.

Other individual lipids also exhibit predictable genetic correlations. In general, individual SFA's of different lengths tend to be positively correlated (Inoue et al., 2011; Nogi et al., 2011). A strong negative genetic correlation is also consistently observed between C18:0 and C18:1 (Inoue et al., 2011; Nogi et al., 2011), which is likely a reflection of stearoyl Co-A desaturase (SCD) variation in the catalysis of C18:0 desaturation into C18:1 (Smith et al., 2006). Individual lipids and lipid classes exhibit a wide range of genetic correlation estimations. Some individual lipids exhibit a genetic correlation of almost 1.0 or -1.0 which is likely due to the pathway being highly dependent on the products from each previous step in the synthesis, elongation, or desaturation of lipid products, as well as a likely over-estimation of the parameter.

Genomic Regions of Interest affecting Fatty Acid Profile

Multiple studies have carried out genome-wide association studies in various breeds of cattle for the total fatty acid fraction in order to identify genomic regions, markers, and genes of interest. One of the most important genes involved in *de novo* synthesis of fatty acids is FASN. This protein is a complex of multiple subunits which are transcribed from a region on chromosome 19 starting at approximately 51,384,900 base pairs (bp). Multiple studies have identified this region as having a high association with saturated fatty acids including C14:0, C16:0, and total SFA (Matsushashi et al., 2011; Uemoto et al., 2011; Ishii et al., 2013; Saatchi et al., 2013; Hayakawa et al., 2015). There have also been multiple detailed studies of this region in relation to the fatty acid profile and there appear to be many different SNP's in the region affecting synthesis of SFA (Li et al., 2012; Oh et al., 2012; Lee et al., 2014). Saatchi et al. (2013) also estimated that markers in this region explain up to 25% of the genetic variance in saturated fatty acids with the highest genetic variance explained in *cis*-9 C18:1. This data suggests there are likely multiple causative mutations in the FASN gene that affect the fatty acid profile in multiple species of cattle (Casas et al., 2001; Casas et al., 2003; McClure et al., 2010).

However, not every species seems to have this association between SFA the FASN loci. Cesar et al. (2014) identified 8 genomic regions explaining approximately 1% of the genetic

variance in SFA's, including C14:0, C16:0, and C18:0. None of these 8 regions were near or overlapped the FASN loci, but they did overlap with previously identified loci affecting marbling score, backfat thickness, and carcass and body weight in Angus cattle. These associations are likely detecting the effect of loci causing variation in carcass fatness, which directly has an effect on percentage of SFA. At different levels of carcass fatness the ratio of SFA to unsaturated fatty acids changes (Warren et al., 2008). This effect can be partially explained by the morphology of adipose cells at different maturity points. In younger animals it can be expected that adipose cells are in a stage of multiplication under conditions of excess energy intake, at which point the ratio of the lipids in the phospholipid membrane to the lipids stored as triacylglycerol is high (Grauagnard et al., 2010). As the adipose tissue ages a higher proportion of the lipids synthesized and incorporated are stored in the triacylglycerol as triglycerides which are generally more saturated in nature than the phospholipid membrane (Smith et al., 1998). Given this shift in lipid storage as a tissue ages, it can be expected that loci affecting carcass fatness and adipose cell morphology would also affect the proportion of SFA.

Saatchi et al. (2013) also identified a region on chromosome 29 starting at about the 18th Mb harboring the candidate gene thyroid responsive hormone (THRSP or SPOT14) to explain the second highest amount of genetic variance in C14:0, C16:0, C16:1, cis-9 C18:1, long chain fatty acids (LCFA), and medium chain fatty acids (MCFA). This gene is known to be involved in SFA and LCFA synthesis through transcriptional activity and possibly by acting as a cofactor to FASN (Cunningham et al., 1998; LaFave et al., 2006). Other studies have also identified an association between fatty acid traits and variation and expression of THRSP (Hudson et al., 2014; Oh et al., 2014). Variation in FASN and THRSP appear to be associated with high genetic variance in SFA and fatty acid synthesis in beef cattle tissues.

Genomic regions associated with percentage of MUFA have also been well characterized. A region on chromosome 26 starting at approximately 21,132,700 bp harbors the SCD gene which is known to be involved in lipid desaturation in mammalian tissues (Marchitelli et al., 2013; Estany et al., 2014). Multiple studies have identified this genomic region as having a significant effect on C14:1, C16:1, C18:1 and other elongated MUFA species through GWAS (Ishii et al., 2013; Saatchi et al., 2013; Cesar et al., 2014). Additional regions have been associated with MUFA containing candidate genes for fatty acid related traits. Cesar et al. (2014) identified a region on chromosome 2 in Nellore cattle near two candidate genes, glutamate

decarboxylase 1 (GAD1) and specificity protein 5-transcription factor (Sp5), which are both involved in general energy metabolism, adipogenesis, and lipogenesis pathways. These studies support the hypothesis that SCD is the main candidate gene responsible for variation in MUFA species in beef cattle tissues.

Results from estimates of genetic parameters and GWAS from PUFA in beef tissues have proven to be the most difficult to obtain among the three major lipid saturation classes due to the low variation observed in these traits. Heritability estimates for the PUFA lipids are the lowest for all lipid species (Inoue et al., 2011; Saatchi et al., 2013; Ekine-Dzivenu et al., 2014). This relatively low variance observed for PUFA species is likely a reflection of the biological importance of these lipids in the cell. Since the majority of these elongated and unsaturated lipids are found in the cell membrane it can be reasoned that variance in this lipid depot would be detrimental to the fluidity and function of the phospholipid bilayer. The low genetic variance estimates for these phenotypes also allow for the discovery of fewer candidate genes explaining genetic variance using a GWAS methodology. This does not indicate that there are fewer genes involved in the synthesis or incorporation of these lipids into adipose tissue, but that it is more difficult to identify them using these methods. Another source of difficulty in identifying candidate genes involved with the PUFA species is that a number of them are not synthesized *in vivo*, but are instead incorporated from dietary sources. Also, the majority of the PUFA synthesis that does occur in mammalian tissues occurs in the liver rather than in adipose. The main pathway leading to PUFA synthesis relies on the conversion of linoleic and alpha linoleic acids to arachidonic (ARA), eicosapentaenoic (EPA), and docosahexaenoic (DHA) through the activity of fatty acid elongases (ELOVLs) and fatty acid desaturases (FADS) (Jump, 2011).

Studies reporting GWAS results for PUFA species in beef cattle have not found an association with the FAD or ELOVL loci, but rather genomic regions harboring or near candidate genes involved in membrane function, membrane adhesion, adipogenesis, or cell signaling. Cesar et al. (2014) identified 9 genomic regions explaining at least 1% of the genetic variance in multiple PUFA species. Candidate genes in the regions included aquaporin 7 (AQP7), lysil oxidase-like 2 (LOXL2), and RAR-related orphan receptor. These candidate genes are involved in cellular component functions such as the PPAR signaling pathway, lean body mass determination in mice, and cellular receptor pathways but no previous association with bovine adipose tissue has been reported. Saatchi et al. (2013) reported associations between

omega-3 and omega-6 fatty acids and regions on chromosomes 23, 14, 26, and 11, but no candidate genes were reported near these regions that had an association to lipid metabolism. There were also no regions of the genome in this study with a posterior probability of inclusion (PPI) greater than 0.9 for total PUFA or any other individual PUFA lipids. Identification of genomic loci affecting PUFA species needs further investigation. It appears that the low phenotypic and genetic variance estimates for this trait hinder the discovery of candidate genes affecting variation.

Other candidate genes affecting fatty acid profile in livestock species have been described in the literature, but have not shown up in GWAS studies in these traits. Graugnard et al. (2010) described the PPAR gamma signaling axis as a major driver of adipogenesis in response to energy abundance under different dietary conditions. Other lipid metabolism genes implicated in through differential gene expression in this study included adiponectin (ADIPOQ), fatty acid binding protein 4 (FABP4), diglycerol acyltransferase 2 (DGAT2), and sterol regulatory element-binding transcription factor 1 (SREBF1). The role of ADIPOQ has been studied as a regulator of lipid synthesis in milk fatty acid synthesis (Singh et al., 2014; Locher et al., 2015), and it would follow that this hormone would likely have a similar role in signaling lipogenesis in adipose. The binding protein FABP4 has also exhibited differential expression in the muscle of cattle fed differing levels of soybean oil or rumen protected fat (Oliveira et al., 2014). There have been a wide variety of genes described in the literature affecting fatty acid traits in beef cattle and other species. Taken together, this set of candidate genes likely contains a large number of causal mutations contributing variation to fatty acid traits in beef cattle.

Gene Network Theory

Complex trait analysis in livestock species has been assisted by recent advances in the generation of genomic and general “omics” related data sets. However, this generation of extremely large datasets has created a need for more complex analysis systems to detect biological phenomena and relate genotype to phenotype. Some of the primary goals in complex trait analysis using these large datasets are to identify causal genes and causal mutations, interactions among these genes and genomic regions, and to assemble these genes and interactions into networks or pathways in a meaningful way that relates to the underlying biology (Feltus, 2014). Such tasks have been the central goal of disciplines such as systems biology or

systems genetics. These systems biology approaches have been developed to identify a variety of genome features such as copy number variation (Jiang et al., 2015), diagnostic features in the cancer genome (Liu et al., 2015a), and causal mutations underlying traits of interest (Hudson et al., 2009; Chen et al., 2014). Causal mutations are of particular importance to the livestock genomics industry due to the development of selection strategies based on genomic data, which can increase in accuracy when causal mutations are included in the prediction (Druet et al., 2014).

One important development in this area has been the incorporation of GWAS data into the generation of regulatory networks underlying multiple related traits of interest. A method developed by Reverter and Fortes (2013) has utilized the inclusion of SNP identified in GWAS to build gene networks highlighting genes of functional relevance to significant biological pathways, rather than just a single phenotype. The method relies on the generation of SNP networks derived from an association weight network tested for interactions by using an algorithm known as partial correlation and information theory (PCIT) (Reverter and Chan, 2008). The major principle behind this method relies on the assumption that SNP having a high impact on multiple related phenotypes are likely of high importance or contain causal mutations.

The first step in the generation of the association weight matrix is to create a matrix of SNP effects for all phenotypes used in the model. A threshold needs to be chosen that incorporates a number of SNP that have a sufficiently high effect on the phenotype of highest importance. Once the initial set of SNP are chosen, the rest of the phenotypes are populated with the same chosen SNP with effects from each respective GWAS. For Bayesian GWAS methods an appropriate threshold might include a posterior probability of association (PPA) of 0.50 to 0.95, depending on the number of SNP that fall within this range. One benefit of the method is that it can be customized to multiple types of omics data that has been generated in association with multiple related phenotypes of interest. Other methods have successfully been used to generate an association weight matrix from data such as the transcriptome (Lehnert et al., 2006; Fortes et al., 2010; Fortes et al., 2012).

The next step is to identify correlations between all SNP or data points in the association weight matrix. The PCIT algorithm was developed specifically to handle this task of identifying associations or correlations among all data points in a large matrix. The matrix consists of columns that correspond to phenotypes in the analysis, and rows that correspond to the SNP

selected from GWAS results with the highest association to the most important phenotype in the analysis. The algorithm first estimates correlations between every pair of SNP in the dataset across all of the phenotypes. Next, the algorithm identifies a partial correlation between each SNP pair and every other SNP, if such a correlation exists. SNP pairs with a partial correlation of 0 to any other SNP are considered isolated and only associated with one another, and subsequently removed from the final output. The algorithm was optimized for use as an R package (Watson-Haigh et al., 2010) and also optimized to run in parallel for high performance computing applications (Koesterke et al., 2013). The final output of the algorithm is a set of SNP pairs and their associated direct correlations which can be utilized in the final visualization of SNP networks.

Network scoring, annotation, and visualization are the final steps in the association weight matrix approach spanning multiple phenotypes. There are many software packages that can handle gene network visualization, but the Cytoscape software package (Shannon et al., 2003) is particularly useful for its ability to score highly interconnected network clusters. A plugin for the Cytoscape software called MCODE (Bader and Hogue, 2003) was developed to score highly interconnected clusters of genes. The clusters are identified by an analysis of cluster density, which is the product of the number of connections in the network and the number of SNP. Clusters with the highest network density are ranked highest in the scoring criteria. These highly interconnected clusters represent the candidate genes or SNP that have the highest impact on the overall phenotype of interest since they contain associated genes or SNP that affect all phenotypes in the model. Annotation of the final networks is necessary to determine if the captured SNP fall in or near genes of functional significance to the overall phenotype in the analysis.

Multiple studies have utilized the association weight matrix approach to analyze quantitative traits in livestock species. A study by Fortes et al. (2012) utilized transcriptome data to build an association weight matrix to analyze first service conception rates in Brangus heifers. Transcriptome data from 10 related growth and fertility traits were used in the construction of the association weight matrix. This approach identified 5 highly interconnected transcription factors hypothesized to be related to overall fertility as well as markers in multiple genes that have been previously associated with fertility traits in beef cattle.

A study by Ramayo-Caldas et al. (2014b) utilized a SNP effect based association weight matrix to analyze intramuscular fat deposition in approximately 10,000 beef cattle from 3 breeds. The study looked at 29 different traits including intramuscular fat, related fat phenotypes, feedlot performance, and various meat quality traits to identify the markers with the highest impact on fat deposition. The resulting networks produced three transcription factors as key regulators of fat deposition and carcass traits: PPARGC1A, HNF4G, and FOXP3. Multiple other markers were identified within genes of biological importance to the pathways regulating these traits of interest as well. Importantly, it was noted that the transcription factors and major genes of interest were not identified in the GWAS as markers with the highest effect associated with any one individual phenotype. The combination of multiple phenotypes with a high throughput genomic data source incorporated into the association weight matrix allowed these markers to be highlighted.

Another study by Ramayo-Caldas et al. (2014a) used SNP effects to create an association weight matrix for intramuscular fatty acid composition in porcine. This study looked at 15 fatty acid phenotypes to identify key regulators of intramuscular fatty acid metabolism. The final network analysis identified the transcription factors NCOA2, FHL2, and EP300 as central regulators of fatty acid metabolism along with many other individual genes of functional significance. This study was unique in that the authors went on to validate the identified transcription factors as having differential expression at the transcriptomic level using real-time PCR. They found expression differences for extreme fatty acid phenotypes in two breeds in liver tissue for 55 genes involved in their association network, including the three identified transcription factors. Also, approximately 60% of the connections identified in the network analysis were validated at the transcriptomic level. Creating the association weight matrix with multiple types of omics data or validating the networks through expression analysis appears to be a robust method for identifying genes of interest in pathways affecting multiple phenotypes of interest. This method appears to be a promising tool for the dissection of complex traits represented by multiple phenotypes, and the flexibility of this method would allow its application across multiple phenotypes of economic importance for beef cattle.

Conclusion and Implication for Genetic Improvement of Beef Cattle

The fatty acid profile of beef is a complex phenotype that would benefit from a systems biology approach to identify the genes of highest impact regulating overall lipid metabolism. The fatty acid profile is associated with economic traits of interest such as intramuscular fat and healthfulness of the final beef product. Previous research across multiple beef cattle breeds, environmental conditions, and muscle tissues has determined that individual lipids and lipid classes exhibit a wide range of heritability estimates. Lipids of higher abundance such as medium chain SFA and MUFA exhibit a moderate to high heritability, which indicates these traits would respond to a genomic selection program. Given the wide range of observed fatty acid phenotypes in various lipid depots (triacylglycerol vs. phospholipid), muscle types, breeds, and feeding programs there is a need to identify the major pathways, transcription factors, and genes responsible for variation within the overall process of lipid metabolism. The identification of the drivers of lipid metabolism has multiple economic implications for the beef cattle industry since the value of the final beef product is highly dependent on lipogenesis during the finishing phase.

The association weight matrix approach provides a robust methodology that can identify the central regulators of a complex metabolic process such as the fatty acid profile of beef. The application of this method across multiple phenotypes and species has demonstrated its adaptability to multiple data types which is an important feature since the nature of “omics” data is constantly and rapidly changing with technological advances. The fatty acid profile has multiple related individual phenotypes that make up the overall fatty acid profile, including the major lipid classes as well as the various individual lipids contained in muscle and adipose tissue. With the introduction and continued use of high density genotype data into genomic selection programs it is becoming increasingly important to have an understanding of the biology and markers of highest importance for economic traits of interest. The beef cattle industry would benefit from an analysis of the genetic parameters and genetic correlations associated with the intramuscular fatty acid profile from the triacylglycerol and phospholipid fatty acid fractions followed by the implementation of the association weight matrix approach to generate a network analysis of lipid metabolism in Angus beef cattle.

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FRANK H. BAKER MEMORIAL SCHOLARSHIP PAST AWARD RECIPIENTS

Name	University	Year
Heather Bradford	Kansas State University	2014
Xi Zeng	Colorado State University	2014
Heather Bradford	Kansas State University	2013
Erika Downey	Texas A&M University	2013
Jeremy Howard	University of Nebraska-Lincoln	2012
Kristina Weber	University of California-Davis	2012
Brian Brigham	Colorado State University	2011
Megan Rolf	University of Missouri	2011
Kent A. Gray	North Carolina State University	2010
Lance Leachman	Virginia Polytechnic Institute and State University	2009
Scott Speidel	Colorado State University	2009
Devori W. Beckman	Iowa State University	2008
Kasey L. DeAtley	New Mexico State University	2008
Gabriela C. Márquez Betz	Colorado State University	2007
Yuri Regis Montanholi	University of Guelph	2007
Amy Kelley	Montana State University	2006
Jamie L. Williams	Colorado State University	2006
Matthew A. Cleveland	Colorado State University	2005
David P. Kirschten	Cornell University	2005
Reynold Bergen	University of Guelph	2004
Angel Rios-Utrera	University of Nebraska	2004
Fernando F. Cardoso	Michigan State University	2003
Charles Andrew McPeake	Michigan State University	2003
Katherina A. Donoghue	University of Georgia	2002
Khathutshelo A. Nephawe	University of Nebraska	2002
Khathutshelo A. Nephawe	University of Nebraska	2001
Janice M. Rumph	University of Nebraska	2001
Paul L. Charteris	Colorado State University	2000
Katherine A. Donoghue	University of Georgia	2000
Janice M. Rumph	University of Nebraska	1999
Bruce C. Shanks	Montana State University	1999
Patrick Doyle	Colorado State University	1998
Shannon M. Schafer	Cornell University	1998
Rebecca K. Splan	University of Nebraska	1997
Robert Williams	University of Georgia	1997
D. H. "Denny" Crews, Jr.	Louisiana State University	1996
Lowell S. Gould	University of Nebraska	1996
D. H. "Denny" Crews, Jr.	Louisiana State University	1995
Dan Moser	University of Georgia	1995
Kelly W. Bruns	Michigan State University	1994
William Herring	University of Georgia	1994

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. He 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 \$1250 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. (From BIF website, www.beefimprovement.org.)



2014 Roy A. Wallace Scholarship Recipients



The Roy A. Wallace Memorial scholarship was awarded to Heather Bradford, Kansas State University, and Maci Lienemann, University of Nebraska. Pictured are (from left) Joe Cassady, executive director of the Beef Improvement Federation; Brian House, Select Sires; Trevor, Torri and Maci Lienemann; Bradford; and Aaron Arnett, Select Sires.

BIF PAST RECIPIENTS OF THE ROY A. WALLACE SCHOLARSHIP AWARD

Name	University	Year
Maci Lienemann (undergraduate)	University of Nebraska–Lincoln	2014
Heather Bradford (graduate)	Kansas State University	2014
Tyler Schultz (undergraduate)	Kansas State University	2013
Loni Woolley (graduate)	Texas Tech	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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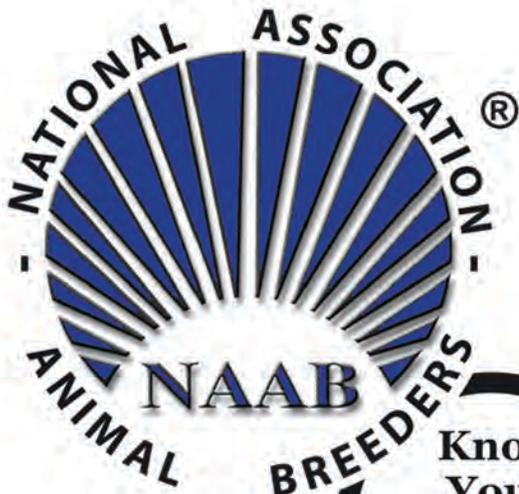
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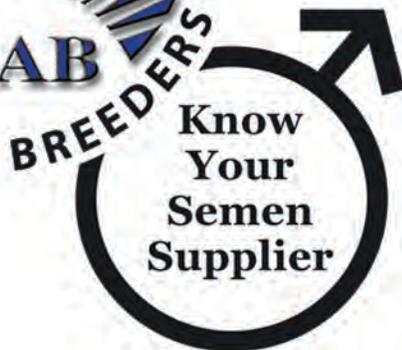


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FRIDAY JUNE 12TH, POST-CONFERENCE TOUR

Tour departs at 7:00 a.m. Planned arrival back at 6:00 p.m. The tour includes the following planned stops:

Grand Bay NERR

The Grand Bay National Estuarine Research Reserve (NERR) was established in 1999 and is managed by the Mississippi Department of Marine Resources as part of the National Oceanic and Atmospheric Administration's National Estuarine Research Reserve System. The Grand Bay NERR is comprised of approximately 18,000 acres and contains pine savannas, salt marshes, salt pannes, bays and bayous as well as terrestrial habitats that are unique to the coastal zone.

For more information, visit: www.grandbaynerr.org.



Seward Farms

Seward Farms is a diversified farm specializing in cattle, horses, peanuts, cotton, and hay. Cattle are a major part of their farming operation. In 2014, they produced upwards of 5,000 head of stocker cattle. The farm also has a big focus on sharing the story of agriculture with the public, and hosts families and school groups for educational trips, summer camps, pig races, and more.

For more information, visit: www.sewardfarms.com.



Tanner Farms

Tanner Farms is a grass roots, registered and commercial Angus operation which originated in Jones County in 1977 and expanded to Noxubee County in 2000. There are approximately 600 registered cows and 800 commercial cows with both a spring and fall calving season. The goal is to produce functional and profitable Angus cattle for their own operation and customers. A fall Angus and Sim Angus bull and female sale is hosted at the farm in Shuqualak, and a Angus and SimAngus bull sale is hosted in January at the farm in Wiggins. For more information, visit www.tannerfarms.net.



Rocking B Cattle

Rocking B Cattle is a registered Polled Brahman cattle ranch that is operated by Shep and Tracey Batson along with their three daughters, Reagan, Hadley, and Arrah Beth. The ranch is located in Wiggins, Mississippi, 25 miles north of the Mississippi Gulf Coast. The Batson Family in Wiggins, Mississippi has been involved in the cattle business since the 1850's. For over 4 generations, the family has been breeding quality cattle on the same ranch. For more information, visit: www.rockingbcattle.com.





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