Beef Improvement Federation

Annual Convention
May 31 - June 3, 2017
Athens, Georgia

UNIVERSITY OF **GEORGIA**
1785

Georgia Cattlemen's ASSOCIATION

UNIVERSITY OF GEORGIA

1785

May 31, 2017

Welcome to the Peach State!

On behalf of the Georgia Cattlemen's Association (GCA) and the University of Georgia (UGA), it is our pleasure to welcome you to the 49th Beef Improvement Federation Annual Meeting and Research Symposium. The annual BIF Meetings, as they are referred to by most of us, not only offer the opportunity to learn about the latest topics affecting beef cattle improvement and profitability, they also provide the chance to interact and network with leaders in several of the different areas that encompass beef improvement in both the U.S. and Canada. The conversations in the hallway have become a highlight for many that regularly attend these meetings as industry leaders, scientists, extension personnel, breed association and company personnel, and producers discuss and debate the future of beef cattle genetic improvement. The BIF Conference planning committee has worked hard to provide a program that will stimulate much thought and discussion.

Most people associate Georgia with peaches, poultry and peanuts, but according to *2015 Georgia Farm Gate Value Report*, beef cattle was the third leading agricultural commodity in the state in terms of farm gate receipts during 2015 and was ahead of both peanuts and peaches. It is important that beef cattle producers in Georgia and elsewhere continue to focus on key technologies, tools and strategies that allow them to be profitable and sustainable. It is our hope that those that attend this year's meetings will take home information that will enhance their enterprises.

The BIF Meeting would not be possible without the support of our sponsors. Please take the time to thank each of them for their contributions. We hope all of you enjoy your time in Athens, home of the University of Georgia, which is the nation's oldest chartered state public university. If you have the time, travel around the state; it has mountains, beaches, a rich history and great natural beauty.

Sincerely,

Ronnie Silcox, PhD
Meeting Coordinator
Associate Professor

Will Bentley
GCA Executive VP

Georgia
Cattlemen's
ASSOCIATION

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Schedule of Events

Wednesday, May 31, 2017
8:00 a.m. – Noon   BIF Board Meeting

10:00 a.m – 7:00 p.m. Registration Opens,
Athens Classic Center Foyer

1:00 – 4:30 p.m.   **Young Producers Symposium**
• Starting from Scratch: Tips for building an operation from the ground up. *Kevin and Lydia Yon, Yon Family Farms, Ridge Spring, SC*
• Smart financial planning: Business planning and loan approval for young cattlemen. *Dr. Curt Lacy, Mississippi State University*
• Marketing Challenges your dad didn't face: Understanding millennial consumers and social marketing strategies. *Amanda Radke, Rancher, Marketing Specialist and Correspondent for BEEF magazine, Mitchell, SD*

5:30 – 7:00 p.m.   **Reception**

7:00 – 9:00 p.m.   **NAAB Symposium**
The Benefits of Proven Genetics & A.I.
Featuring Dr. Les Anderson of the University of Kentucky and Dr. Dave Patterson from the University of Missouri

Thursday, June 1
7:00 a.m. – 5:00 p.m. Registration,
Athens Classic Center Foyer

7:00 – 8:00 a.m.   Breakfast

8:00 a.m. – Noon   General Session I:
The Current Value and Future Promise of Genomics for Beef Improvement
Moderator: Dr. Keith Bertrand, The University of Georgia

8:00 a.m.   Opening comments

8:15 a.m.   The promise of genomics for beef improvement.
Dr. Daniela Lourenco, The University of Georgia

9:00 a.m.   What the beef industry can learn about genomics use from other industries.
Dr. Tom Lawlor, Holstein Association USA

9:45 a.m.   Question and Answer Session

10:00 a.m.   Break

10:30 a.m.   Where we are going with genomics and genetic improvement.
Dr. Matt Spangler, University of Nebraska and Dr. Alison Van Eenenaam, University of California – Davis

11:30 a.m.   What you heard
Dr. Bob Weaber, Kansas State University

12:00 – 2:00 p.m.   Awards Luncheon
Presentation of BIF Commercial Producer, American Angus Assn. Presentation of BIF Pioneer, Frank Baker and Larry Cundiff Scholarships

2:00 – 5:30 p.m.   Breakout Sessions
Advancements in Genomics and Genetic Prediction
Chair: Dr. Mark Thallman, USDA-ARS-MARC
• 2:00 – 2:45   Genomic prediction developments at American Angus
Stephen Miller, American Angus Association
• 2:45 - 3:30   A new cow fertility prediction, Bruce Golden, Theta Solutions
• 3:30 – 4:15   Considerations for adjusting carcass traits to differing endpoints
Matt Spangler, University of Nebraska
• 4:15 – 5:00   BIF sub-committee report on across-breed EPD programs: proposed improvements
Larry Kuehn, US Meat Animal Research Center

Advancements in Producer Applications
Chair: Dr. Darrh Bullock, University of Kentucky
• 2:00 – 3:30   Panel Discussion
Implications of multi-breed evaluations and across-breed EPDs for commercial cattlemen
    Bruce Golden, Theta Solutions
    Larry Kuehen, US Meat Animal Research Center
    Matt Spangler, University of Nebraska
    Joe Epperly, North American Limousin Foundation
• 3:30 – 4:15   Local genetic adaptation project
Jared Decker, University of Missouri
• 4:15 – 5:00   Genetics of reproduction project
Alison Van Eenennaam, University of California – Davis

Advancements in Efficiency and Adaptability
Chair: Dr. Mark Enns, Colorado State University
• 2:00 – 2:45   Evaluating sustained cow production: Alternate definitions of stayability.
Scott E. Speidel, Assistant Professor, Department of Animal Sciences, Colorado State University
• 2:45– 3:30   Cow and bull fertility in a fescue challenged environment.
Justin Rhinehart, Assoc. Professor and Extension Beef Cattle Specialist, Department of Animal Sciences, University of Tennessee.
• 3:30 – 4:15   Beef cattle climate adaptability: How can genomics help?
Raluca Mateescu, Associate Professor of Quantitative Genetics & Genomics, Department of Animal Sciences, University of Florida

Schedule of Events

• 4:15 – 5:00   Feed intake in Brangus cattle: Experiences and Recommendations
Lisa Kriese-Anderson, Extension Specialist and Associate Professor, Department of Animal Sciences, Auburn University

6:30 p.m.   Evening Social/Dinner

Friday, June 2

7:00 a.m. – Noon   Registration, Athens Classic Center Foyer

7:00 – 7:45 a.m.   Breakfast

7:30 – 7:45 a.m.   Welcome and News of the Day

7:45 a.m. – Noon   General Session II: Profitability Using the Tools We Have
Moderator: Dr. Lawton Stewart, The University of Georgia

7:45 a.m.   Strategic use of heterosis
  Dr. Todd Thrift, University of Florida

8:30 a.m.   The power of index based selection:
  Dr. Darrh Bullock, University of Kentucky;
  Donnell Brown, R. A. Brown Ranch;
  Larry Keenan, Red Angus Association of America

9:15 a.m.   Question and Answer Session

9:30 a.m.   Break

10:00 a.m.   Investing in the future, heifer development for longevity
  Dr. Justin Rhinehart, University of Tennessee

10:30 a.m.   Factors affecting feedlot profitability
  Gary Fike, Tri County Steer Carcass Futurity Cooperative and Red Angus Association of America

11:00 a.m.   Question and Answer Session

11:15 a.m.   BIF caucuses and elections

12:00 – 2:00 p.m. Awards Luncheon
What you heard, Dr. Dan Moser, American Angus Assn. Presentation of Seedstock Producer Awards, Continuing Service and Ambassador Awards, Roy Wallace Scholarships, Introduction of newly elected BIF Board of Directors, Invitation to BIF 2018

2:00 – 5:30 p.m.   Breakout Sessions
  Advancements in Emerging Technology
    Chair: Dr. Megan Rolf, Kansas State University

• 2:00 – 2:45   Update on the GGP-F250 and loss of function lethals
Jerry Taylor, University of Missouri-Columbia
• 2:45 - 3:30   How genome editing could synergistically accelerate animal genomics
Alison Van Eenennaam, University of California – Davis
• 3:30 – 4:15   Economic risk analysis of embryo transfer programs through stochastic simulation
Dustin Aherin, Kansas State University
• 4:15 – 5:00   Basics and prospects in epigenetics
Chad Niederhuth, The University of Georgia

Advancements in End Product Improvement
Chair: Dr. Tommy Perkins, International Brangus Breeders Association
• 2:00 – 2:45   Field testing $BEEF in Purebred Cattle
Tom Brink, Red Angus Association of America
• 2:45 – 3:30   Insights from ongoing beef flavor research
Bridget Wasser, Meat Science & Technology, NCBA, a Contractor to the Beef Checkoff Program
• 4:00 – 4:45   Genetic improvement of carcass traits in *Bos indicus* influenced cattle
Raluca Mateescu, University of Florida
• 4:45 – 5:30   Transcriptome data supporting early prediction of carcass merit in young cattle
Heather Dunn and Matt Burns, Clemson University

Advancements in Selection Decisions
Chair: Dr. Bob Weaber, Kansas State University
• 2:00 – 2:40   Genomic analysis of udder traits in tropically adapted beef cows
Mallory Tollenson, Clare Gill, Andy Herring, Penny Riggs, Jason Sayer, Jim Sanders and David Riley, Texas A&M University
• 2:40 – 3:20   Exploring variation in beef cattle water intake and utilization
Cashley Ahlberg, Kansas State University
• 3:20 – 3:30   Break
• 3:30 – 4:10   Making the most of genetic selection in a challenging environment
David Genho, President and General Manager, Conservation and Environmental Resources, Alico, Inc.
• 4:10 – 4:50   Development of genomic pipeline for IGS BOLT genetic evaluations
Mahdi Saatchi, International Genetic Solutions

5:30 p.m.   BIF board meeting and board photo

Saturday, June 3
8:00 a.m.   Tour of Georgia beef industry

General Session Speakers

Daniela Lourenco is an Assistant Professor in animal breeding and genetics at the University of Georgia. She was born and raised in Brazil, where she earned her M.S. and PhD degrees in animal breeding and genetics from Maringa State University. Daniela has been working in this field since 2004 and has published over 150 scientific papers and proceedings. Daniela's research has focused on improving livestock production using genomic information, developing methods for genetic evaluation, and addressing issues related to the implementation of genomic selection in beef and dairy cattle, poultry, swine, and fish. Although she works with several species, beef cattle breeding is her passion. She has been recently working on the implementation of single-step genomic evaluation for several American and Canadian beef cattle associations.

Dr. Tom Lawlor is the Executive Director of Research and Development at Holstein USA. He works quite closely with the association's Genetic Advancement Committee and is a regular contributor to the Journal of Dairy Science, winner of their J.L. Lush Award in Animal Breeding and Genetics and co-author of the most-cited breeding and genetics paper in 2013. Tom also serves as a technical advisor to the U.S.'s Council on Dairy Cattle Breeding, Interbull and the World Holstein Friesian Federation.

Matt Spangler grew up on a diversified crop and livestock farm in Kansas. He received degrees from Kansas State University (B.S.; 2001), Iowa State University (M.S.; 2003), and the University of Georgia (PhD; 2006) and is currently an Associate Professor and Extension Beef Genetics Specialist at the University of Nebraska. He works as part of a team with colleagues at UNL and US MARC to improve genetic/genomic selection tools and methods.

Dr. Alison Van Eenennaam is a Cooperative Extension Specialist in the field of Animal Genomics and Biotechnology in the Department of Animal Science at University of California, Davis. She received a Bachelor of Agricultural Science from the University of Melbourne in Australia, and both an M.S. in Animal Science, and a PhD in Genetics from UC Davis. Her publicly-funded research and outreach program focuses on the use of animal genomics and biotechnology in livestock production systems. Her current research projects include the development of genomic approaches to select for cattle that are less susceptible to disease, the development of genome editing approaches for livestock, and applied uses of DNA-based information on commercial beef cattle operations. She has given over 450 invited presentations to audiences globally, and uses a variety of media to inform general public audiences about science and technology. She frequently provides a credentialed voice on controversial topics including cloning and genetically engineered plants and animals. Dr. Van Eenennaam was the recipient of the 2014 Council for Agricultural Science and Technology Borlaug Communication Award, and the 2016 Beef Improvement Association Continuing Service Award.

Darrh Bullock was raised on a commercial beef cattle/watermelon farm in north-central Florida. He earned a B.S. in Animal and Dairy Sciences and M.S. degree in Animal Breeding and Genetics from Auburn University and he earned his Ph.D. in Beef Cattle Breeding and Genetics from the University of Georgia. Dr. Bullock has been on faculty at the University of Kentucky for 25 years and holds the rank of Professor, specializing in beef cattle genetics. He coordinates the Beef Group in the department and has recently served as the Animal and Food Sciences Extension Coordinator and on the college promotion and tenure committee. The majority of Dr. Bullock's appointment is Extension, however, he is responsible for teaching the department's Beef Cattle Sciences course. National and international activities include membership on the eBEEF.org team, Educational Program Committee for the National Beef Cattle Evaluation Consortium, board member and committee chair of the Beef Improvement Federation, past Southern Region ASAS Extension Chair and past representative of the United States to the International Committee for Animal Recording and InterBeef Beef Working Group. Dr. Bullock has received the MD Whiteker Award for Extension Excellence from the University of Kentucky, the Southern Region American Society of Animal Science (ASAS) Extension Award and the national ASAS Extension Award..

General Session Speakers

Justin Rhinehart is an Associate Professor and Extension Beef Cattle Specialist in the University of Tennessee Department of Animal Science. He was raised in east Tennessee working with livestock and tobacco. Justin earned his B.S. in Agriculture and Extension Education from the University of Tennessee. He received his M.S. in Reproductive Physiology from the University of Kentucky where he investigated the use of dietary fat supplementation to alleviate the negative effects of endophyte-infected tall fescue on reproductive performance of beef heifers. He then earned his Ph.D. from the Faculty of Reproductive Physiology at West Virginia University where his dissertation focused on pregnancy loss in cattle associated with changes in steroid hormone concentrations and placental development. After completing his terminal degree, Dr. Rhinehart served for three years in the Mississippi State University Department of Animal & Dairy Sciences as an Extension Beef Cattle Specialist. During his academic career, Justin has developed a strong desire to apply his education through the Extension arm of the Land-Grant system. Specifically, his goal is to translate research findings into management practices that improve the profitability of beef cattle production.
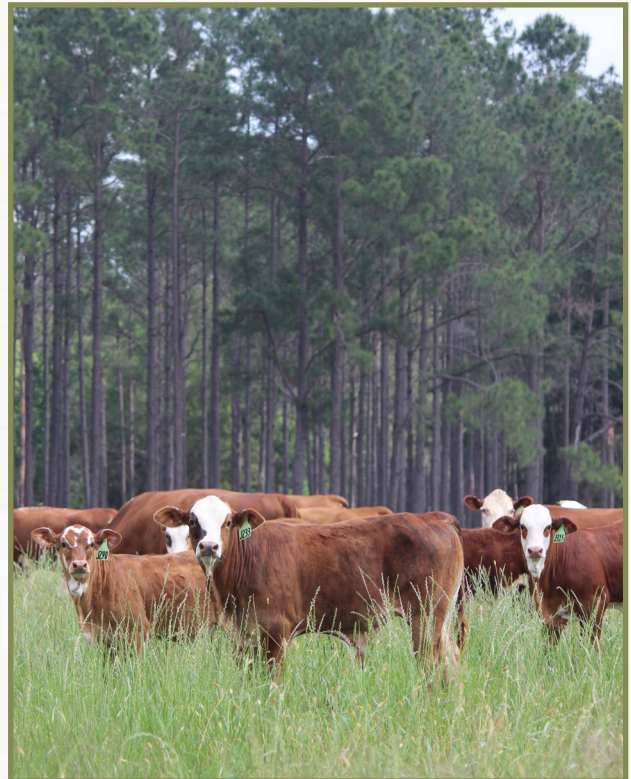
Gary Fike was raised on a family farm in central Kansas. He received his B.S. in Agricultural Education from Panhandle State University in 1983 and his M.S. degree from Kansas State University in 1995. He has worked in several extension positions including county agent in Kansas, county extension director in Iowa, area beef/forage specialist at Iowa State University, and Quality Assurance Extension Associate for the Ohio State University. In 2004, he took a position as a Beef Cattle Specialist with Certified Angus Beef LLC (CAB) at their Manhattan, KS field office and served there for 10 years before joining the Red Angus Association of America (RAAA) in December of 2014 as the Director of Commercial Marketing. In his present position, he leads a small team of dedicated individuals who help commercial producers market their calves through their process verified Feeder Calf Certification Program tags; assists with DNA collection for validation/comparative purposes, and advises cattle producers on various aspects of marketing their calves. He also assists producers in evaluating carcass data and grids, and works with packers, sale barn owners, and video livestock auctions to develop more marketing avenues for Red Angus influenced cattle. Gary and his wife, Karol, live near Westmoreland, KS, have three children, Jackson, Marshall, and Grace, and run a few commercial and purebred cows.

Todd Thrift was raised in Lexington Kentucky. He obtained his B.S. from the University of Kentucky, his M.S. from Oklahoma State University, and his Ph.D. from Texas A&M University. Upon graduation he worked for Texas A&M for five years as a Beef Cattle Specialist in the eastern portion of the state. Since 2001 he has worked at the University of Florida in a teaching and extension role. He teaches Cow Calf Production, Stocker and Feedyard Management, Beef Practicum, Beef Nutrition and Introduction to Animal Science. His extension focus is in the area of Beef Quality Assurance, Cow Calf Management, and Utilization of *Bos inducus* Genetics. Todd and his wife Dayla have three children and maintain a small commercial cattle operation west of Gainesville.

Commercial Producer Award Nominees

Megehee Cattle Company
Owners: Jacob and Martha Megehee
Manager: Jacob Megehee
Macon, Mississippi

Megehee Cattle Company is a commercial cow/calf and stocker operation located in East Central Mississippi, only fourteen miles from the Alabama border. Owned by Jacob and Martha Megehee, Megehee Cattle Company began in 1970 at the conclusion of Jacob's service in the United States Army.

With $10,000, 6 brood cows, two children, and a degree from Mississippi State University in Dairy Production, the Megehees purchased their farm in 1967, but leased out until 1970. While Jacob finished his Masters degree in Ag Economics, he and Martha ran stocker calves. Upon graduation, the Megehees used their stockers and six cows as collateral and purchased 99 bred, black baldy heifers for $195 each. From there, the operation peaked at 800 head.

Megehee Cattle Company is currently made up of 329 owned acres and 126 lease acres for hay and pasture. The herd consists of 140 mature cows, 80 bred heifers, and 62 open replacement heifers with a heavy Brangus influence. Approximately half of the herd calves in the spring and half in the fall. The Megehees market bred heifers in the state's most exclusive, highly regarded bred heifer sale. They also market bred heifers in the invitation-only Town Creek Farm Annual Production Sale. Steers have been marketed in the Mississippi Homeplace Feeder Calf Board sale since the sale's inception in 2008.

The Megehee Cattle Company is proudly nominated by the Mississippi Beef Cattle Improvement Association.

Mundhenke Beef
Owners/Managers: John and Gina Mundhenke
Lewis, Kansas

Mundhenke Beef is located in southwestern Kansas in eastern Edwards County near Lewis. Owners John and Gina Mundhenke both grew up on Kansas ranches that were established more than 100 years ago, with each representing the fourth generation of their respective families to work in the livestock industry. In fact, Gina's family's homestead is just a few miles away from their ranch. They operate irrigated and dryland farms, native grassland, backgrounding yards, and have interest in Kinsley Feeders LLC and Star Alfalfa Inc.

The focus of Mundhenke Beef is on efficient production from conception to consumption. The ranch calves 300 registered Angus cows and 200 commercial Angus cows in the spring. In addition, they develop and artificially inseminate (AI) 200 Angus heifers for customers. They also provide genetic selection and influence the management of animal health protocols and marketing for Gina's family's 1,100-head Angus-based commercial cow herd. They raise their own Angus bulls for their use and sell a few to others.

Calves are marketed through value-added programs, with the majority grading Prime or Choice on a consistent basis. This falls in line with the overall goal of Mundhenke Beef, which is efficient production from conception to consumption. They strive to improve the sustainability of the ranch, the well-being of the cattle and to ensure the endproduct is the best eating experience for their beef consumers.

The Kansas Livestock Association is proud to nominate Mundhenke Beef.

Commercial Producer Award Nominees

Timber Stream Cattle Company, LLC
Owners: Guttau Family
Manager: Joshua Guttau
McClelland, Iowa

    The Guttau family has been involved for multiple generations in the cow/calf industry with the homestead in Treynor, Iowa, going back to current manager Josh's great-great grandfather and their Glenwood location, purchased in 2014, being originally settled by his fourth great grandfather in the 1850s.

    Josh's grandfather ran commercial Hereford cows and all his father's 4H breeding heifers were absorbed into the family herd during his college years and while serving in Vietnam. After he returned home, he took over a local community bank and was unable to return the beef industry he loved.

    It has been an honor for Josh to return the Guttau family 'knee deep' into the cow/calf industry starting with his 8th grade 4H project, through an expansion to 75 cows during college in cooperation with his brother-in-law and further expansion to 500 head in 2010. The operations uses extensive pasture improvement and management to maintain consistent efficient production using Limousin and Lim-Flex bulls on British based cows with the goal of a black baldy phenotype with enhanced growth and cutability and uncompromised beef quality.

    The expansion has coincided with taking their community banking operation to the next level and to launch the family head first into the production side of agriculture where they are hoping to keep their family and future banking leaders fully aligned with the ag producer and have them be as comfortable wearing boots as suits.

Timber Stream Cattle Company is proudly nominated by the North American Limousin Foundation.

BIF Commercial Producer of the Year

Name	State	Year
Plum Thicket Farms	Nebraska	2016
Woodbury Farms	Kansas	2015
CB Farms Family Partnership	Kansas	2014
Darnall Ranch, Inc.	Nebraska	2013
Maddux Cattle Company	Nebraska	2012
Quinn Cow Company	Nebraska	2011
Downey Ranch	Kansas	2010
JHL Ranch	Nebraska	2009
Kniebel Farms and Cattle Company	Kansas	2008
Broseco Ranch	Colorado	2007
Pitchfork Ranch	Illinois	2006
Prather Ranch	California	2005
Olsen Ranches, Inc.	Nebraska	2004
Tailgate Ranch	Kansas	2003
Griffith Seedstock	Kansas	2002
Maxey Farms	Virginia	2001
Bill & Claudia Tucker	Virginia	2000
Mossy Creek Farm	Virginia	1999
Giles Family	Kansas	1999
Mike & Priscilla Kasten	Missouri	1998
Randy & Judy Mills	Kansas	1998
Merlin & Bonnie Anderson	Kansas	1997
Virgil & Mary Jo Huseman	Kansas	1996
Joe & Susan Thielen	Kansas	1995
Fran & Beth Dobitz	South Dakota	1994
Jon Ferguson	Kansas	1993
Kopp Family	Oregon	1992
Dave & Sandy Umbarger	Oregon	1991
Mike & Diana Hopper	Oregon	1990
Jerry Adamson	Nebraska	1989
Gary Johnson	Kansas	1988
Rodney G. Oliphant	Kansas	1987
Charles Fariss	Virginia	1986
Glenn Harvey	Oregon	1985
Bob & Sharon Beck	Oregon	1984
Al Smith	Virginia	1983
Sam Hands	Kansas	1982
Henry Gardiner	Kansas	1981
Jess Kilgore	Montana	1980
Bert Hawkins	Oregon	1979
Mose Tucker	Alabama	1978
Mary & Stephen Garst	Iowa	1977
Ron Baker	Oregon	1976
Gene Gates	Kansas	1975
Lloyd Nygard	North Dakota	1974
Pat Wilson	Florida	1973
Chan Cooper	Montana	1972

Seedstock Producer Award Nominees

Barrett Cattle
Owners/Managers: Gene, Anna, Payden and Ella Barrett
Grantville, Kansas

Barrett Cattle has been a registered Angus seedstock provider for more than 18 years, having evolved from a set of 20 commercial heifers to their current inventory of more than 200 registered Angus females. In addition to their cow herd, they custom artificial inseminate (AI) 6,500 to 7,000 head of cattle each year. They live and winter their cattle in the same area that Anna's family homesteaded more than 150 years ago, with their children working as the sixth generation along the banks of Prairie Creek near Grantville, KS, in southwestern Jefferson County.

The beef industry is their history and their future, with a diverse background in many aspects of the agriculture industry on both sides of the family. Gene's grandfather and great-grandfathers were meat cutters and owned meat shops from the late 1800s to the mid-1900s. Family, hard work, commitment to their trade and helping others is their foundation. They are proud to carry this forward and strive to develop their operation and their lives with respect to the hard work that has come before them. They don't consider themselves a large operation, but their current size allows them to know every animal and appreciate the importance of the day-to-day visual knowledge of their cows.

Their 1,100 acres are spread between two counties, with their summer grass along the very edge of the Flint Hills in northern Shawnee County and their fescue-brome-based winter grass in Jefferson County. Their cows are managed as a commercial herd would be. Their bulls and replacements are better because of this management style; and their customers appreciate it, too. They begin calving in late August and, with the first calf of the season, consider this day one of their operational year.

Barrett Cattle is proudly nominated by the Kansas Livestock Association.

Gates Limousin Ranch
Owner: Mary Gates
Manager: Gary Gates
Roscoe, Montana

Gates Limousin Ranch is a family owned and operated ranch located in the shadows of the Beartooth Mountains in southern Montana. The Gates Family has run a commercial cow/calf operation in Stillwater and Sweetgrass Counties of Montana for over 50 years.

In 2002, Mary brought the first registered Limousin female home to the ranch signaling the start of the seedstock portion of the operation. Since that time Gates Limousin has put together a solid registered herd to compliment the commercial females. With a focus to add genetics that look as good on paper as they do in the pasture, the registered herd has experienced modest but guided growth. Currently, there are about 140 commercial cows and 70 registered cows roaming the ranch.

As we continue to expand the registered herd, Gates Limousin Ranch has focused on producing bulls that will work for commercial cattlemen. In attempts to better serve the commercial market, Gates Limousin Ranch has also expanded its product line to include Lim-Flex® cattle. If the bulls they raise aren't good enough for use on their own commercial herd, they wouldn't think about selling them to their customers. Gates Limousin Ranch is nothing without its customers, and they strive to provide the best customer service possible.

The North American Limousin Foundation is proud to nominate Gates Limousin Ranch.

Seedstock Producer Award Nominees

Hillside Angus Farm
Owners/Managers: Dale and Judy Parris
Albertville, Alabama

Hillside Angus Farm, owned and operated by Dale and Judy Parris, is located on Sand Mountain in northeast Alabama. Hillside Angus Farm purchased their first registered Angus cows in 1982 and joined the American Angus Association and the Alabama Angus Association soon after. Performance record keeping through the Angus Herd Improvement Record (AHIR) Program began in 1986. The first calf crop resulted in an average 205-day weight for bulls of 550 pounds and for heifers an average of 472 pounds. Through dedication to genetic improvement and diligent record keeping for the past 30 years, the 2015-16 calf crop resulted in an average 205 day weight of 770 pounds for bulls and 652 pounds for heifers.

A fall calving season is planned annually beginning the first of September, to market bulls and females in spring sales. Artificial insemination with estrus synchronization is used to capture top-performing Angus genetics with a clean-up bull to complete the breeding season. Embryo transfer has also been utilized at different times in the past 25 years for genetic advancement of the herd. A long term goal of the farm is to further genetic improvement, continuing to collect complete performance data, and utilizing all available genetic selection tools, such as genomic testing, genomic-enhanced EPDs and carcass ultrasound.

Dale Parris serves in many leadership roles throughout the cattle industry. He is a past president of the Alabama Angus Association and currently serves as a director. At present, he also serves as president of the Marshall County Cattlemen's Association. He is one of the founders and prominent leader of the Northeast Performance Breeders Angus Sale, which just completed its' 20th anniversary event.

The Alabama Beef Cattle Improvement Association is proud to nominate Hillside Angus Farm.

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

"Conserve the land for the future generations, keep current and knowledgeable on the leading cattle issues, high quality cattle for a fair price, and treat people with honesty and integrity." The Charles Hunt Family operation began in the 1960s after Charlie attended the University of Nebraska. With a love for God, family, the land, and cattle Charlie and Nancy were ready for the opportunity to do then what they still enjoy doing today, over 56 years later, raising cattle. Currently, the 6,500 acre diversified operation consists of dryland and irrigated corn, soybeans, alfalfa, wheat and grass land which supports 300 cows, private treaty bulls, and replacement females. Genetics have been placed all over the globe, including Canada, Mexico, Australia and New Zealand. Bulls have been on display at the National Western Stock Show for the past 32 years and the Hunts have attended many BIF, NCBA, and numerous other Ag conferences. Charlie has been the recipient of many awards including the first ever Commercial Marketing Supporter Award from the North American Limousin Foundation. One of their most prestigious awards was being inducted into the Nebraska Cattlemen's Hall of Fame.

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

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

Hunt Limousin Ranch is proudly nominated by the Nebraska Cattlemen.

Seedstock Producer Award Nominees

Suhn Cattle Company
Owners/Managers: Vernon and Vicki Suhn
Eureka, Kansas

Vernon Suhn was raised on a large commercial operation in South Dakota where they incorporated some of the first large scale use of AI and utilized several of the continental breeds upon their introductions in the 70s. From there they went on to manage purebred Angus operations for Ankony Shadow Isle in California and Loos Angus in Nebraska. In 1980, Vicki and Vernon moved to Texas and went to work as operation manager for Brinks Brangus. While at Brinks Brangus, Vernon was instrumental in establishing a bull development program from which he started marketing bulls at 12 months of age and worked with Glenn Brinkman and K-State in developing ultrasound technology.

In 1990, Vernon and Vicki purchased their own place in the Flint Hills of Kansas near Eureka. What began with 15 head of Brangus and Angus females has grown to 350 Brangus and Ultrablack females. The majority of their growth has been through the genetics of six cow families and utilizing an extensive AI and embryo transplant program. They employ both a spring- and fall-calving season to best utilize their combination of native bluestem and fescue grasses.

From their beginning, they established a bull development facility where they developed and merchandized not only their own bulls but also those of a select group of other smaller breeders. All bulls and females are ultrasound scanned as yearlings and in the past several years they have also incorporated parent verification and DNA technology in their evaluation process. 2017 will be their 24th bull sale and their eighth sale under the GENETRUST Marketing Alliance, which they helped form in 2009 and Vernon served as president of and has grown to currently rank number fifteen in Beef Magazine's top 100 seedstock producers.

The International Brangus Breeders Association is proud to nominate Suhn Cattle Company.

Waukaru Farms
Owners: Barry & Anita, Mark & Heidi, and Toby & Jodi Jordan
Manager: Toby Jordan
Rensselaer, Indiana

Waukaru Farms Inc., a diversified family farming operation in Northwest Indiana, began using registered Shorthorn bulls in 1902. From the early 1900s - 1940s three breeds of cattle (Angus, Hereford, and Shorthorn) grazed the sandhills and marsh ground at Waukaru. Today our Waukaru herd consists of 200 Shorthorn females calving in the spring, another 50 in the fall, and 1,300 acres of corn. The top 50% of the bulls sell through the annual bull sale in March; ownership is retained on steers and carcass data collected. In September, Waukaru holds the longest running female sale in the breed.
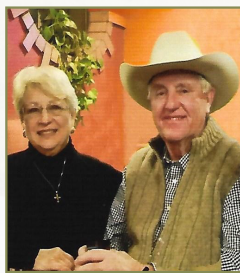
Waukaru, a Shorthorn breed leader in data submission, began performance testing and collecting carcass data in 1960. The 1970s brought wide use of artificial insemination and then non-surgical embryo transfer. Data from a multitude of environments across the US and Australia is used in structured progeny tests since the 1980s. Waukaru was involved in the discovery and validation of tests for genetic defects, de-worming products, fescue tolerance, Johne's disease eradication programs, timed AI systems, and carcass tenderness, in cooperation with MARC, Purdue University, Oklahoma State University, University of Illinois, Iowa State University, and Kansas State University among others. Performance and carcass data collected at Waukaru since the 1960s was important in the development of the breed's first sire summary. Today Waukaru includes DNA submission for GE-EPDs as vital technologies. Waukaru genetics can be found in 40 of the 50 U.S. states, Canada, Argentina, Brazil, Uruguay, Australia, New Zealand, England, Ireland, South Africa, and China.

Waukaru Farms is proudly nominated by the American Shorthorn Association.

BIF Seedstock Producer of the Year

Name	State	Year
Shaw Cattle Company	Idaho	2016
McCurry Angus Ranch	Kansas	2015
Schuler Red Angus	Nebraska	2014
Bradley 3 Ranch	Texas	2013
V8 Ranch	Texas	2012
Mushrush Red Angus	Kansas	2011
Sandhill Farms	Kansas	2010
Harrell Hereford Ranch	Oregon	2009
Champion Hill	Ohio	2009
TC Ranch	Nebraska	2008
Pelton Simmental Red Angus	Kansas	2007
Sauk Valley Angus	Illinois	2006
Rishel Angus	Nebraska	2005
Camp Cooley Ranch	Texas	2004
Moser Ranch	Kansas	2003
Circle A Ranch	Missouri	2002
Sydenstricker Genetics	Missouri	2001
Fink Beef Genetics	Kansas	2000
Morven Farms	Virginia	1999
Knoll Crest Farms	Virginia	1998
Flying H Genetics	Nebraska	1998
Wehrmann Angus Ranch	Virginia	1997
Bob & Gloria Thomas	Oregon	1997
Frank Felton	Missouri	1996
Tom & Carolyn Perrier	Kansas	1995
Richard Janssen	Kansas	1994
R.A. "Rob" Brown	Texas	1993
J. David Nichols	Iowa	1993
Leonard Wulf & Sons	Minnesota	1992
Summitcrest Farms	Ohio	1991
Douglas & Molly Hoff	South Dakota	1990
Glynn Debter	Alabama	1989
W.T. "Bill" Bennett	Washington	1988
Henry Gardiner	Kansas	1987
Leonard Lodoen	North Dakota	1986
Ric Hoyt	Oregon	1985
Lee Nichols	Iowa	1984
Bill Borror	California	1983
A.F. "Frankie" Flint	New Mexico	1982
Bob Dickinson	Kansas	1981
Bill Wolfe	Oregon	1980
Jim Wolf	Nebraska	1979
James D. Bennett	Virginia	1978
Glenn Burrows	New Mexico	1977
Jorgenson Brothers	South Dakota	1976
Leslie J. Holden	Montana	1975
Jack Cooper	Montana	1975
Carlton Corbin	Oklahoma	1974
Mrs. R. W. Jones, Jr.	Georgia	1973
John Crowe	California	1972

BIF Ambassador Award Recipients

Name	Publication	State	Year
Bob Hough	Freelance writer	Colorado	2016
E. C. Larkin	Gulf Coast Cattlemen	Texas	2015
John Maday	Drovers CattleNetwork	Colorado	2014
A.J. Smith	Oklahoma Cowman Magazine	Oklahoma	2013
Burt Rutherford	BEEF Magazine	Texas	2012
Jay Carlson	BEEF Magazine	Kansas	2011
Larry Atzenweiler	Missouri Beef Cattlemen	Missouri	2010
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

BIF Pioneer Award

2016
Doug Hixon, University of Wyoming
Ronnie Green, University of Nebraska
Bill Rishel, Rishel Angus

2015
Paul Genho, Florida
Tom Woodward, Texas

2014
Merlyn Nielsen, Nebraska
Gary Bennett, Nebraska
Steve Radakovich, Iowa

2013
Keith Bertrand, Georgia
Ignacy Misztal, Georgia
Glenn Selk, Oklahoma

2012
Sally Buxkemper, Texas
Donald Franke, Louisiana
Leo McDonnell, Montana

2011
Mike Tess, Montana
Mike MacNeil, Montana
Jerry Lipsey, Montana

2010
Richard McClung, Virginia
John and Bettie Rotert, Missouri
Daryl Strohbehn, Iowa
Glen Klippenstein, Missouri

2009
Bruce Golden, California
Bruce Orvis, California
Roy McPhee (posthumously), California

2008
Donald Vaniman, Montana
Louis Latimer, Canada
Harry Haney, Canada
Bob Church, Canada

2007
Rob Brown, Texas
David and Emma Danciger, Colorado
Jim Gosey, Nebraska

2006
John Brethour, Kansas
Harlan & Dorotheann Rogers, Mississippi
Dave Pingrey, Mississippi

2005
Jack and Gini Chase, Wyoming
Jack Cooper, Montana
Dale Davis, Montana
Les Holden, Montana
Don Kress, Montana

2004
Frank Felton, Missouri
Tom Jenkins, Nebraska
Joe Minyard, South Dakota

2003
George Chiga, Oklahoma
Burke Healey, Oklahoma
Keith Zoellner, Kansas

2002
H.H. "Hop" Dickenson, Kansas
Martin & Mary Jorgensen, South Dakota
L. Dale Van Vleck, Nebraska

2001
Larry Benyshek, Georgia
Minnie Lou Bradley, Texas
Tom Cartwright, Texas

2000
PJ. David Nichols, Iowa
Harlan Ritchie, Michigan
Robert R. Schalles, Kansas

1999
Joseph Graham, Virginia
John Pollak, New York
Richard Quaas, New York

1998
John Crouch, Missouri
Bob Dickinson, Kansas
Douglas MacKenzie Fraser, Canada

1997
Larry V. Cundiff, Nebraska
Henry Gardiner, Kansas
Jim Leachman, Montana

1996
A.L. "Ike" Eller, Virginia
Glynn Debter, Alabama

1995
James S. Brinks, Colorado
Robert E. Taylor, Colorado

1994
Tom Chrystal, Iowa
Robert C. DeBaca, Iowa
Roy A. Wallace, Ohio

1993
James D. Bennett, Virginia
M.K. "Curly" Cook, Georgia
O'Dell G. Daniel, Georgia
Hayes Gregory, North Carolina
Dixon Hubbard, Virginia
James W. "Pete" Patterson, North Dakota
Richard Willham, Iowa

1992
Frank Baker, Arkansas
Ron Baker, Oregon
Bill Borror, California
Walter Rowden, Arkansas

1991
Bill Long, Texas
Bill Turner, Texas

1990
Donn & Sylvia Mitchell, Canada
Hoon Song, Canada
Jim Wilton, Canada

1989
Roy Beeby, Oklahoma
Will Butts, Tennessee
John W. Massey, Missouri

1988
Christian A. Dinkle, South Dakota
George F. & Mattie Ellis, New Mexico
A.F. "Frankie" Flint, New Mexico

1987
Glenn Burrows, New Mexico
Carlton Corbin, Oklahoma
Murray Corbin, Oklahoma
Max Deets, Kansas

1986
Charles R. Henderson, New York
Everett J. Warwick, Maryland

1985
Mick Crandell, South Dakota
Mel Kirkiede, North Dakota

1984
Bill Graham, Georgia
Max Hammond, Florida
Thomas J. Marlowe, Virginia

1983
Jim Elings, California
W. Dean Frischknecht, Oregon
Ben Kettle, Colorado
Jim Sanders, Nevada
Carroll O. Schoonover, Wyoming

1982
Gordon Dickerson, Nebraska
Mr. & Mrs. Percy Powers, Texas

1981
F.R. "Ferry" Carpenter, Colorado
Otha Grimes, Oklahoma
Milton England, Texas
L.A. Maddox, Jr., Texas
Charles Pratt, Oklahoma
Clyde Reed, Oklahoma

1980
Richard T. "Scotty" Clark, Colorado
Bryon L. Southwell, Georgia

1979
Robert Koch, Nebraska
Mr. & Mrs. Carl Roubicek, Arizona
Joseph J. Urick, Montana

1978
James B. Lingle, Maryland
R. Henry Mathiessen, Virginia
Bob Priode, Virginia

1977
Ralph Bogart, Oregon
Henry Holsman, South Dakota
Marvin Koger, Florida
John Lasley, Missouri
W. L. McCormick, Georgia
Paul Orcutt, Montana
J.P. Smith, Missouri
H.H. Stonaker, Colorado

1976
Forrest Bassford, Colorado
Doyle Chambers, Louisiana
Mrs. Waldo Emerson Forbes, Wyoming
C. Curtis Mast, Virginia

1975
Glenn Butts, Missouri
Keith Gregory, Nebraska
Braford Knapp, Jr., Montana

1974
Reuben Albaugh, California
Charles E. Bell, Jr., Virginia
John H. Knox, New Mexico
Paul Pattengale, Colorado
Fred Wilson, Montana
Ray Woodward, Montana

1973
Jay L. Lush, Iowa

BIF Continuing Service Award

Name	Orgainzation/State	Year	Name	Orgainzation/State	Year
John Pollak	U.S. MARC	2016	Gary Johnson	Kansas	1999
Alison Van Eenennaam	UC - Davis	2016	Norman Vincil	Virginia	1999
Alison Sunstrum	GrowSafe	2016	Keith Bertrand	Georgia	1998
Steve Kachman	University of Nebraska-Lincoln	2016	Richard Gilbert	Texas	1998
Joe Cassady	South Dakota State University	2015	Burke Healey	Oklahoma	1998
Andy Boston	Indiana	2015	Glenn Brinkman	Texas	1997
Lois Schreiner	Kansas State University	2015	Russell Danielson	North Dakota	1997
Chris Shivers	American Brahman Breeders Assn.	2015	Gene Rouse	Iowa	1997
Larry Kuehn	US MARC	2014	Doug L. Hixon	Wyoming	1996
Wade Shafer	American Simmental Assn.	2014	Harlan D. Ritchie	Michigan	1996
Warren Snelling	US MARC	2014	Paul Bennett	Virginia	1995
Susan Willmon	American Gelbvieh Association	2014	Pat Goggins	Montana	1995
Ben Eggers	Sydenstricker Genetics	2013	Brian Pogue	Canada	1995
Brian House	Select Sires	2013	Bruce E. Cunningham	Montana	1994
Lauren Hyde	American Simmental Assn.	2013	Loren Jackson	Texas	1994
Jerry Taylor	University of Missouri	2013	Marvin D. Nichols	Iowa	1994
Jack Ward	American Hereford Association	2013	Steve Radakovich	Iowa	1994
Tom Field	Nebraska	2012	Doyle Wilson	Iowa	1994
Stephen Hammack	Texas	2012	Robert McGuire	Alabama	1993
Brian McCulloh	Wisconsin	2012	Charles McPeake	Georgia	1993
Larry Olson	South Carolina	2012	Henry W. Webster	South Carolina	1993
Tommy Brown	Alabama	2011	Jack Chase	Wyoming	1992
Mark Enns	Colorado	2011	Leonard Wulf	Minnesota	1992
Joe Paschal	Texas	2011	John Crouch	Missouri	1991
Marty Ropp	Montana	2011	Robert Dickinson	Kansas	1990
Bob Weaber	Missouri	2011	Roger McCraw	North Carolina	1989
Bill Bowman	Missouri	2010	Bruce Howard	Canada	1988
Twig Marston	Nebraska	2010	Bill Borror	California	1987
David Patterson	Missouri	2010	Jim Gibb	Missouri	1987
Mike Tess	Montana	2010	Daryl Strohbehn	Iowa	1987
Darrh Bullock	Kentucky	2009	Larry Benyshek	Georgia	1986
Dave Daley	California	2009	Ken W. Ellis	California	1986
Renee Lloyd	Iowa	2009	Earl Peterson	Montana	1986
Mark Thallman	Nebraska	2009	Jim Glenn	IBIA	1985
Doug Fee	Canada	2008	Dick Spader	Missouri	1985
Dale Kelly	Canada	2008	Roy Wallace	Ohio	1985
Duncan Porteous	Canada	2008	James Bennett	Virginia	1984
Craig Huffhines	Missouri	2007	M.K. Cook	Georgia	1984
Sally Northcutt	Missouri	2007	Craig Ludwig	Missouri	1984
Jimmy Holliman	Alabama	2006	Art Linton	Montana	1983
Lisa Kriese-Anderson	Alabama	2006	J.D. Mankin	Idaho	1982
Dave Notter	Ohio	2006	Mark Keffeler	South Dakota	1981
Jerry Lipsey	Montana	2005	Glenn Butts	PRI	1980
Micheal MacNeil	Montana	2005	Jim Gosey	Nebraska	1980
Terry O'Neill	Montana	2005	C.K. Allen	Missouri	1979
Robert Williams	Missouri	2005	William Durfey	NAAB	1979
Chris Christensen	South Dakota	2004	James S. Brinks	Colorado	1978
Robert "Bob" Hough	Texas	2004	Martin Jorgensen	South Dakota	1978
Steven M. Kappes	Nebraska	2004	Paul D. Miller	Wisconsin	1978
Richard McClung	Virginia	2004	Lloyd Schmitt	Montana	1977
Sherry Doubet	Colorado	2003	Don Vaniman	Montana	1977
Ronnie Green	Virginia	2003	A.L. Eller, Jr.	Virginia	1976
Connee Quinn	Nebraska	2003	Ray Meyer	South Dakota	1976
Ronnie Silcox	Georgia	2003	Larry V. Cundiff	Nebraska	1975
S.R. Evans	Mississippi	2002	Dixon D. Hubbard	Washington, DC	1975
Galen Fink	Kansas	2002	J. David Nichols	Iowa	1975
Bill Hohenboken	Virginia	2002	Frank H. Baker	Oklahoma	1974
William Altenburg	Colorado	2001	D.D. Bennett	Oregon	1974
Kent Andersen	Colorado	2001	Richard Willham	Iowa	1974
Don Boggs	South Dakota	2001	F. R. Carpenter	Colorado	1973
Ron Bolze	Kansas	2000	Robert DeBaca	Iowa	1973
Jed Dillard	Florida	2000	E.J. Warwick	Washington, DC	1973
Bruce Golden	Colorado	1999	Clarence Burch	Oklahoma	1972
John Hough	Georgia	1999			

Baker / Cundiff Award
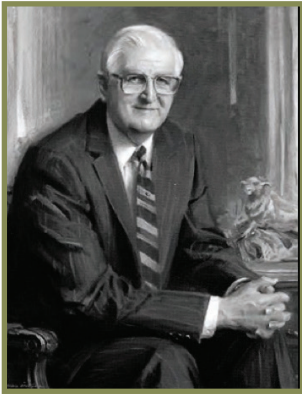
Frank H. Baker 1923-1993
(Photograph of portrait in Saddle and Sirloin Club Gallery; Everett Raymond Kinstler, artist)

Dr. Frank H. Baker is widely recognized as the "Founding Father" of the Beef Improvement Federation (BIF). Frank played a key leadership role in helping establish BIF in 1968, while he was Animal Science Department Chairman at the University of Nebraska, Lincoln, 1966-74. The Frank Baker Memorial Scholarship Award Essay competition for graduate students provides an opportunity to recognize outstanding student research and competitive writing in honor of Dr. Baker.

Frank H. Baker was born May 2, 1923, at Stroud, Oklahoma, and was reared on a farm in northeastern Oklahoma. He received his B.S. degree, with distinction, in Animal Husbandry from Oklahoma State University (OSU) in 1947, after two and a half years of military service with the US Army as a paratrooper in Europe, for which he was awarded the Purple Heart. After serving three years as county extension agent and veterans agriculture instructor in Oklahoma, Frank returned to OSU to complete his M.S. and Ph.D. degrees in Animal Nutrition. Frank's professional positions included teaching and research positions at Kansas State University, 1953-55; the University of Kentucky, 1955-58; Extension Livestock Specialist at OSU, 1958-62; and Extension Animal Science Programs Coordinator, USDA, Washington, D.C., 1962-66. Frank left Nebraska in 1974 to become Dean of Agriculture at Oklahoma State University, a position he held until 1979, when he began service as International Agricultural Programs Officer and Professor of Animal Science at OSU. Frank joined Winrock International, Morrilton, Arkansas, in 1981, as Senior Program Officer and Director of the International Stockmen's School, where he remained until his retirement. Frank served on advisory committees for Angus, Hereford, and Polled Hereford beef breed associations, the National Cattlemen's Association, Performance Registry International, and the Livestock Conservation, Inc.

His service and leadership to the American Society of Animal Science (ASAS) included many committees, election as vice president and as president, 1973-74. Frank was elected an ASAS Honorary Fellow in 1977, he was a Fellow of the American Association for the Advancement of Science, and served the Council for Agricultural Science and Technology (CAST) as president in 1979. Frank Baker received many awards in his career, crowned by having his portrait hung in the Saddle and Sirloin Club Gallery at the International Livestock Exposition, Louisville, Kentucky, on November 16, 1986. His ability as a statesman and diplomat many awards in his career, crowned by having his portrait hung in the Saddle and Sirloin Club Gallery at the International Livestock Exposition, Louisville, Kentucky, on November 16, 1986. His ability as a statesman and diplomat for the livestock industry was to use his vision to call forth the collective best from all those around him. Frank was a "mover and shaker" who was skillful in turning "Ideas into Action" in the beef cattle performance movement. His unique leadership abilities earned him great respect among breeders and scientists alike. Frank died February 15, 1993, in Little Rock, Arkansas.

Larry Cundiff
(Photograph taken at BIF 2014, by Angus Journal)

Dr. Larry Cundiff retired in January 2007 after 40 years of service as a Research Geneticist with the U.S. Department of Agriculture, Agricultural Research Service. He was Research Leader of the Genetics and Breeding Research Unit at the U.S. Meat Animal Research Center from 1976 until 2005, when he accepted an interim eight-month appointment as Acting Center Director.

Larry Cundiff was born in Kansas in 1939, received his B.S. from Kansas State University in 1961, his M.S. and Ph.D. from Oklahoma State in 1964 and 1966. He married his wife, Laura, in 1960. They have three children. He was on the faculty at the University of Kentucky from 1965 to 1967, before working as a research geneticist in the USDA.

Cundiff has not only designed, conducted and published some of the most important beef breeding research of the 20th century, but also has lead in the transfer of new technology to the beef industry through his continued work in BIF and his presentations made across the nation and around the world.

His research efforts have involved evaluation and utilization diverse breeds, effects and utilization of heterosis through alternative crossbreeding systems, and evaluation and effectiveness of selection for traits of economic importance in beef production. Since his retirement, he has continued service as a collaborator at the U.S. Meat Animal Research Center assisting with preparation of research reports and speaking at beef industry meetings and conferences. Dr. Cundiff has served as chairman of the Beef Improvement Federation (BIF) Committee on Genetic Prediction from 1973 until 2007, and as the Agricultural Research Service, USDA representative on the BIF Board of Directors from 1981 until 2007. He has served as editor of the Beef Improvement Federation's 9th Edition of Guidelines for Uniform Beef Improvement Programs.

Past Recipients

Name	University	Year
Kathleen Ochsner	University of Nebraska-Lincoln	2016
Kashly Schweer	University of Nebraska-Lincoln	2016
Justin Buchanan	Oklahoma State University	2015
Jamie Parham	South Dakota State University	2015
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 & 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.

Roy loved what BIF stood for – an organization that brings together purebred and commercial cattle breeders, academia and breed associations, all committed to improving beef cattle. Wallace was honored with both the BIF Pioneer Award and BIF Continuing Service Award and co-authored the BIF 25-year history, Ideas into Action. This scholarship was established to encourage young men and women interested in beef cattle improvement to pursue those interests as Mr. Wallace did, with dedication and passion.

Proceeds from the Roy A. Wallace Beef Improvement Federation Memorial Fund will be used to award scholarships to graduate and undergraduate students currently enrolled as fulltime students in pursuit of a degree related to the beef cattle industry. Criteria for selection will include demonstrated commitment and service to the beef cattle industry. Preference will be given to students who have demonstrated a passion for the areas of beef breeding, genetics, and reproduction. Additional considerations will include academic performance, personal character, and service to the beef cattle industry.

Two scholarships will be offered in the amount of $1,250 each. One will be awarded to a student currently enrolled as an undergraduate and one will be awarded to a student currently enrolled in a master of science or doctoral program.

2017 Recipients

Graduate: Dustin Aherin, Kansas State University
Undergraduate: Tanner Aherin, Kansas State University

Past Recipients

Name	University	Year
Will Shaffer (graduate)	Oklahoma State University	2016
Ryan Boldt (undergraduate)	Colorado State University	2016
Joshua Hasty (graduate)	Colorado State University	2015
Matthew McIntosh (undergraduate)	University of Connecticut	2015
Heather Bradford (graduate)	Kansas State University	2014
Maci Lienemann (undergraduate)	University of Nebraska-Lincoln	2014
Loni Woolley (graduate)	Texas Tech	2013
Tyler Schultz (undergraduate)	Kansas State University	2013
Ky Polher (graduate)	University of Missouri	2012
Natalie Laubner (undergraduate)	Kansas State University	2012
Jessica Bussard (graduate)	University of Kentucky	2011
Cassandra Kniebel (undergraduate)	Kansas State University	2011
Paige Johnson (graduate)	Texas Tech University	2010
Sally Ruth Yon (undergraduate)	South Carolina	2010

2016-2017 *Board of Directors*

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303-884-3900 (C)
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816-261-1490 (C)
dMoser@angus.org

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417-860-6757 (C)
tperkins@gobrangus.com

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713-349-9795 (F)
cshivers@brahman.org

Jack Ward
American Hereford Association
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Kansas City, MO 64101
816-842-3757 (O)
816-842-6931 (F)
jward@hereford.org

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605-439-3100 (F)
605-216-8169 (C)
craig@bieberredangus.com
Also serves as ***Past President**

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12227 Mystic Hill Lane
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540-937-0029 (C)
cattleclark@gmail.com

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Woodville, VA 22749
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Leachman Cattle of Colorado
2056 West CR70
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970-219-8519 (C)
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Strong City, KS 66849
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620-340-7461 (C)
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mattperrier@dalebanks.com

Others

NCBA Representative
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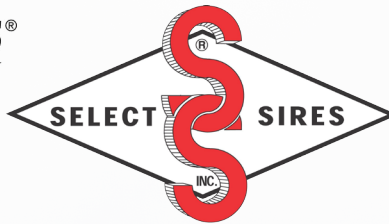
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Notes

Tour

Gretsch Brothers Angus

Fred and Anne Gretsch are first generation cattle ranchers. Their family operation began in 1988 with commercial cattle while working public jobs. By 2000 Fred and Anne's sole income came from their farming operations including poultry, hogs, timber, hay, and cattle. In 2007, the operation began to use embryo transfer to transition to a registered Angus operation. During the development of their Angus business the Gretsch family used consignment sales and worked as a cooperator herd for a larger more established Angus operation to market their bulls and females. In 2013 Fred and Anne held their first Bull and Commercial female sale marketing 35 bulls and 50 commercial females, and in January of 2017 they marketed over 100 bulls and close to 100 commercial females. This October 21st GBA will hold its second registered female and 2-year-old bull sale.

Living in Oglethorpe County they are considered to be in the Piedmont region of the state. The Gretsch operation consists of approximately 500 acres of owned land and 1000 acres of rented farms all located in Oglethorpe County. The Gretsch family has approximately 250 registered females including 50 replacement heifers and works with 4 recipient herds and 4 cooperators. Fred has served at the state and local level of the Georgia Cattlemen's Association. Fred is an active board member for the Georgia Angus Association. With proximity to UGA, many college interns have worked with the Gretsch family and have moved on to Veterinarian, Animal Science, and Ag Education as careers. "We love what we do and we are constantly trying to learn new and better ways to do things!" Fred Gretsch says. "We would like to thank everyone that has helped us along our journey, and we hope that we can pass that knowledge along."

Partisover Ranch

Dr. Dan Daniel and son Randy Daniel founded Partisover Ranch in 1970 located in Colbert, GA. "Dr. Dan" moved his family from Oklahoma to Georgia to lead the University of Georgia's Department of Animal Science Extension Program in 1958. By his 1981 retirement as Animal Science Department Head and Division Chairman, he had succeeded in building a nationally renowned beef cattle performance program as well as Georgia's successful youth livestock program. In 2001, Dr. Dan was inducted into the prestigious Saddle and Sirloin Club. His portrait is displayed at the Kentucky State Fair & Exposition Center in Louisville, KY.

Partisover Ranch started with the purchase of a small, select group of heifers from Spur Ranch in Oklahoma. From that purchase grew the Partisover Burgess and Partisover Witch families that are seen in many popular performance pedigrees today. As breed priorities shifted over time, Partisover remained a consistent source for maternally driven, functional females with balanced EPDs. In order to complement their proven Angus genetics, Partisover began to search for elite Simmental herd sires. This quest led to the acquisition of Macho, Mo Magic and Upgrade who have each proven to be valuable assets and have taken their program to the next level. The cattle operation has also produced industry leading genetics in the Gelbvieh breed. Currently, expansion of the Angus herd is underway. ET and AI calves will be 90 percent of the fall calving herd. To date the majority of the bull calves go to Stucky Ranch in Kansas. The mission of the ranch has been to produce practical cattle that cover as many business basics as possible for maximum output from minimum inputs. Selling profit orientated bulls and females to seedstock and commercial producers alike are the backbone to the program. Combining their passion for the youth program, they are happiest when they can provide young people with highly competitive show heifers that go on to be valuable and productive cows. Randy and wife, Beth, have two children. Their son Buck and wife Jenna have a son. Their daughter and son in-law Adam are due with their first child this summer. Partisover Ranch welcomes BIF participants and appreciates being included in the tour program.

Innisfail Farm

Innisfail Farm is a Registered Hereford operation located in Madison, GA and is owned by Whitey and Weyman Hunt. The first registered Herefords at Innisfail arrived in the early 70's and were purchased to test the waters. They fit so well, the herd was expanded. Today they breed around 200 females and implant around 100 embryos for cooperator herds. All females are AI'd once and then exposed to the best Hereford bulls they can get their hands on. Innisfail's cleanup bulls are a combination of in-herd genetics and purchases from some of the top breeders in the US. All females are retained through their first breeding season before they select the sale groups. Innisfail Farm tries to accelerate their genetic progress by keeping their cow herd young. With the exception of a handful of donors, all the cows are sold by the time they reach 7 years.

Most of the cattle are marketed private treaty and include around 75 females and 35 bulls. The balance of the bull crop is steered and sent to feed yards in Iowa where they retain ownership and collect carcass data. This "real-world" data is combined with 25+ years of ultrasound data to select genetics that excel in carcass merit. The average cow will be around 5 times breed average in Marbling while maintaining 1.5 times breed average on REA. Their main customers will be commercial cattlemen in the Southeast but more and more of their genetics are sought after by registered breeders across the country. Over the last 40+ years they have been selecting for performance cattle with great maternal qualities that excel in their environment. These animals will be in the top end of the breed for all their EPD's and will have the phenotype to match. For more information please visit their web site at www.innisfailfarm.com or visit them on Facebook or Instagram. See you at the farm.
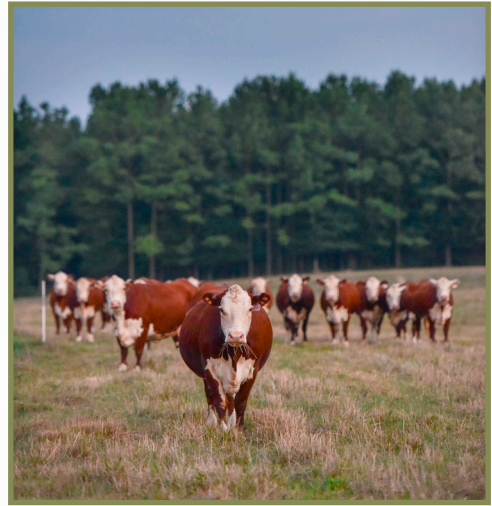
2016 *Winners*

2016 Commercial Producer of the Year Winners
Plum Thicket Farms, Nebraska

2016 Seedstock Producer of the Year Winners
Shaw Cattle Company, Idaho

2016 BIF Ambassador Award Winner
Bob Hough, Freelance Writer, Colorado

2016 Baker/Cundiff Award Winners
Kathleen Ochsner, University of Nebraska-Lincoln and
Kashly Schweer, University of Nebraska-Lincoln

2016 Wallace Memorial Scholarship - Undergraduate
Ryan Boldt, Colorado State University

2016 Wallace Memorial Scholarship - Graduate
Will Shaffer, Oklahoma State University

2016 *Winners*

Doug Hixon, University of Wyoming

2016 BIF Pioneer Award Winners
Ronnie Green, University of Nebraska

Bill Rishel, Rishel Angus

John Pollak, U.S. MARC

2016 BIF Continuing Service Award Winners
Alison Van Eenennaam, U.C. - Davis

Alison Sunstrum, GrowSafe

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The Promise of Genomics for Beef Improvement

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Long before genomics found its way into livestock breeding, most of the excitement pertaining to research into livestock improvement via selection involved developments in the BLUP mixed model equations, methods to construct the inverse of the pedigree relationship matrix recursively (Henderson, 1976; Quaas, 1988), parameter estimation and development of new, measureable traits of economic importance. In particular for several decades (1970's through the early 2000's), lots of resources were invested in finding the most useful evaluation model for various traits. Since the American Simmental Association published the first sire summary in 1971, the use of pedigree and phenotypic information has been the major contributing factor to the large amount of genetic progress in beef industry.

During the late 1970's and early 1980's, geneticists developed techniques that allowed the investigation of DNA, and they discovered several polymorphic markers in the genome. Soller and Beckmann (1983) described the possible uses of new discovered polymorphisms, and surprisingly, their vision of using markers was not much different than how DNA is used today in the genetic improvement of livestock. They surmised that markers would be beneficial in constructing more precise genetic relationships, followed by parentage determination, and the identification of quantitative trait loci (QTL; genes that affect a quantitative trait). The high cost of genotyping animals for such markers probably prevented the early widespread use of this technology. However, valuable information came along with the first draft of the Human genome project in 2001 (The International SNP Map Working Group, 2001): the majority of the genome sequence variation can be attributed to single nucleotide polymorphisms (SNP).

After all, what are SNPs? The genome is composed of 4 different nucleotides (A, C, T, and G). If you compare the DNA sequence from 2 individuals, there may be some positions were the nucleotides differ. The reality is that SNPs have become the bread-and-butter of DNA sequence variation (Stonecking, 2001) and they are now an important tool to determine the genetic potential of livestock. Even though several other types of DNA markers have been discovered

(e.g., microsatellites, RFLP, AFLP) SNPs have become the main marker used to detect variation in the DNA. Why is this so? An important reason is that SNPs are abundant, as they are found throughout the entire genome (Schork et al., 2000). There are about 3 billion nucleotides in the bovine genome, and there are over 30 million SNPs or 1 every 100 nucleotides is a SNP. Another reason is the location in the DNA: they are found in introns, exons, promoters, enhancers, or intergenic regions. In addition, SNPs are now cheap and easy to genotype in an automated, high-throughput manner because they are binary.

One of the benefits of marker genotyping is the detection of genes that affect traits of importance. The main idea of using SNPs in this task is that a SNP found to be associated with a trait phenotype is a proxy for a nearby gene or causative variant (i.e., a SNP that directly affects the trait). As many SNPs are present in the genome, the likelihood of having at least 1 SNP linked to a causative variant greatly increases, augmenting the chance of finding genes that actually contribute to genetic variation for the trait. This fact contributed to much initial excitement as labs and companies sought to develop genetic tests or profiles of DNA that were associated with genetic differences between animals for important traits. Suddenly, marker assisted selection (MAS) became popular. The promise of MAS was that since the test or the profile appeared to contain genes that directly affect the trait, then potentially great genetic improvement could be realized with the selection of parents that had the desired marker profile. It is not hard to see this would work very well for traits affected by one or a couple of genes. In fact, several genes were identified in cattle, including the myostatin gene located on chromosome 2. When 2 copies of the loss-of-function mutation are present, the excessive muscle hypertrophy is observed in some breeds, including Belgian Blue, Charolais, and Piedmontese (Andersson, 2001). Another example of that has been shown to have a small, but appreciable effect on beef tenderness pertains to the Calpain and Calpastatin (Page et al., 2002) and a genetic test was commercialized by Neogen Genomics (GeneSeek, Lincoln, NE) and Zoetis (Kalamazoo, MI). It is important to notice that all those achievements were based on few SNPs or microsatellites because of still high genotyping costs.

Although there were a few applications in beef cattle breeding, MAS based on a few markers was not contributing appreciably to livestock improvement simply because most of the traits of interest are quantitative and complex, meaning phenotypes are determined by thousands of genes

with small effects and influenced by environmental factors. This goes back to the infinitesimal model assumed by Fisher (1918), where phenotypic variation is backed up by a large number of Mendelian factors with additive effects. Some lessons were certainly learned from the initial stab at MAS: some important genes or gene regions (quantitative trait loci or QTL) were detected; however, the same QTL were not always observed in replicated studies or in other populations, meaning most of them had small effects on the traits (Meuwissen et al., 2016). In addition, the number of QTL associated with a phenotype is rather subjective and depends on the threshold size of the effect used for identifying QTL (Andersson, 2001). Simply put, it appears there are only a few genes that contribute more than 1% of the genetic variation observed between animals for any given polygenic trait.

Initial allure of MAS led to a massive redirecting of grant funds to this type of research, greatly contributing to the current shortage of qualified quantitative geneticists in animal breeding (Misztal and Bertrand, 2008). Despite some of the initial setbacks using MAS, in 2001, some researchers envisioned that genomic information could still help animal breeders to generate more accurate breeding values, if a dense SNP assay that covers the entire genome became available. Extending the idea of incorporating marker information into BLUP (using genotypes, phenotypes and pedigree information), introduced by Fernando and Grossman (1989), Meuwissen et al. (2001) proposed some methods for what is now termed genome-wide selection or genomic selection (GS). This paper used simulation data to show that accuracy of selection was doubled using genomic selection compared to using only phenotypes and pedigree information. With the promise of large accuracy gains, this paper generated enormous excitement in the scientific community. Some conclusions from this study included: 1) using SNP information can help to increase genetic gain and to reduce the generation interval; 2) the biggest advantage of genomic selection would be for traits with low heritability; 3) animals can be selected early in life prior to performance or progeny testing. With all of this potential, genomic selection was an easy sell.

However, it took about 8 years from the publication of the Meuwissen et al. (2001) paper until the dense SNP assay required for genomic selection became available for cattle. Researchers from USDA, Illumina, University of Missouri, University of Maryland, and University of Alberta developed a SNP genotyping assay, allowing the genotyping of 54,001 SNP in the

bovine genome (Illumina Bovine50k v1; Illumina, San Diego, CA). The initial idea of this research was to use the SNP assay or chip for mapping disease genes and QTLs linked to various traits in cattle (Matukumalli et al., 2009). In 2009, a report about the first bovine genome entirely sequenced (The Bovine Genome Sequencing and Analysis Consortium et al., 2009) was published as an output of a project that cost over $50 million and involved about 300 researchers. With the cattle sequence known, it was possible to estimate the number of genes in the bovine genome: somewhere around 22,000. Armed with the tools to generate genomic information, GS became a reality.

Among all livestock industries in USA, the dairy industry was the first to use genomic selection. More than 30,000 Holstein cattle had been genotyped for more than 40k SNP by the end of 2009 (https://www.uscdcb.com/Genotype/cur_density.html). In January of 2009, researchers from AGIL-USDA released the first official genomic evaluation for Holstein and Jersey. Still in 2009, Angus Genetics Inc. started to run genomic evaluations, but with substantially fewer genotypes, which was also true for other livestock species. After the first validation exercises, the real gains in accuracy were far less than those promised in the paper of Meuwissen et al. (2001). This brought some uncertainties about the usefulness of GS that were later calmed by understanding that more animals should be genotyped to reap the full benefits of GS. VanRaden et al. (2009) showed an increase in accuracy of 20 points when using 3,576 genotyped bulls, opposed to 6 points when using 1,151 bulls. Now, in 2017, Holstein USA has almost 1.6 million (Figure 1) and the American Angus Association has more than 300,000 (Figure 2) genotyped animals.

When GS was first implemented for dairy breeding purposes, all the excitement was around one specific Holstein bull nicknamed Freddie (Badger-Bluff Fanny Freddie), which had no daughters with milking records in 2009 but was found to be the best young genotyped bull in the world (VanRaden, personal communication). In 2012 when his daughters started producing milk, his superiority was finally confirmed. Freddie's story is an example of what can be achieved with GS, as an animal with high genetic merit was identified earlier in life with greater accuracy. With the release of genomic predicted transmitting abilities or genomic enhanced expected progeny differences (GE-EPD), the race to genotype more animals started.
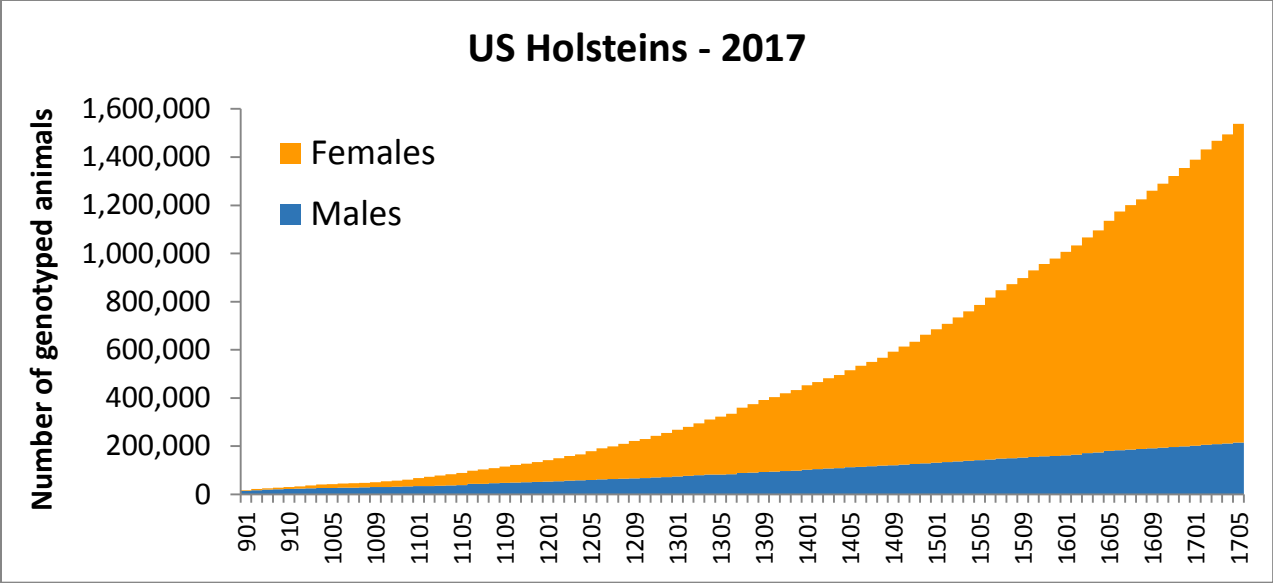
Figure 1. Number of genotyped US Holsteins over the years
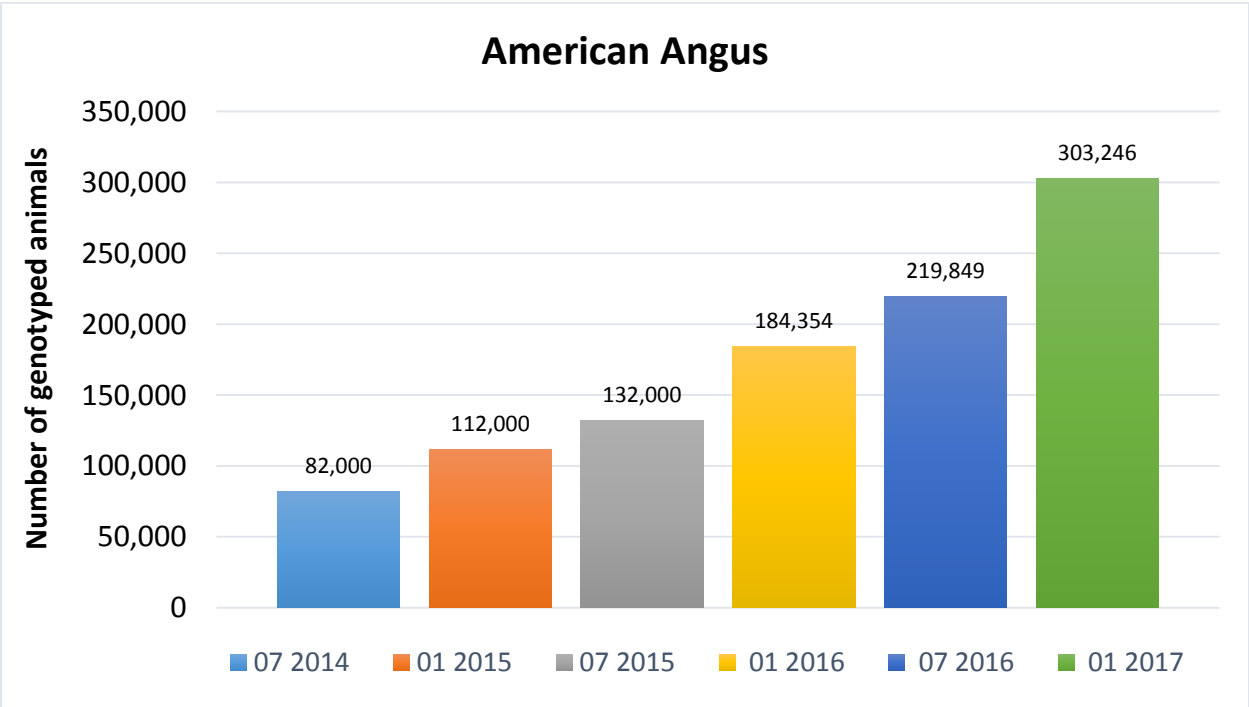(https://www.uscdcb.com/Genotype/cur_density.html)

Figure 2. Number of genotyped Angus over the years (AGI Inc., 2017)

The availability of more genotyped cattle drove the development of new methods to incorporate genomic information into national cattle evaluations. The first method was called multistep

(Figure 3), and as the name implied, this method required multiple analyses to have the final GE-EPDs. Distinct training and validation populations were needed to develop molecular breeding values (MBV), which were blended with traditional EPDs or included as correlated traits (Kachman et al., 2013). This multistep model was the first one to be implemented for genomic selection in the USA. Several studies examining the application of multistep in beef cattle evaluation have been published (Saatchi et al., 2011; Snelling et al., 2011). The main advantage of this approach is that the traditional BLUP evaluation is kept unchanged and genomic selection can be carried out by using additional analyses. However, this method has some disadvantages: a) MBV are only generated for simple models (i.e., single trait, non-maternal models), which is not the reality of genetic evaluations; b) it requires pseudo-phenotypes (EPDs adjusted for parent average and accuracy); c) pseudo-phenotypes rely on accuracy obtained via approximated algorithms, which may generate low quality output; d) only genotyped animals are included in the model; e) MBV may contain part of parent average, which leads to double counting of information.
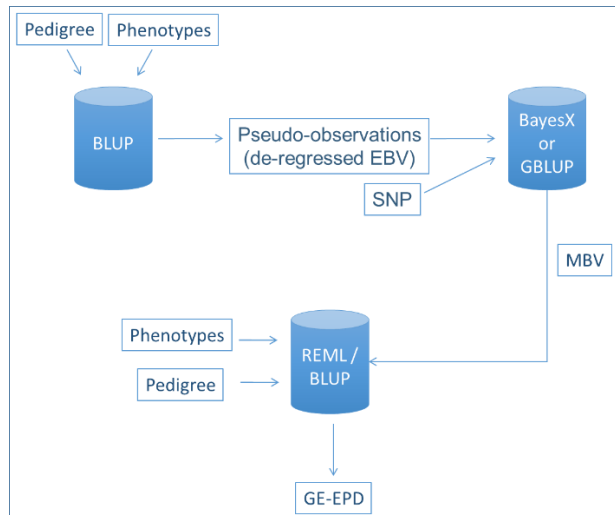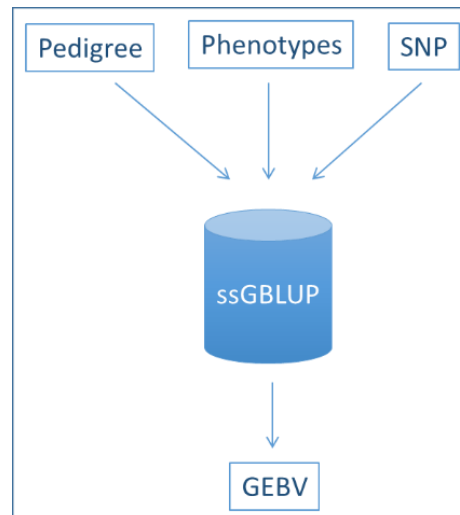

Figure 3. Multistep genomic evaluation

Figure 4. Single-step GBLUP

As only a fraction of livestock are genotyped, Misztal et al. (2009) proposed a method that combines phenotypes, pedigree, and genotypes in a single evaluation (Figure 4). This method is called single-step genomic BLUP (ssGBLUP) and involves altering the relationships between

animals based on the similarity of their genotypes. As an example, full-sibs have an average of 50% of their DNA in common, but in practice this may range from 20% to 70% (Lourenco et al., 2015a). ssGBLUP has some advantages over multistep methods. It can be used with multi-trait and maternal effect models, it avoids double counting of phenotypic and pedigree information, it ensures proper weighting of all sources of information, and it can be used with both small and large populations and with any amount of genotyped animals. Overall, greater accuracies can be expected when using ssGBLUP compared to multistep methods. Not long after the implementation of GS, single-step was first applied to a dairy population with more than 6,000 genotyped animals (Aguilar et al., 2010; Christensen and Lund, 2010).

An early application of ssGBLUP in beef cattle used simulated data with 1500 genotyped animals in an evaluation for weaning weight with direct and maternal effects (Lourenco et al., 2013). Although a small number of genotyped animals was used, gains in accuracy were observed for both direct and maternal weaning weight. Next ssGBLUP was applied to a real breed association data set (Lourenco et al., 2015b). This study showed a comprehensive genomic evaluation for nearly 52,000 genotyped Angus cattle, with a considerable gain in accuracy in predicting future performance for young genotyped animals. This gain was on average 4.5 points greater than the traditional evaluations; however, it was much lower than the 10-fold gain obtained by Meuwissen et al. (2001). Going back to their study, we observed that the number of genotyped animals was small (~2,000) and some of the QTL effects generated in their simulation model were very large, meaning few QTL were explaining nearly all the genetic variation. This is unrealistic for most of the traits of interest in livestock breeding, which we know are controlled by several, small effect QTL, as it is shown in Figure 5. The percentage of genetic variance explained by each one of the 54,000 SNP is in the Y-axis. Although we can see several peaks in this Manhattan plot, meaning there are lots of SNP associated with weaning weight, the variance one SNP explains alone is at maximum 0.7%.

More interesting than finding peaks of SNP in Manhattan plots, is that those peaks are seldom observed in the next generations. In addition, many peaks seem to capture population structure or effect of important ancestors instead of proper QTL effect. Fragomeni et al. (2014) investigated the top SNP windows explaining the genetic variance of 3 traits in broilers. Surprisingly, the peaks were not consistent across generations, meaning selection should not be performed based

on SNP regions, unless a large effect QTL is conclusively identified. Therefore again for polygenic traits that are influenced by many SNPs, where each SNP has a small effect, it is more practical to simply include a large number of SNPs in a genetic evaluation method, such as ssGBLUP, than trying to estimate SNPs directly and providing them separately.
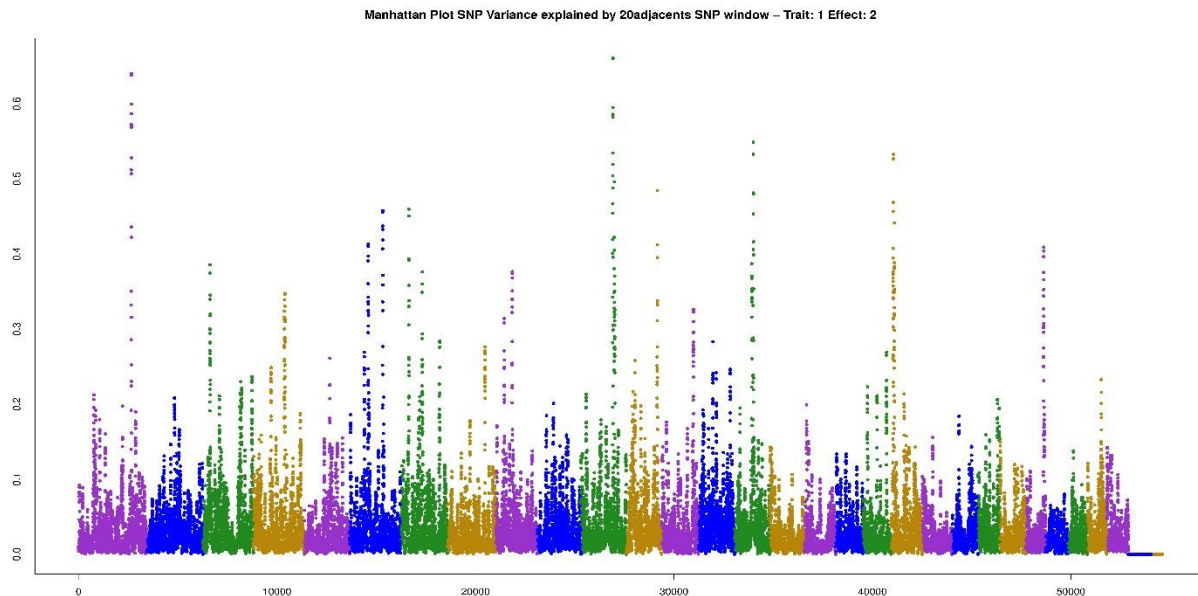

Figure 5. Manhattan plot for weaning weight in American Angus, using nearly 52,000 genotyped animals. Y-axis shows percentage of genetic variance explained by the SNP; X-axis has SNP number. Each chromosome is represent by different colors.

The American Angus Association has been using genomic information since 2009 in a multistep process that treats MBVs predicted from a separate data set as a correlated trait with the phenotypic data in the Angus data base. Now the beef industry has started moving to single-step. Organizations are now running or testing single-step using all types of models: single and multiple-trait, maternal effects, multi-breed using external EPDs, linear and categorical traits. The American Angus Association's official release of GE-EPD using ssGBLUP (using software developed at UGA; http://nce.ads.uga.edu/software) is scheduled for July 7, 2017. In the beginning of 2017, International Genetic Solutions (IGS) released the first GE-EPD from single-step in a single-trait, multi-breed evaluation for stayability using BOLT, a software developed by Theta Solutions (Bruce Golden and Dorian Garrick), and about 100,000 genotyped animals (http://simmental.org/site/index.php/component/k2/item/209-multi-breed-stayability-first-epds-

). The implementation of single-step for the IGS evaluation uses the approach developed by Rohan Fernando's group (see Fernando et al., 2014), although BOLT has also implemented the approach developed by Ignacy Misztal's group (see Aguilar et al., 2010). In terms of accuracy, GE-EPDs outperformed traditional EPDs in single-step or multistep approaches. Also, the two implementations of single-step (Misztal's approach or Fernando's approach) produce similar accuracies (Fernando et al., 2014). The higher accuracy delivered by single-step, the simplicity of the method, and the ability to work with virtually any number of genotyped animals is the responsible for the move towards single-step.

We can see the statement made in 2009 that "more animals should be genotyped if the objective is to get the full benefits of GS" is still currently in practice. Computationally speaking, prior to 2014 ssGBLUP could not be implemented for a data set with more than 150,000 genotyped animals because the genomic relationship matrix had to be created via inversion. Misztal et al. (2014) extended the algorithm to construct the inverse of the pedigree relationship matrix, proposed by Quaas (1988), to work for the construction of the inverse of the genomic relationship matrix. This method of constructing the inverse of the genomic relationship matrix is termed the "algorithm for proven and young" (APY) and enables implementation of ssGBLUP for millions of genotyped animals. Single-step with APY has been successfully implemented for 570,000 genotyped Holsteins in a practical analysis time (Masuda et al., 2016).

The idea of this method came from the fact that although millions of animals can be genotyped, the dimension of the genomic information is limited. In a statistical language, some genotyped animals are linearly independent (core) and some are linearly dependent (noncore) and the inverse is constructed directly only among the independent animals and the number of independent animals is relatively fixed no matter how many animals are genotyped. The genome of a particular animal contains large segments inherited from recent and earlier ancestors. In Angus, about 12,000 segments explain 100% of the genetic additive variance, with 3,000 largest segments explaining 90% of the variance (Pocrnic et al., 2016). When estimating SNP effects, we indirectly estimate effects of the segments, with many SNPs corresponding to one segment. This is why with two analyses using the same data but different methods for SNP estimation, SNP effects can be weakly correlated whereas EPDs are highly correlated. While 12,000

segments are hard to identify, 12,000 animals are likely to contain nearly all combinations of those segments.

Several studies have shown that including genomic information increases the accuracy of prediction particularly among young animals (Aguilar et al., 2010; Christensen and Lund, 2010; Lourenco et al., 2014; Lourenco et al., 2015b). This increase in accuracy at younger ages can also lead to greater numbers of young bulls selected, which reduces generation interval. So using genomic information helps to increase accuracy and to reduce generation interval, which were two early state benefits of including genotypic information in genetic evaluation programs. Another benefit of using genotypic information that was initially offered by some was once we know genotypes there would not be a need to collect phenotypes. If we are looking at the differences in DNA sequence that can contribute to phenotypic differences, the only way to do that is to have both SNP and phenotypes. Without SNP we cannot unravel the molecular basis of phenotypic diversity, and without phenotypes we cannot link the polymorphisms to this phenotypic diversity. If we go back to Figures 3 and 4, we can see that both single-step and multistep methods currently used for genomic selection need phenotypes. Consider the multistep approach. The training population needed genotypes and phenotypes to develop prediction equations, meaning both pieces of information are essential to GS. Several studies showed a decrease in accuracy of genomic predictions if phenotypes are not recorded for several generations (Muir, 2007; Wolc et al., 2011). So, it is important that phenotypes continue to be collected in every generation.

Among all the research that has been done in beef cattle genomics, there is one topic that remains unclear: multibreed evaluation. Different breeds are selected for different purposes and with different intensity; therefore, the allele frequencies and linkage disequilibrium are different. This makes the prediction of GE-EPD for a breed that is not included in the reference set (used to estimate SNP effects) challenging. Some authors reported low accuracy of predicting across beef cattle breeds using multistep methods (Kachman et al., 2013), and some reported reasonable accuracies when the breeds are only few generations apart (De Roos et al., 2009). In a study that involved predictions in Holsteins and Jerseys, better predictions for Jerseys after including the Holstein data (Harris and Johnson, 2010) could be due to the fact that important Jersey bulls are descendants of Holstein bulls. Since the number of segments per breed is small, the chip with

50,000 SNP has enough capacity to account for a few breeds at slightly low accuracy. A comprehensive approach for crossbred or multibreed genomic evaluation in beef, analogous to the traditional approach proposed by Legarra et al. (2007), is the use of metafounders (Legarra et al., 2015). Meuwissen et al. (2016) stated that having a greater number of SNP, which means reading about 30 million SNP in the cattle DNA, would help to better predict across breeds. This leads to another promise for the beef cattle industry: sequence data could help to increase accuracy and find causative variants in the genome. The 1,000 bull genomes consortium was created in 2012 with the objective to sequence 1,000 animals and more easily identify QTL for complex traits (Daetwyler et al., 2014). The project is still ongoing and the number of sequenced beef and dairy cattle is around 2.000. The use of sequence data is a big promise, although very small increase in accuracy was reported when moving from 50K to 777K SNP for genomic selection (VanRaden et al., 2011) or even when moving to 30 million SNP (actually ~ 3 million qualified SNP) (MacLeod et al., 2016). In a recent study, VanRaden et al. (2017) selected about 17,000 SNP that had higher effect on 34 dairy traits and included them in the 50K SNP data. The maximum increase in accuracy was 2.2 points for body depth, and the average gain for the 34 traits was 1.6 points. Maybe sequence data can help us to find true causative variants; however, the best use of these data is still unclear. Consequently, the race for finding the best use for this information has just started.

For the beef cattle industry, as well as the other livestock industries, some of the initial stated benefits associated with the use of genomic information have been delivered, while others have not been realized. Technology continues to develop and mature with new ideas coming from a variety of fields. It is important to keep investing in all areas of research related to genomics and to be ready for the new developments yet to come.

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"What the Beef Industry Can Learn about Genomics From Another Livestock Industry"

Thomas J Lawlor, Director of Research, Holstein Association USA

Introduction

Genomic evaluations have been a great benefit to the dairy industry. And to my friends in the other livestock groups, it seems as though everything has been easy. Phenotypes are easy to obtain. Our main trait of interest, milk production, is measured two to three times a day. And we have millions of animals who are genotyped.

Hardly a week goes by without some type of popular press article reporting on another genomic tested dairy calf selling for a high price. A recent article from Australia (www.beefcentral.com) stated "will we ever see a $251,000 12-week-old calf? Maybe genomic testing is the answer?"

Even in the scientific Journal of Animal Breeding and Genetics, Jerry Taylor et al (2016) stated "As it turns out, Genomic Selection was a technology waiting to be invented for the US dairy industry." Well, that is partially true. We have certainly welcomed it and we do ask ourselves "what would we do without it?"

So, let's review the dairy genomic journey. You may be surprised that your dairy friends had to "cowboy up" several times to the bumps and challenges along the way.

The science of utilizing genomic information.

As in life, scientific pursuits often start off with some grand "what if" ideas. In genomics, our question was…. What if we had a lot of genetic markers equally spaced across the genome? How would we use that information to better select animals? Two noteworthy papers addressing this question were Nejati-Javaremi et al. (1997) and Meuwissen et al. (2001). It was the latter paper that stimulated the thinking of others on just how important genomic selection could become. Recognizing that affordable large scale genotyping would soon become a reality, Schaeffer (2006) discussed its benefits, which included a reduction in the costs of traditional progeny testing, having more accurate predictions on young animals, selecting them earlier and using them intensively, thereby decreasing the generation interval and increasing the rate of genetic improvement.

Curt Van Tassell was our cheer leader, motivator and sometimes arm-twister in getting the scientific know-how, funding and industry support behind the development of the Bovine SNP50 Van Tassell et al. (2008) and Matukumalli et al. (2009). The work of VanRaden (2008) provided the framework for genomic predictions which launched the genomic selection revolution in the dairy industry. Unofficial genomic predictions were first provided to the owners of genotyped animals in 2008, with an official public release and start of routine evaluations in January 2009.

The management and storage of the growing amount of genomic data was described by Wiggans et al. (2010). Although USDA had complete access to tremendous resource for research, it was beginning to become apparent that running a complete genomic evaluation required a large amount of time commitment for maintenance of this growing database, and the necessity to provide a service to the individual breeders and private breeding companies. Additionally, there were growing concerns about the privacy of sensitive traits, such as, incidence of disease and other health events. And the large amount of financial investment in genotyping and

Availability of genomic information has changed the dairy industry forever. Along with a renewed interest, enthusiasm and appreciation of genetic information came the commercialization of the genetic evaluation system and increasing discussion over the financial commitment to obtain genotypes and phenotypic data, the ownership of that data, and who and when others can have access to the resulting genomic information. The initial introduction of genomic evaluations were a bit controversial, as only members of the original seven AI companies who agreed to genotype their bulls and provide access to USDA, were permitted to obtain a genomic evaluation on bull calves for a 5-year-period.

In 2014, the running of the national genetic evaluations moved from being publicly funded and run by USDA-AIPL to the privately funded Council on Dairy Cattle Breeding (CDCB). In addition to paying for a genotyping service, breeders must now pay for the genomic evaluation. Prices vary depending upon sex - with the logic that bulls have the potential to provide a large financial return to the owner; as well as, the amount of phenotypic data that the farm or organization has contributed to the national database or more specifically to the reference population. Countries, such as Canada and Germany, have followed this open system with differential pricing. Some other countries run an exclusive system where an owner of animal must belong to a domestic organization, in order, to submit a genotype and obtain a genomic evaluation.

Protection of intellectual property in the form of many genotypes tied to a large amount of phenotypic data has become a concern. Countries with long time marketing relationships with one another have formed alliances and pooled their reference populations together. Currently three major international consortiums are in place. The needs of the international dairy community which has had a long-time tradition of pooling data, obtaining a genetic evaluation with a higher accuracy, and having an evaluation expressed on each country's domestic scale has changed.

The within-country genomic evaluations of the major exporting countries provide more accuracy, are available on a more frequent and timely basis, and access can be governed by a country's own domestic policy. Interbull, the international organization which has provides a service of performing the task of running a Multiple Across Country Evaluation (MACE) for our traditional (pedigrees and phenotypic data only) has struggled to find the proper business model in the genomics era.

The need for research into the modelling of genetic evaluations is at a level not seen in decades. And there is a shortage of well-trained quantitative geneticists to meet this demand. Although there are many ways to categorize research, a simple grouping is accuracy versus bias. Improvements in accuracy have been made by advances in imputation, fully sequencing influential ancestors,

Controlling bias is often connected with evaluating different groups fairly and equitably. For example, young animals versus older, domestic versus foreign, genotyped versus non-gentoyped, selected versus culled, etc.. Identifying a bias in different segments of a population takes a combination of skills; observing differences and forming a hypothesis on why different groups of animals may be handled differently by the current genetic evaluation model. Knowing how to properly categorize the population to address a concern. And having the skill set to develop the theory and a solution which can be programmed and implemented. Some good examples are adjusting cow variances and trait heritabilities (VanRaden, 2016), to control genomic pre-selection ssGBLUP (Aquilar et al, 2010))and incorporating foreign data that may be missing from your domestic genomic evaluation (**Vandenplas, 2017**).

Genomic information allows us to make genetic improvement on the more difficult traits, i.e. lowly heritable traits (Table 1) and those traits that are costly to collect data. Private organizations saw a business opportunity in creating one's own reference population by collecting valuable but costly phenotypes on a limited group of animals and providing an opportunity to access the genomic information. Four different sources of proprietary information on health traits are now available from Zoetis (Wellness Traits), ABS Global (TransitionRight), Genex (Exclusive Health Traits) and Semex (Immunity Plus). The CDCB is developing a national genetic evaluation, but, it's yet to be determined if any of the existing data sets will be pooled together.

As expected, the acceptance, utilization and accuracy of genomic information varies across the dairy industry. Genomic predictions were first officially available for Holsteins and Jerseys in January 2009; followed by Brown Swiss in August 2009, Ayrshire in April 2013, and Guernsey in April 2016. As of May 2017, 1.5 million Holsteins have a genotype; followed by 0.2, 0.03, 0.007, and 0.003 million, respectively for Jerseys, Brown Swiss, Ayrshire and Guernsey.

Presently, the SNP effects are breed specific. Which means greater accuracy in the Holstein breed does not get conveyed to the others. Additionally, the Holstein breed is much larger, on both a domestic and international basis, providing greater selection intensity. The difference in the genetic merit of the top Holstein bulls versus the Jersey bulls continues to widen over time (Table 2). The Holstein breed is pulling away, genetically, from the other breeds.

In addition to genetic evaluations, the dairy industry also receives information on parentage verification and/or discovery; identification of desirable and undesirable alleles; and indication of breed purity. Although, there is a very limited amount of crossbreeding in the dairy industry,

there are differences in the rules on how unregistered animals may enter the different herd books. A percentage value called the Breed Base Representation (BBR) provides a measure of the admixture of genes from different breeds. The BBR values on many of the top Jersey bulls indicate that Jersey breeders have introgressed Holstein genes into their elite cows.

The business of genomics.

Within a breed, breeders must decide on whether to use the younger and genetically superior genomic tested bulls as opposed to the older bulls with milking daughters. Whether they will participate in genomic testing and to what extent. And whether they will use sexed semen, embryo transfer, IVF, IVM or other reproductive technologies. These decisions will influence not only the herd's rate of genetic improvement and its ability to be successful in a competitive industry, but it will also determine their ability to be a provider of elite genetics.

Today's seed stock providers are breeding to young genomic bulls, genomic testing, and using advanced reproductive tools extensively. To obtain an extreme genetic outlier, high additive genetic merit of the parents is required, as well as, high Mendelian sampling. The latter component is simply a matter of the number of matings being made. The more embryoes a breeder obtains from the top parents, the more likely they are to obtain a high sample of better chromosome segments from each parent. A lack of ready access to a large number of recipients is the limiting factor for many of the current elite breeders. Without an opportunity to create a lot offspring, the odds are stacked against them to obtain an extreme outlier. For this reason, we've seen a large shift away from the smaller or moderate size farms to larger ones.

Genomics has changed the business of dairy cattle genetics. As with all technologies, there are early adopters and latter ones. In our industry, different AI companies approached this new technology differently. Several AI companies, were quite aggressive, by using young genomic bulls as sires of sons, buying and owning females, changing the way that semen was released, and establishing closer and often contractual business relationships with farmers. In the last five years, the registration of animals from these more aggressive AI companies, as well as new upstart companies, has grown by 14% at the expense of the more conservative companies. Couple this domestic change with large changes in the international sale of semen and we have a genetics industry in transition.

The growth in the investment in dairy cattle genetics has led to an increase desire to protect that investment and control the distribution of its product. Using the top genetics, early and exclusively, within one's own nucleus breeding program. And then selling sexed-sorted semen is a strategy that some studs have implemented.

Figure 1 shows the registration of male and female offspring from one of the breed's top young sires. All of the bulls born during the pre-release period are either owned by the AI company or under contract for first right of refusal at a set price. Then the commercial product that is sold is sexed-sorted semen, which is good for the commercial farmer looking for dairy replacements and

not so good for seed-stock producers or competing AI companies looking for bulls. This strategy does provide the owner with early access to the sons of an elite sire, but, given enough breeding by others, elite sons are still available to their competitors with a six-month delay in availability.

The current time in the business of genetics is quite exciting. Companies who were either slow in their initial uptake of an aggressive genomic breeding, or, were aggressive at the beginning and are being fueled by initial success and the desire to capture more market share are paying large prices for elite genetics. Seed-stock breeders are putting IVF facilities on their farm, negotiating their own contracts with AI companies, consulting with geneticists, studying consumer and economic trends, and trying to predict where our industry is headed.

However, the real driver behind the pursuit for faster genetic gain are the improved genetics they bring into their herd. These large farms realize that the occasional lucrative sale is merely frosting on the cake. The real money is made from milking those elite genetics. This is the true success of the genomic era. Farmers are more convinced than ever of the importance of good genetics in their herds. Many are investing heavily in it and are convinced that their herd will be more profitable due to their genomic breeding program.

The use of genetic advisors has increased within the dairy industry. A frequent request is for the design of a genomic breeding program whereby a small percentage of the elite females will be put into an IVF program. The next tier of females will be breed with sexed semen followed by females that will be used as recipients or bred to beef bulls, and finally the low end who will be culled. Many farms have become quite adept at producing embryos and are achieving high transfer rates. The cost of purchasing high genetic level embryos has dropped to the point where many believe that embryos will soon rival semen as the most economical way of disbursing genetics throughout the industry.

The future:

Information on sequence data available from the 1000 Bull Genome Project has identified informative SNPs in close linkage to causative genetic variants. These SNPs are being included on next production run of SNP chips.

Personalized nutrition is becoming more popular. With a growth in genotyping amongst both humans and cows, the ultimate personalized nutrition program is one where the genotype of the consumer is matched with a dairy product that best complements their needs. Dairy farms have grown to where several tanker trucks of milk per day will be filled. If a certain milk protein is deemed desirable by a certain portion of consumers, farmers can easily genotype their cows, segregate them into subgroups, and fill a complete milk-tanker with a specified milk protein.

The dairy cattle breeding industry has a history of being open to new technologies. For example, gene editing and cloning have been successfully demonstrated in dairy cows. Their acceptance

and utilization is ultimately dependent upon its cost effectiveness, long-term sustainability, and consumer acceptance.

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Vandenplas Jeremie. 2017 Can MACE and national ssGBLUP integrating MACE cohabitate without double-counting? Interbull

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Table 1. Lowly heritable traits benefit more from the addition of genomic information.

Trait	Extra Daughter Equivalents from SNP effects
Production	25
Conformation	25
Calving Ease	38
Somatic Cell Score	58
Productive Life	80
Fertility	140

Table 2. USDA Sire Summary, April 2017. Genomic tested young bulls being marketed

Breed	Number	PTAM	PTAF%	PTAF	PTAP%	PTAP	SCS	PL	DPR	NM$	FM$	CM$
Holstein	2215	1105	0.06	58	0.03	42	2.81	5.2	1.6	635	586	656
Jersey	394	691	0.08	48	0.05	33	2.93	4.2	0	445	387	469
Ayrshire and Red	39	981	0.06	51	0.04	40	2.92	1.3	1.1	392	344	412
Brown Swiss	51	749	0.01	32	0.02	28	2.87	3.5	0.9	364	332	377
Red and White	28	335	0.05	25	0.04	21	2.88	2.8	0.7	332	278	354
Guernsey	8	504	-0.02	20	-0.02	12	2.96	1.4	-0.3	169	178	165

Figure 1. Use of restricted access to pre-release unsorted semen, followed by the commercial sale of sex-sorted semen, in an effort to control the access and usage of an AI company's top genetics.
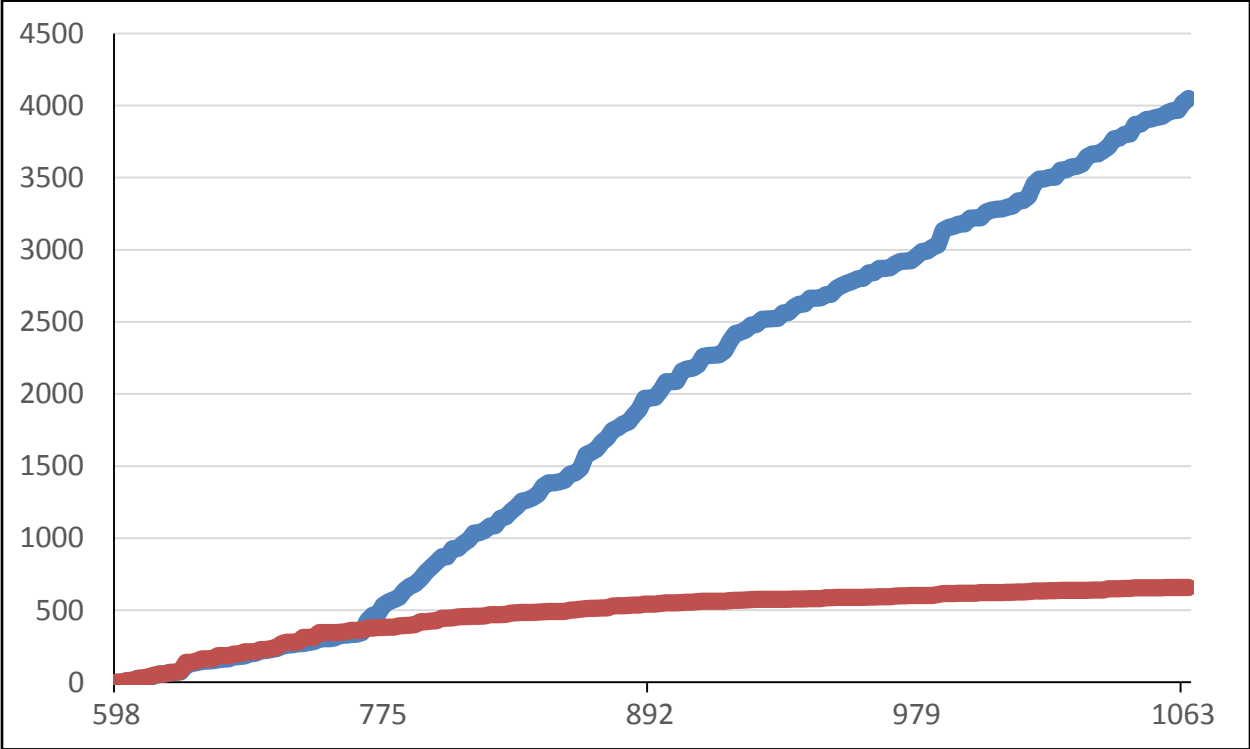
Where We Are Going with Genomics and Genetic Improvement:

Matt Spangler, University of Nebraska-Lincoln and Alison Van Eenennaam, University of California-Davis

Historical Summary

It has become clear that that real-time changes in genetic merit estimates, also known as Expected Progeny Differences (**EPD**), are not well accepted by many in the beef industry. Increasing the accuracy of prediction much earlier in life does not allow for an extended time horizon to justify changes in EPD based on empirical evidence (e.g., visualizing differences in offspring). This, coupled with changes in prediction methodology that have taken longer to implement than desired, have led many to question the validity of genomic selection and the entire infrastructure for National Cattle Evaluation (**NCE**). However, we contend that tremendous progress has been made in a relatively short amount of time, and that the scientific issues we currently face pale in comparison to the issues created by an overall lack of cohesion in the beef sector and the general reluctance to adopt technology.

Before we prognosticate about what the future may hold, let us take a look back to see how we got to the point at which we are currently. As different breed associations began including genomic information (primarily genotype data from the 50,000 (**50K**) single nucleotide polymorphism (SNP) chip) into their NCE, the nuances related to methodology for doing so increased. The method used by the American Angus Association (AAA) was first proposed by Kachman (2008) and used by MacNeil et al. (2010) in their prototype evaluation. This became known as the "correlated trait approach" and assumed that the linear combination of the 50K SNP genotypes known as the Molecular Breeding Value (**MBV**) could be fitted as a correlated indicator trait in existing multiple-trait models. A primary benefit of this was the familiarity of the concept to breed associations. It also allowed for genomic information to influence the predictions of animals in the pedigree that were not genotyped.

As other breeds began to include genomic information into their NCE, "new" methods of doing so were being developed. It is important to note that the choice of inclusion method was arguably based on the genetic service provider (entity that conducted NCE) and not through purposeful model comparison. The majority of breeds that followed implemented a blending (indexing) approach whereby the MBV and EPD were indexed together to produce a "genomically enhanced" EPD (**GE-EPD**). This has primarily been done post evaluation and consequently only impacted the prediction of the genotyped animal. This created the largest difference between blending and the correlated trait approach. All of these methods are essentially variations on the same two-step theme; estimate the SNP effects using a large data set of genotyped and phenotyped animals from the same "breed" to train the MBV and then fit them into NCE. Since 2009, many breeds have made tremendous investments in this technology and currently offer GE-EPD. Table 1 represents counts of genotyped animals as of fall 2016.

Table 1. Number of Animals Genotyped, use of Low-Density (LD) Panels for Imputation, Method of Incorporation of Genomic Data into National Cattle Evaluation (NCE), and Genotyping Service Provider by Breed.

Breed	Samples Included in NCE[1]	LD Panel to Impute	Method[2]	Service Provider[3]
Angus	264,656	Yes	Corr	G,Z
Hereford	~23,000	Yes	Blend	G
Red Angus	22,791	Yes	Blend	G,Z
Charolais	2,454	No	Corr	G
Gelbvieh	10,162	Yes	Blend	G
Limousin	3,340	Yes	Blend	G
Simmental	32,629	Yes	Blend	G
Shorthorn	~1,000	Yes	Blend	G
Brangus[4]	3,909	Yes	ssGBLUP	G,Z
Santa Gertrudis[4]	3,160	No	ssGBLUP	G

[1]These are the number of either high density or low density samples included into NCE. Some breeds have access to additional genotyped animals for training and research purposes. These counts do not include legacy 384 SNP panels, although for Angus these are being included (n=26,282; unknown number of duplicates with higher density panels).

[2]Corr=A correlated trait approach; Blend = post-evaluation indexing; ssGBLUP = single-step Genomic Best Linear Unbiased Prediction.

[3]G=GeneSeek; Z=Zoetis

[4]Updates as of Oct. 2016

We know that the inclusion of genomic information into NCE can add accuracy to EPD, particularly for young animals. The benefit of increased accuracy, and perhaps the salesmanship associated with being a technology adopter, has spurred rapid genotyping in several breeds as evidenced by the counts in Table 1. The availability and use of low-density (**LD**) panels (fewer SNP and less expensive) has also aided in the increased rate of genotyping but more importantly in the fraction of animals within a contemporary group that are being genotyped. The ad hoc selective genotyping strategy whereby only the "best" animals were genotyped was undoubtedly a disservice to NCE and genomic selection. Early prediction equations were built based on a highly-selected subset of animals and as a consequence bias was introduced. The ability to affordably genotype entire contemporary groups can resolve this issue. However, the technology will need to continue to decrease in cost toward commodity based pricing before the strategy of genotyping every animal becomes pervasive. We suspect collective bargaining, with all breed associations engaged and on the same side of the table, could help to drive the cost of genotyping down.
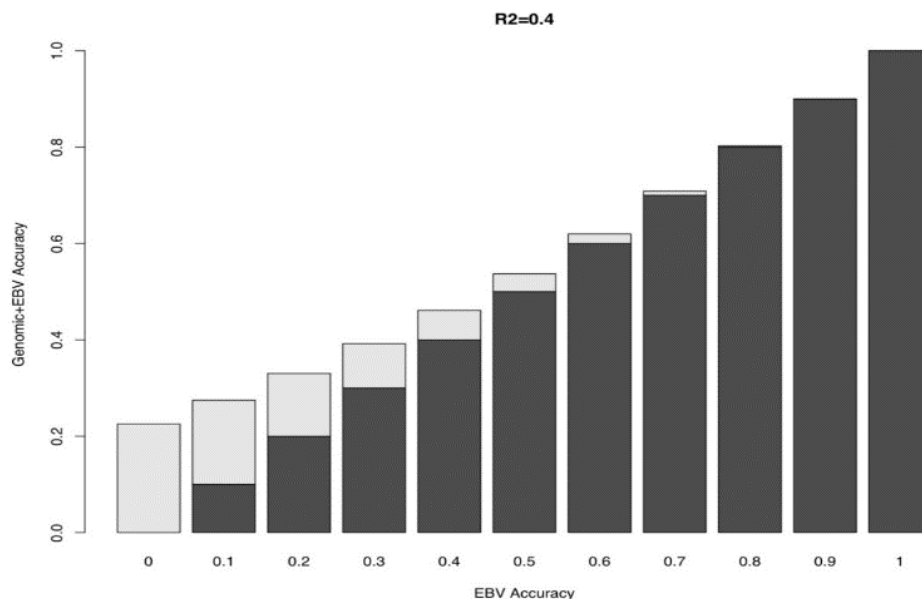
Figure 1. Increase in EPD Accuracy Resulting from Inclusion of Genomic Information That Explains 40% of the Genetic Variation (GV; squared genetic correlation). The darker portion of the bars shows the EPD accuracy before the inclusion of genomic information and the lighter colored portion shows the increase in accuracy after the inclusion of the MBV into the EPD calculation. As the %GV explained by the genomic information increases, the increase in EPD accuracy becomes larger.

The use of LD SNP panels presented a critical question to breed associations relative to the enabling of imputation going forward in time. For example, if the use of LD panels (e.g. 20,000 SNP) becomes commonplace and the target SNP density for inclusion into NCE is of higher density (e.g. 50K) how would breed associations ensure that imputation could be performed given that the animals with actual HD genotypes would become further and further removed from the target population? This issue made breed associations decide to re-genotype critical animals (e.g. prominent sires) with a high density panel to ensure imputation could proceed with an acceptable degree of accuracy. This re-genotyping is often subsidized by the breed association. To our knowledge, the choice of which animals to re-genotype is done by setting a relatively arbitrary threshold relative to the number of daughters in production, calves registered, accuracy of a certain EPD, etc. Gains in efficiency could be achieved by using more advanced criteria, such as calculating the relatedness of the genotyping candidate to the rest of the population and approximating the gain in imputation accuracy that could be achieved by re-genotyping an individual. It is unclear if the resulting cost savings would justify the added effort of doing so.

The methods of inclusion of genomic information into NCE have been relatively static over the past 5 years despite a considerable amount of research. The ongoing research is focused on the commercial scale implementation of various "single-step" methods, some that allow variable weighting of different SNP effects and others that do not. Presumably, all beef breed associations will move to one of these two methods (software provided by University of Georgia or Theta Solutions) by early July of 2017 (this timeline is a prediction and not a guarantee). This is an exciting evolution, particularly given some breed associations currently use software for

NCE that is decades old and that has undergone several "patches" along the way to keep it afloat. It will also be beneficial to move away from the possibility of using MBV or "percentile ranks" based on MBV alone as selection criteria.

It will also benefit any breeds that are using differing prediction equations from multiple labs, which creates confusion at best and at worst adds unwanted heterogeneity and differing sources of bias to post blended EPD. However, these are not truly single step methods, and they still rely on imputation to a common density. In some cases, this means data are cast aside if, for example, the target density is the 50K and animals are genotyped with a higher density. Although data are being cast aside, we suppose it is arguable that information may not be lost given panels with a density higher than 50K have not yielded substantial increases in accuracy.

Priority Areas

Despite the tremendous progress that has been made over the past several years, challenges still exist. Although not an exhaustive list, we believe the three bullet points below summarize the current hurdles to further refine genomic selection.

1) Improve the portability of genomic predictions.

It is well known that the accuracy of genomic predictions erode as the target population becomes more distantly related to the training population. This can occur over time, but perhaps the larger concern is across differing breeds. Kachman et al., (2013) clearly illustrated that a 50K-based genomic predictor for weight (either yearling or weaning) that was trained in Angus was not predictive in Red Angus. The issue of robustness, or portability, of genomic predictions across breeds is critical for three reasons: 1) Not all breeds will have the resources to adequately estimate markers effects for all traits, 2) prediction in non-pedigree commercial populations will remain elusive unless this issue is resolved, and 3) The transfer of genomic information from research settings for novel traits to industry populations will not occur otherwise.

Initially there existed hope that simply increasing the marker density (e.g., going from 50,000 SNP to 770,000 SNP) would alleviate this problem. It did not. Simply adding more markers actually reduces statistical power when the number of genotyped animals does not increase proportionally and results suggest that any gains in using higher density panels are negligible at best both within and across breeds. The new hope comes from a growing body of whole-genome sequence information. The omnipresent thought is that "functional" variants can be identified from sequence data and used to construct lower-density panels. If truly functional variants are identified, they should not be subject to the reliance on linkage disequilibrium (non-random association of alleles at different loci in a given population) that plagues the use of markers alone, and thus they should be valuable predictors across populations. This is easier said than done.

First, we must develop a system of categorizing DNA variants that provides more resolution than is currently used (e.g., a variant is classified as important—but how important is it, and what is the evidence of this?). This will help narrow the list of candidate variants. Secondly, given a pragmatic view of how well we can identify functional variants, we must refine the methodology we use to estimate genomic predictors. For example, there is evidence that haplotype based models may be more robust in admixed populations in terms of prediction accuracy and resolution of QTL locations (e.g., Schweer et al., 2016). Additionally, encouraging results using

identified variants from whole genome sequence information that are contained on the new GGP-F250 panel are becoming available (e.g., Snelling et al., 2017). In this paper, Snelling and colleagues reported that 293 variants explained 36% of birth weight genetic variation in the Germ Plasm Evaluation project (GPE) at the US Meat Animal Research Center, and molecular breeding values trained using GPE effects had genetic correlations with birth weight in other populations ranging from 0.25 to 0.44. Similar correlations were obtained from a subset of SNP that contained only 11 variants. Genetic correlations between birth weight and genotypes for the single most significant variant in GPE were between 0.17 and 0.34 in the independent populations. Although we have a considerable amount of work yet to do, the incorporation of biological information into our predictions of genetic merit using genomic data seems encouraging.

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

The principal reasons that genomic selection has worked well in dairy cattle are that Holstein is a homogeneous population, and the selection objective focuses primarily on sex-limited traits (e.g., milk production). In contrast, the majority of EPD in the beef industry are not sex-limited and represent phenotypes, or indicators of the desired phenotype, that can be collected on bulls at or before 12 months of age. Exceptions include heifer pregnancy and measures of sustained cow fertility (e.g., stayability). Although fertility EPDs do exist in some form for several beef breed associations, the information content is not sufficient. This is due to a combination of factors including the lowly heritable nature of these traits, and both the quantity and quality of data reported. In other words, phenotypic data collection needs to be ramped up.

There are other traits that are economically relevant to the commercial industry that are either sparsely collected or non-existent in current breed association databases. Traits such as disease susceptibility (Bovine Respiratory Disease (BRD), pinkeye, etc.), carcass data including primal yields, mature cow weights, male fertility, cow feed intake, and the list could go on. The majority of these phenotypes exist in the commercial sector (cow/calf, feedlot, and packer) and are collected in some form every day. To fully capitalize on genomics, we must exploit the data that exists in our industry and ensure it enters into NCE. It is obvious that breeds without a solid NCE foundation cannot make use of genomics, and for many traits of economic importance all breeds fall into this category. Unfortunately, these are the traits for which genomics could help the most—those that are expensive to collect, collected on older animals, or sex-limited. It is not the entity that genotypes the largest number of animals, or the entity that first implements single step genomic selection that will win the NCE race. Rather it is the entity that is able to fully exploit commercial level data in genetic prediction that will gain the most from genomic selection.

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

Psychology might be a better degree to hold to solve this issue as compared to quantitative genetics. The implementation of genomic selection is only advantageous if breeders, particularly nucleus breeders, believe in and utilize traditional EPD and selection indices. Moreover, commercial producers must value increases in EPD accuracy as a means of mitigating risk. If these two qualifications are not met, genomic selection in beef cattle is futile.

Currently, there are people in leadership positions who believe publishing the actual MBV is valuable, in addition to publishing GE-EPD. This illustrates that continued educational efforts

relative to genomic selection and the outputs of NCE have somehow fallen short. Perhaps part of this can be attributed to the survey findings of Weaber et al. (2014) regarding where beef producers seek genetic selection information. Interestingly, Weaber and colleagues reported that unpaid consultants, such as neighbors or friends, were most frequently (38.9%) identified by respondents as valuable sources of breeding and genetics information followed by veterinarians (29.7%), extension professionals (29.5%), seedstock producers (27.7%), internet search (18.9%), farm supply or feed store staff (18.1%), breed association personnel (14.7%), AI stud personnel (11.7%), popular press sources (9.3%) and paid consultants (2.1%). These results suggest that it is important to educate not only traditional information providers (veterinarians and extension educators), but also commercial producer peers and their seedstock suppliers about genetic and breeding principles as these entities are often consulted as trusted sources of genetic selection information (Weaber et al., 2014).

The traditional vehicle for outreach has been face-to-face delivery of educational and written material. These delivery approaches are generally targeted towards increasing knowledge and awareness. Unfortunately, despite decades of effort using these two traditional approaches to outreach, little has been accomplished relative to attitude and behavior changes. Survey results suggest that upwards of 70% of U.S. beef cattle producers in the commercial sector do not utilize genetic merit estimates, EPD, as their primary selection criterion (e.g., Weaber et al. (2014)).

Using the thesis that current adoption of fundamental genetic selection tools by bull buyers is archaic, and that traditional means of outreach have not been able to penetrate the beef industry such that behavior changes have occurred, a new approach was deemed necessary to ensure technology adoption of emerging tools like genomics. A hands-on approach where beef cattle producers could 'learn by doing' was trialed to augment traditional outreach vehicles. Moreover, this approach leant itself to training beef cattle producers and breed association personnel to be effective educators themselves. The latter point is critical given the general lack of outreach personnel in the United States that are trained in quantitative genetics/genomics.

In 2009, an integrated effort between the National Beef Cattle Evaluation Consortium (NBCEC), the University of Nebraska, and the 7 largest beef breeds in the U.S. (Angus, Hereford, Red Angus, Charolais, Gelbvieh, Limousin, and Simmental) was initiated in an effort to develop an educational program centered on genomics and to build a resource population for the development and evaluation of genomic predictors and related methodology. These 7 breed associations 'nominated' seedstock producers (n=24) in the Northern Plains region of the U.S. to participate in the project. Initially, producers agreed to provide hair samples on all 2009 born bull calves. These animals were genotyped with a reduced assay for weaning weight and post-weaning gain. The SNP discovery for this reduced assay occurred in the Cycle VII population at US Meat Animal Research Center (**USMARC**). Given the early focus on weight traits as proof of concept, the project was named the Weight Trait Project (**WTP**).

In subsequent years, producer-owned herd bulls were genotyped with the 50K, and MBV and marker-assisted EPD were provided back to producers for growth and carcass traits. The MBV were trained using currently available genotypes in the NBCEC database using both within-breed and across-breed training sets. All genotypes generated were provided to the respective breed associations to aid in the development of training sets that would eventually be used to generate MBV that were included into NCE.

As part of the WTP, a two-day meeting has been held annually at the USMARC, with the first day focused on short (approx. 20 minute) presentations accompanied by brief (2-page) handouts. Talks on the first day of the meeting have focused on the current status of genomic selection in beef cattle, novel trait discovery and, in more recent years, considerations related to selection for improved feed utilization. All talks have been recorded and posted at www.beefefficiency.org. All attendees of the first day meeting were asked to complete an anonymous survey indicating levels of knowledge gained and any likely behavior changes as a result of the presentations. They were also asked to provide an indication of numbers of beef cattle they owned or for which they directly influenced management decisions. On the second day, activities centered on project aims and results, and upcoming project activities. This forum allows for direct industry feedback from progressive seedstock producers and breed association personnel related to the direction of genomics research and issues of technology adoption.

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

A survey was conducted by Spangler et al. (2011) to gauge changes in knowledge, practices, and behavior; the survey was sent to participants in the WTP. The 17 respondents indicated that collectively they own 20,125 beef cows. Increases in knowledge were rated from 0 (none) to 4 (significant). Mean survey results were 1.5, 2.8, 2.0, 3.4, 2.4, 2.7, 2.8, and 2.9 for EBV, genomics terminology, parentage verification, marker assisted selection, across breed genomic predictions, whole genome selection and panel development, test validation, and accuracy improvement of EBV, respectively. Producers indicated adoption of methods to improve the following production practices: making mating decisions (40%), efficient use of DNA technology (75%) and selection (bull buying) decisions (47%). Mean responses for changes in behavior (1 = none; 5 = very likely) were 3.9, 3.8, 4.3, and 4.6 for making more informed selection decisions, better educating their clientele, feeling comfortable with terminology, and desiring to stay abreast of DNA technology, respectively.

 A critical outcome of this integrated project is the development of a forum for researchers, breed association personnel, and seedstock producers to continue a dialogue regarding genomic technology, implementation methods for genomic selection, and discovery for novel traits. Consequently, these types of activities are likely better suited at generating behavior change than classical extension talks during an industry-sponsored meal.

Emerging Technologies in Beef Cattle Breeding

Genome Editing

Genome editing is a category of new methods that can be used to precisely edit or change the sequence of DNA or the genetic code. As the name "genome editing" suggests, these technologies enable researchers to add, delete, or replace letters in the genetic code. In the same way that spell check identifies and corrects single letter errors in a word or grammar errors in a sentence, gene editing can be used to identify and change the letters that make up the genetic code (i.e. DNA) within an individual.

Gene editing has many potential applications. For example, it can be used to correct diseases and disorders that have a genetic basis. It could also be used to change a less desirable form of a gene (called an allele) to a more desirable allele without the need to introgress (repeatedly backcross) or bring in that allele through outcrossing with an animal that carries the desirable allele. Therefore gene editing is really more like precision breeding where breeders can introduce the specific sequences that they would like to select for using gene editing technologies.

Gene editing is different from "traditional" genetic engineering. Continuing with the analogy of a word processor, genetic engineering enables a gene sequence of "foreign DNA" to be "cut and pasted" from one species to another; typically the location where the new DNA sequence inserts into the genome is random. Gene editing can add, delete, or replace a series of letters in the genetic code at a very precise location in the genome.

Without the addition of template DNA, the double stranded breaks created at a precise location in the genome by the nucleases are repaired by the cell's natural DNA repair mechanism in a process called "nonhomologous end joining" (NHEJ; Figure 2). This typically results in single nucleotide changes, deletions or small (1-2 nucleotide) insertions at the DNA cut site. In this case, although the location of the cut site is very precise, the exact change that occurs when the DNA is repaired is random and so a number of different outcomes representing minor sequence changes are possible.
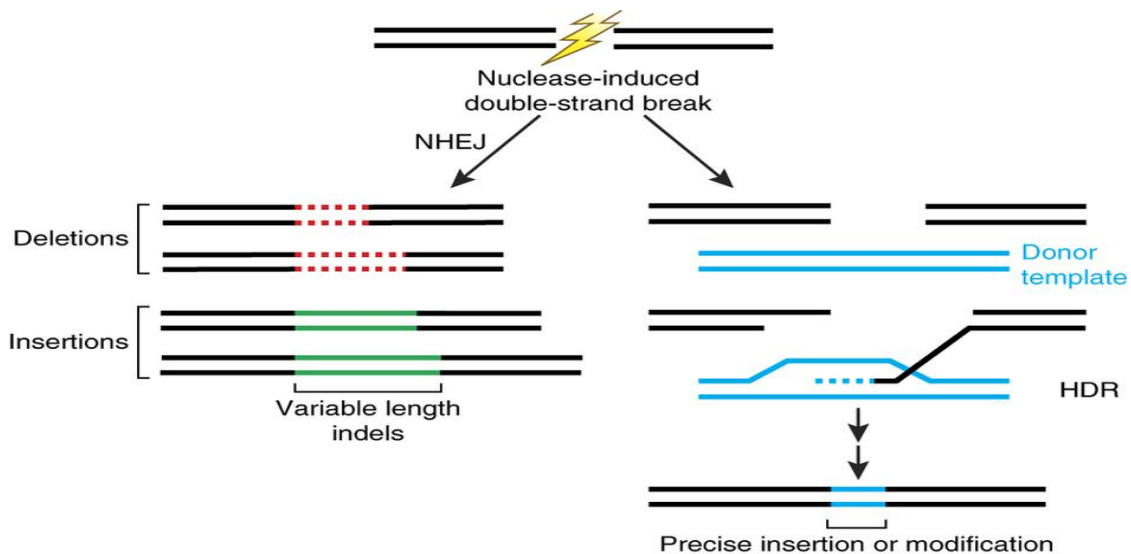
Figure 2. Nuclease induced double-strand breaks (DSBs) can be repaired by "nonhomologous end joining" (NHEJ) or "homology directed repair" (HDR) pathways. Imprecise NHEJ-mediated repair can produce variable-length insertion and deletion mutations at the site of the DSB. HDR-mediated repair can introduce precise point mutations or insertions from a single-stranded or double-stranded DNA donor template (blue). Image from (Sander and Joung, 2014).

Supplied with a nucleic acid template, however, the double stranded breaks initiated by the nucleases are repaired via the cell's "homology directed repair" (HDR; Figure 2) pathway whereby the template dictates the sequence resulting from the repair, allowing the introduction of the DNA sequence dictated by the template into the host genome. Such changes might range

from nucleotide-specific changes, to large (whole gene) insertions or substitutions depending upon the template. The end result of this maybe a targeted SNP edit (e.g. the nucleotide A at a given location in the genome is deliberately replaced by T), the replacement of one naturally occurring allele with another naturally occurring allele at a targeted genetic locus in that species, or the introduction of a novel DNA sequence as encoded by the template at the target location in the genome.

The currently available set of gene editing tools (zinc finger nucleases (ZFNs), transcription activator-like effector nucleases (TALENs), and clustered regulatory interspersed short palindromic repeats (CRISPRs) associated system) have been used for a relatively small number of livestock applications to date. Several recent reviews describe the potential to use these tools in food animals for agricultural purposes (Bosch et al., 2015; Laible et al., 2015; Murray and Maga, 2016; Tan et al., 2016), and include detailed descriptions of their mechanics and relative efficiencies.

Gene editing has been used to produce genetically hornless Holstein dairy cattle by replacing the Holstein "horned" allele with the naturally-occurring Angus "polled" allele at the gene that is responsible for horn development (Carlson et al., 2016), and to generate pigs with a single base deletion in a gene that may confer resilience to African Swine Fever Virus (Lillico et al., 2016). Recently a paper was published showing that gene edited pigs were protected from porcine respiratory and reproductive syndrome (PRRS) virus, a particularly devastating disease of the global pork industry (Whitworth et al., 2016). It has also been used to introduce changes in the *myostatin* gene in sheep and cattle (Proudfoot et al., 2015). As the Latin origin of the word *myostatin* (muscle/stop) suggests, turning off this gene results in muscle growth. Naturally-occurring mutations in this gene have historically been selected by conventional animal breeders and are the genetic basis for the "double muscled" phenotype that is seen in cattle breeds like the Belgian Blue, and the "bully" phenotype in whippet dogs.

In this way, gene editing really mimics the natural processes that form the basis of selective breeding programs, and for that matter, natural selection. Breeders work with the genetic variation that exists within a species, and that genetic variation ultimately arises from naturally-occurring mutations. Although the word "mutation" sounds negative, it simply refers to variations in DNA sequences. These variations, or mutations, are responsible for virtually all genetic differences which exist between individuals, such as having blue eyes instead of brown.

Although different mammals have many of the same genes, many people do not appreciate that the genetic code that makes up those genes differs among animals of different breeds, and even among animals within the same breed. In fact, with the exception of identical twins, there are literally millions of DNA sequence variations between two individuals of any species. For example, an enormous number of genetic variants have accumulated within cattle since the advent of domestication and selective breeding due to the naturally-occurring processes that lead to a small number of mutations each generation. In one recent analysis of whole-genome sequence data from 234 taurine cattle representing 3 breeds (Daetwyler et al., 2014), more than 28 million variants were observed, including insertions, deletions and single nucleotide variants. Most of these mutations are silent and have no impact on traits of importance to breeding programs. Occasionally, such mutations result in a genetic condition such as red or black coat color or an undesirable disease condition such as dwarfism.

Sequence Data

Some of the large-scale genomic and sequencing projects have revealed a number of single nucleotide polymorphisms (SNPs) and haplotypes in which one naturally-occurring allele results in superior performance to that observed to be associated with an alternative allele. Consequently, an animal's genome could theoretically be edited to the superior allele at one or more genomic locations. To date, targeting different genes simultaneously has allowed bi-allelic modification of as many as three genes at once. Multiple favorable alleles are rarely found in a single individual, and gene editing offers an advantage over conventional selection by efficiently increasing the frequency of desirable alleles in an individual, or even an entire breed, by moving naturally-occurring alleles without also bringing along all of the unwanted alleles that come along with conventional crosses to introduce a desired allele. This is referred to as "linkage drag" and is used to describe the (usually undesirable) effects of alleles at genes located adjacent to the allele we are trying to introgress. If a desirable allele for trait X lies close to an undesirable gene affecting trait Y, you will want to "break" the linkage drag – that is, separate the good allele from the bad.

In order for gene editing to be an important factor for genetic change, it must integrate smoothly into conventional animal breeding programs and reliably edit the germline of single cell zygotes that will form the breeding stock of the next generation. Gene editing could theoretically be applied to many different traits in livestock, including known fertility impairing haplotypes, and to correct known Mendelian genetic defects, in conjunction with conventional selection methods to continue making progress towards a defined selection objective. It also provides a means by which the discovery of causative SNPs (Quantitative Trait Nucleotides; QTNs) through sequencing projects and the information obtained from various genome wide association studies (GWAS) could be translated into valuable genetic variation for use in animal breeding programs. In one simulation study, response to selection was improved four-fold after 20 generations as a result of the combined use of gene editing and traditional genomic selection (Jenko et al., 2015). At best, gene editing will be used to complement conventional breeding programs; it will not replace them.

Although these methods offer many advantages, it is important to understand that hundreds, if not thousands, of different genes and their interactions impact complex traits. As a result, not all of the genes that influence these traits have been identified, so the sequences of the desirable alleles are not always known. For now, it is likely that relatively large effect loci and known targets will be the focus of editing in efforts to correct genetic defects or decrease disease susceptibility. The backbone of breeding programs will continue to be conventional selection in which selection for many small effect loci that impact complex traits will contribute to the breeding objective.

There have been a multitude of genome wide association studies (GWAS) performed over the past decade on all manner of traits, and large scale whole genome sequencing projects. Yet despite all of this information there are few obvious targets for editing at the current time, other than those associated with simple qualitative traits where one allele has a known affect (e.g. polled). As we develop a more sophisticated understanding of gene networks and quantitative trait variation, additional targets will likely be identified. In the future we may use editing to introduce specific alleles into maternal lines, without diluting the genetics that makes them superior maternal lines. We may even make maternal lines homozygous at certain alleles, and terminal lines homozygous at alternative alleles so that every mating results in a heterozygous individual with maximal heterosis. It may be used to ensure maternal lines have adequate

carcass merit by making targeted edits in loci associated with meat quality, yet continue to excel in maternal traits.

To emphasize it relative role in a breeding program, we can envision breeding programs as an ice-cream sundae as shown in Figure 3. Genome editing can be analogized as the cherry on top of all of the other components that are part of genetic improvement programs in the beef industry.
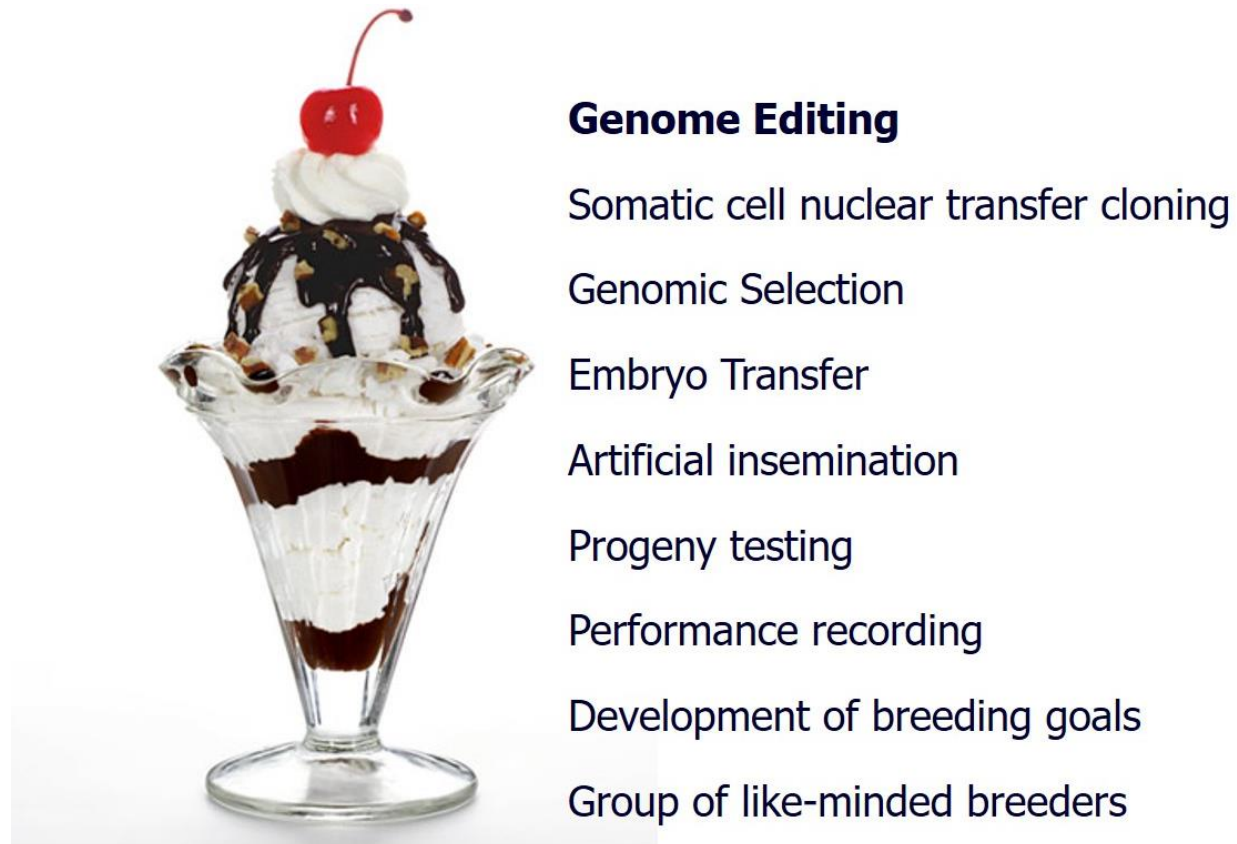

Figure 3. Schematic representation of genetic improvement programs in beef cattle. There are many requisite and interacting components that must be in place to drive genetic improvement.

Combining Advanced Reproductive Technologies with New Breeding Methods

It is perhaps underappreciated how much assisted reproductive technologies (ART) such as ovum-pick up and in vitro production (OPU-IVP) are being combined with the use of genomic selection (GS) in beef cattle breeding. While GS can decrease the generation interval in conventional cattle breeding by allowing for the more accurate genetic evaluation and use of young bulls, the expected benefits of combining GS and OPU-IVP far exceed the benefits achieved by either GS or OPU-IVP alone due to the very large reduction in generation interval (Kadarmideen et al., 2015).

In 2013 the global bovine embryo market reached 1,275,874 embryos, of which 40.6% (517,587 produced embryos) were IVP embryos. Brazil was responsible for 70.8% (366,517) of these IVP of embryos. In 2013, 45.7% (167,452 embryos) were obtained from dairy donors (88.6% from *Bos taurus* females) and 54.3% (199,065 embryos) from beef cattle (86.8% from *Bos indicus*

females; Viana et al., 2015; University of São Paulo, Brazil; unpublished data) (Kadarmideen et al., 2015).

Given there are so many OPU-IVP embryos being used in cattle breeding, editing may also have a role in reducing genetic lag. Genetic lag is defined as the time it takes for any genetic improvement made in the selection program of the top tier of the breeding pyramid (i.e. the nucleus seedstock sector) to trickle down to commercial sector. If genome editing can be reliably used to produce the desired edits in developing embryos, it could be routinely used to introduce useful genetic variants into newly fertilized embryos that are going to be part of an embryo transfer program.

In livestock to date, the primary method to deliver nuclease-mediated genetic changes has been cell culture followed by somatic cell nuclear cloning (SCNT). This method is advantageous because it allows for genotyping and/or screening of the gene edited cell line before it is transferred into the enucleated oocyte. This ensures that only the desired edits are made. On the downside, SCNT is associated with well-documented drawbacks such as early embryonic losses, postnatal death, and birth defects. Figure 4 shows how editing could fit into a selection program using advanced reproductive technologies combined with genomic selection (Van Eenennaam, 2017).

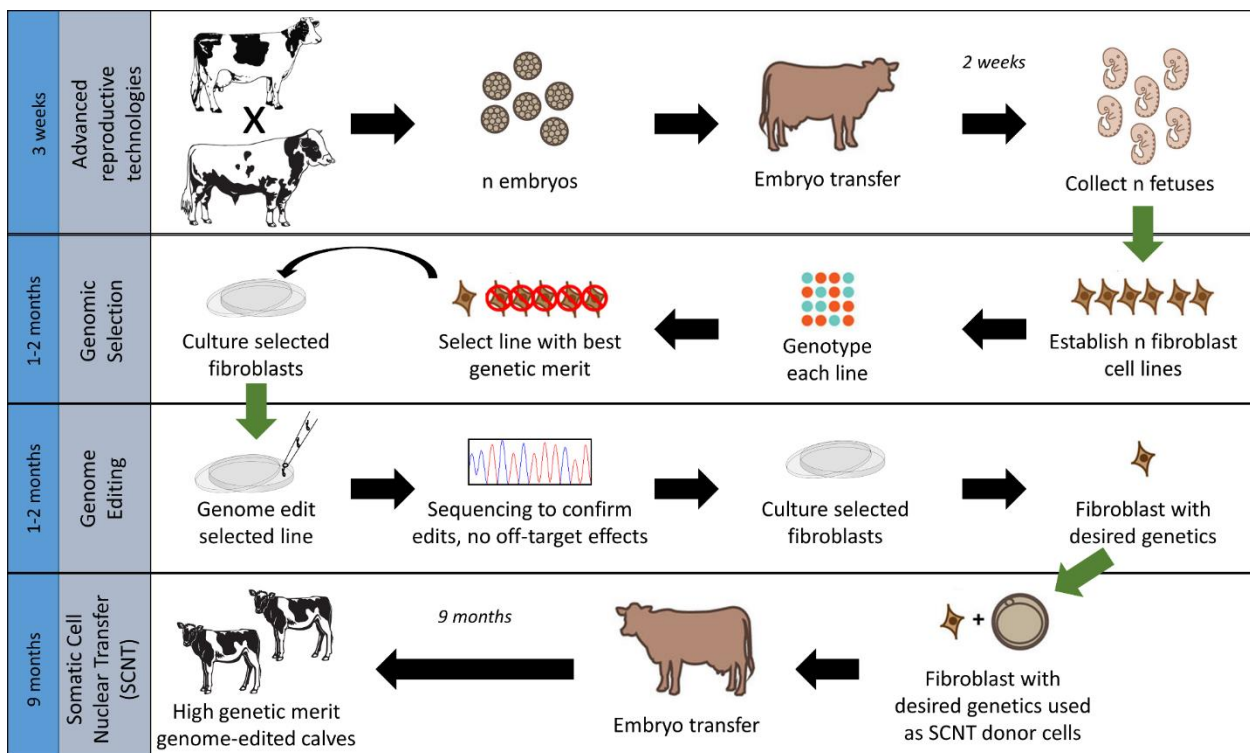**Figure 4.** Production of high genetic merit calves using a range of biotechnologies and showing where gene editing might fit into the process. Collection of day 21-23 early stage embryos and the establishment of cell lines from them allows rapid determination of genetic merit for a large number of candidate embryos, the best of which would be selected for subsequent editing. Image from (Van Eenennaam, 2017)

Alternatively, editing of single-cell zygotes offers an approach to introduce edits directly into the next generation; however, the disadvantage is that not all of the embryos will be correctly edited. Despite this, direct editing is more desirable than SCNT since edited embryos gave a two times higher pregnancy rate, and fewer embryos are required, on average, to achieve the desired result (Tan et al., 2016). Direct editing of zygotes has successfully been used to knock-in entire interspecies allele substitutions (Peng et al., 2015; Lillico et al., 2016). Issues with mosaicism, meaning that some of the cells are edited and some are not as the edit occurred only in a subset of cells after the embryo began dividing, have been associated with this method, but researchers are developing approaches to edit the one cell embryo prior to the first cell division to minimize this problem.

How will gene editing be regulated?

Animal breeding *per se* is not regulated by the federal government, although it is illegal to sell an unsafe food product regardless of the breeding method that was used to produce it. Gene editing as a tool does not necessarily introduce any foreign genetic DNA or "transgenic sequences" into the genome, and many of the changes produced would not be distinguishable from naturally-occurring alleles and variation. As such, many applications will not fit the classical definition of "genetic engineering". For example, many edits are likely to edit alleles of a given gene using a template nucleic acid dictated by the sequence of a naturally-occurring allele from the same species. As such there will be no novel recombinant DNA (rDNA) sequence present in the genome of the edited animal, and likewise no novel phenotype associated with that sequence. It is not evident what unique risks might be associated with an animal that is carrying such an allele given the exact same sequence and resulting phenotype would be observed in the breed from which the allele sequence was derived.

In January 2017, the FDA expanded the scope of its "Guidance for Industry #187" for producers and developers of genetically improved animals and their products to address animals whose DNA has been intentionally altered through use of genome editing techniques. The new guidance (Food and Drug Administration, 2017) entitled, "**Regulation of Intentionally Altered Genomic DNA in Animals**" triggers mandatory, pre-market FDA new animal drug approval of ANY "intentionally altered genomic DNA" sequence in an animal. This altered DNA sequence trigger seems to be aimed squarely at breeder intention and human intervention in the DNA alteration.

The guidance states that "*intentionally altered genomic DNA may result from random or targeted DNA sequence changes including nucleotide insertions, substitutions, or deletions*"; however, it clarifies that selective breeding, including random mutagenesis followed by phenotypic selection, are not included as triggers. The new FDA Guidance contends that "*a specific DNA alteration is an article that meets the definition of a new animal drug at each site in the genome where the alteration (insertion, substitution or deletion) occurs. The specific alteration sequence and the site at which the alteration is located can affect both the health of the animals in the lineage and the level and control of expression of the altered sequence, which influences its effectiveness in that lineage. Therefore, in general, each specific genomic alteration is considered to be a separate new animal drug subject to new animal drug approval requirements.*" So every SNP is potentially a new drug, if associated with an intended alteration.

To put this in perspective, as was mentioned earlier, whole-genome sequence data from 234 taurine cattle representing 3 breeds revealed > 28 million variants comprising insertions, deletions and single nucleotide variants (Daetwyler et al., 2014). A small fraction of these mutations have been selected owing to their beneficial effects on phenotypes of agronomic importance. None of them is known to produce ill effects on the consumers of milk and beef products, and few impact the well-being of the animals themselves. In other words, there are a lot of SNP variations when comparing two healthy animals.

What is not clear is how developers are meant to determine which alterations are due to their "intention" and which result from spontaneous *de novo* mutations that occur in every generation. Certainly breeders can sequence to confirm the intended alteration especially if they are inserting a novel DNA sequence, but how can they determine which of the random nucleotide insertions, substitutions, or deletions are part of the regulatory evaluation, and which are exempt as they occurred spontaneously due to random mutagenesis. And if there is risk involved with the latter, why are only the random mutations associated with intentional modifications subject to regulatory evaluation? And what if the intended modification is a single base pair deletion (meaning the regulatory trigger would be the absence of a SNP) – something that is not there?

Many proposed gene editing applications will result in animals carrying desirable alleles or sequences that originated in other breeds or individuals from within that species (e.g. hornless Holsteins were edited to carry the Celtic polled allele found in breeds like Angus). As such, there will be no novel combination of genetic material or phenotype. The genetic material will also not be altered in a way that could not be achieved by mating or techniques used in traditional breeding and selection. It will just be done with improved precision and minus the linkage drag of conventional introgression.

It does not make scientific sense to regulate hornless dairy calves differently to hornless beef calves carrying the exact same allele at the polled locus (Carroll et al., 2016). Nor does it make sense to base regulations on human intent rather than product risk. Regulatory processes should be proportional to risk and consistent across products that have equivalent levels of risk.

There is a need to ensure that the extent of regulatory oversight is proportional to the unique risks, if any, associated with the novel phenotypes, and weighed against the resultant benefits. This question is of course important from the point of view of technology development, innovation and international trade, as well as the ability of the animal breeding community to use genome editing.

Currently there is only a single genetically engineered animal containing a heritable rDNA construct approved for food consumption anywhere in the world. In December 2015 the United States Food and Drug Administration (FDA) approved the AquAdvantage salmon for human consumption, although it is still not commercially available in the United States until the FDA publishes labeling guidelines for the fish. In 2016 Health Canada gave approval for the AquAdvantage salmon to be produced, sold and consumed in Canada. Animal breeders are therefore painfully aware of the chilling impact that regulatory gridlock can have on the deployment of potentially valuable breeding techniques. While regulation to ensure the safety of

new technologies is necessary, in a world facing burgeoning animal protein demands, overregulation of safe breeding methods is an indulgence that global food security can ill afford.

Conclusion

A plethora of technologies are currently at hand, with more to come. Our charge to the industry is to effectively make use of them towards improved animal populations. Animal breeding programs should position themselves to capitalize on a combination of advanced biotechnologies such as genomic information and advanced reproductive technologies to accelerate the rate of genetic gain. Ultimately these biotechnologies complement the genetic improvement that can be accomplished using traditional selection techniques and, if judged acceptable, offer an opportunity to synergistically accelerate beef cattle genetic improvement. Perhaps the bigger challenge is to improve the understanding and utilization of genetic selection tools both among those making selection decisions in the beef cattle industry, and in those groups seeking to influence public opinion. Many animal breeding goals have the potential to address sustainability challenges including improved animal well-being, efficiency and reduced environmental footprint. Something we would argue aligns with the shared, common values of a large segment of both cattle producers and the consuming public.

Acknowledgements

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Strategic Use of Heterosis

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Traditionally, in the beef cattle industry from 1920-1960's, crossing two breeds of beef cattle was considered an undesirable mating plan. Progressive cattlemen of this era had purebred Herefords, Shorthorns, or Angus. Any commercial producer that had crossbred animals quickly "graded up' to the breed of their choice and high levels of linebreeding were common. Dr. Lush (1945) suggested that crossbreeding was very common with swine and sheep breeders, becoming common with poultry and "rarer in cattle and horses".

Early work in crossing cattle in the Gulf Coast recognized the value of combining different breeds particularly when the survival of existing purebreds was very low. Crossbreeding has been practiced with great success in the Gulf Coast for nearly 100 years. Even during times when it was considered highly undesirable by many in the cattle business.

With the coming of the Continental breeds to the United States in the 1960's a whole new era of crossbreeding occurred. Introduction of large-framed fast growing European cattle resulted in a huge shift in cattle type. New genes from Continental cattle resulted in improved performance and often much of this performance was attributed to the new, breed. In fact some of the improvement in performance was likely a result of heterosis. It was often said that "I tried some of those new Simmentals, or Charolais, or Limousins, (or any continental breed) and man they are good….calves grow like crazy." Some of this increase in performance was certainly additive gene action. Some was no doubt heterosis. After one breed was used for a few years then a switch was often made to the next "hot" breed. This resulted in a repeat of the cycle as new genes where brought in from a different breed often resulting in improved performance and as a by-product, heterosis. In the process, the beef industry learned a hard lesson in genotype by environment interactions. Large framed, high-milking cows resulted as heifers from these crosses were kept. These cattle as a whole were fertile until the feed resources became limited during times of drought. What had resulted from this random crossing of breeds was an infusion of new genetics, a general increase in cow size and milk yield, increased nutrient requirements, some level of heterosis, and a rainbow of coat color patterns.

In the 1990's it was suggested that crossbreeding might be to blame for creating the problem of too much variation in the beef cattle industry. Certainly, crossing breeds did contribute to the variation in coat color. But coat color has never been a good indicator of uniformity. The 1991 Beef Quality Audit (Lorenzen et al., 1993) showed that beef was too variable in many carcass traits. These carcass traits are mostly moderate to highly heritable. Improvement in highly heritable traits is best accomplished via selection. Several breeds have been highly successful at improving carcass traits via this method. While focused selection for carcass traits was occurring in the last 25 years some in the cattle industry rekindled the theory of cattle that are one color are less variable in composition. Great strides have been made at improving carcass

traits in the purebred cattle industry and the breeding and selection decisions of the last two decades are now being realized as improvements in beef quality. But reproductive traits have not had similar improvement. In our estimation, there may even be a general decline in reproductive performance which has been masked by the effects of environmental modification most often in the form of available feed resources. Today's cow has better nutrition, but improvements in weaning weight have been marginal and reproduction has been stagnant. Reproduction is low in heritablity but subject to high levels of heterosis when breeds are crossed. The crossbred cow has been shown to be superior in many aspects including age at puberty, reproduction, and longevity. Despite this questions are still being raised "does heterosis still exist?"

Heterosis or hybrid vigor is simply defined as the improved performance of the crossbreds as compared to the average of the two purebreds that were used to make the cross. Higher levels of heterosis are realized when there is a large difference in the gene frequency between the breeds crossed for the trait of interest. Simply put, the more diverse the two breeds are the more heterosis is realized in the cross.

Crossbreeding systems are designed to combine various breed strengths (or minimize weaknesses) and take advantage of heterosis. Much of the early crossbreeding work was conducted with English crosses in the 1960's. Suggestions have been made that heterosis was valuable only when English type cattle were small and slower growing. Today's English type cattle are larger and in fact the data would suggest as large as many Continental cattle in mature cow size evaluations. Implications have been made that heterosis is no longer needed to improve production.

Studies that were specifically designed to evaluate heterosis of crossing different breed are less common today. Current research relating to genetic evaluations is focused on genomics and the search for genes controlling phenotypes. At one time, many states had large research herds of cattle to estimate the relative effects of breeds and crosses. These studies involved large numbers of breeds across many geographic regions. Data published from these studies formed the basis for much of what is known today about animal breeding and crossbreeding. Unfortunately these experiments are long term and by the time full results are obtained the industry has already moved on to the "next great breed." The early work with crossbreeding serves as a solid foundation still today and the results are still completely applicable to modern cattle production. Crossbreeding, and the accompanying heterosis, is still a valid and highly effective means of improving pounds of calf weaned per cow exposed. Its effects are mediated predominantly through increased fertility of the crossbred cow, increased survival of the crossbred calf, and longevity of the crossbred cow. These effects are often 20-25% (35% when using *Bos indicus* x *Bos taurus*) improvement in pounds of calf weaned per cow exposed. No other technology in the beef production provides this type of return from both biological and economic perspectives.

Certainly crossbreeding is not as simple as placing two breeds together. Depending on the system utilized there are requirements for extra pastures, calving ease bulls for yearling heifers, and marketing multiple types of offspring that may be multiple colors. Many of the more complicated systems only function appropriately with 500 or more cows. Ninety percent of the

cow calf producers in the US have less than 100 cow herd size. These obstacles result in low adoption of true crossbreeding programs. Instead what often results is a corrective mating plan that results in some heterosis but rarely maximizes hybrid vigor.

The lack of adoption of crossbreeding in the beef cattle industry is a result of several factors. Many producers crossbred and receive the benefits of crossing in the form of heterosis. However, very few utilize a planned crossbreeding program. Many of these mating systems have been well established for over 75 years. A full outline of these systems is beyond the scope of this article. An overview of breeding systems has been provided by Hammack (2011). Experimental results have repeatedly shown great benefit but execution of the systems is often difficult.

Crossbreeding systems may be divided into three types: Terminal, Rotational, or Composite. There are also combinations of these systems that work to generally increase heterosis.

In general, terminal sire systems maximize heterosis but do not produce their own replacement heifers. Many terminal systems are used in theory but often fall apart when a producer decides to keep some "big, good-looking, replacement heifers" from a terminal mating. Numerous examples of this occurred in the 1980-90's.

Rotational systems provide some level of hybrid vigor and produce replacement females. Often herd size is a limiting factor and these systems work best in large herds with ability to market different types and colors of offspring.

Composite systems have the advantage of some hybrid vigor and the production of replacements with the simplicity of straightbreeding. Some have suggested that the composite program would work best for small producers (1-2 bull herds). Successful examples of these systems are in place in the United States. Many of the composites that were initially formed used the red recessive gene to set color pattern. The price discrimination of non-black cattle in the US has limited the acceptability of some of the composite populations. It should be noted that the suggestion is not for a producer to develop his or her own composite but rather utilize a composite that has been developed by a larger purebred breeder. Composite formation is complex and requires a large number of cows to avoid inbreeding depression. Utilization of an existing composite is simple and similar to straightbreeding. Many of the early composite breeds like Brangus, Beefmaster and Santa Gertrudis were formed to provide a specific mix of *Bos indicus* and *Bos taurus*. Residual heterosis that resulted was a bonus but not the initial game plan. More recent development of composites from 4 breeds (25% each breed) result in more heterosis. Most of these composites have been developed in temperate climates and very few are available in tropical or subtropical regions. One quarter to one third of cows in the United States are in the South and face the challenges of heat stress for a large percentage of the year. However, beef industry structure may not lend itself to large scale adaption of composite systems. History has shown that many producers do not stick with a breed (or system) long enough to realize the benefits. Too often the lure of some new breed or cross often diverts the attention from the original plan. A historical review of beef industry trait selection would suggest that we often blow with the wind and almost always overshoot our target.

There is a belief that the only crossbred female that is worthwhile to have is the F1. In reality she is the Cadillac of females and will express maximal heterosis. But she is expensive to create from existing populations of purebreds. However, crossbreeding systems do not have to be started with purebreds. A simple sorting based on phenotype is all that is required. A producer might sort cattle into red and black coat color. The red cattle might receive an Angus bull and the black females receive a Herford bull. They will receive these sire types the rest of their productive lives and one has effectively started a two breed rotation.

In the Gulf Coast, the sort most common would be cows with *Bos indicus* influence (more ear) and those with minimal *Bos indicus* (less ear). The appropriate breeds may be picked to produce a calf of desirable type while keeping a specific level of *Bos indicus* percentage AND get some level of heterosis. Crossbreeding systems that are simple often have greater success even though they may not maximize heterosis. It is important to remember that the haphazard crossing of breeds is not a crossbreeding system.

Another serious impediment to crossbreeding has been our failure to have frank discussions about breeds and their strengths and weaknesses. For years it was taboo to say negative things about breeds for fear of hurting feelings or reducing a breeder's ability to merchandise cattle. There is not one breed that rises above all others in terms of maternal, growth and carcass in all environments. Many breeds excel at two of those categories and some in three categories. But no one breed excels in all three categories to be a perfect fit for all environments. The value of heterosis that is often forgotten and which we have found experimentally is that the **heterosis realized is often greatest in the harshest environments**.

The strategic use of heterosis requires a long term plan. Many small producers (<100 cows) would benefit from the use of a terminal sire system. They should purchase crossbred replacement heifers that fit their environment and resources. The independence of many of our cattle producers often interferes with the application of this plan. "I can't buy as good as I can raise" is often heard as the reason why terminal systems are not more popular. The fallacy in this plan is that only about half of the cows can exist in a terminal system. The other half of the cows must be in a system that makes replacement females. Rotational systems produce replacement heifers, but to function they require larger herd sizes and more pastures during the breeding season. Composite systems offer the merit of producing replacement heifers and providing hybrid vigor at some level.

It is possible to put together strategic crossbreeding plans using the breeds that exist in large numbers in the US. These plans have been laid out for 100 years yet adoption still remains only moderate. It must be stressed to producers that these plans are a 20 year decision. Some level of crossbreeding should continue to exist as the benefits to reproduction, calf survival and cow longevity are well established.

The dairy and egg industries have had great success in straightbreeding. Both of these industries work in a controlled environment and predominantly select for one trait. The modern dairy cow is a milk machine, but it is well documented that fertility, longevity and survival have all declined resulting in higher replacement cost to the dairy industry. The beef industry must

function in multiple environments and select for multiple traits. The most important of those traits is reproduction which is highly improved by crossbreeding. Regardless of breeding plan selected, the commercial industry should adopt the use of a crossbred cow. The benefits of early puberty, increased fertility, earlier calving, greater lbs. of calf /cow exposed and improved cow longevity are too great to be overlooked. As producers look for increased production and economic efficiencies, they already have the largest tool at their disposal in the breeding system they implement.

The most practical crossbreeding programs for small producers who want to raise their own replacements heifers is a two breed rotation or composite system. Larger more complicated systems yield more heterosis but often fail due to complexity of implementation. Regardless of the system utilized, much of the benefit to be realized from crossing breeds is a result of the use of a crossbred cow. Mating systems that emphasize the crossbred cow offer much advantage.

Mention of breeds in this publication is solely for illustration purposes. No endorsement is implied.

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The Power of Economic Selection Indices to Make Genetic Change in Profitability

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Introduction

The Beef Improvement Federation defines selection as "Choosing some individuals and rejecting others as parents of the next generation of offspring" (Beef Improvement Federation, 2016). This is a very simple, but accurate, way to describe one of the most important things we do in the cattle industry. Through selection, we have the power to control the flow of genetics that will ultimately determine the beef herd of the future. Cattlemen have historically used the best information available at the time to make genetic improvements to their herds. Granted, the train has fallen off the tracks a few times, but those same or improved selection tools were there to get us back on track. We contend that one of the best tools available for selection today, selection indices, is being underutilized.

Historically, selection was first practiced based on visual appearance and adaptation to local environments, which ultimately led to the development of breeds. This remained the basis of selection for many years until early in the twentieth century when the concept of heritability was applied to livestock species and expanded selection to some production traits based on actual or adjusted measurements. From the 1930's through the 1980's cattlemen used the knowledge of heritability to change cattle, sometimes in drastic ways from the extremely short, blocky cattle of the 1950's to the extremely large framed cattle of the 1980's. Single trait selection seemed to be the norm and took the cattle industry on some wild pendulum rides. National Cattle Evaluations and the publishing of Expected Progeny Differences (EPDs) started in the 1970's. They received widespread adoption and became the selection tool of choice throughout the 80's and 90's providing cattlemen with a more dependable means of making genetic change. For the first time cattlemen were able to make their decisions based on estimates of genetic merit across herds and years. In the mid 2000's, DNA/molecular technology was developed and its initial release caused a level of confusion for cattlemen because it was presented as a competing technology with EPDS. Eventually, methodologies were developed to permit incorporation of the molecular data into NCE with the result being EPDs with greater accuracies.

Expected Progeny Differences incorporating molecular technology, has given us an extremely powerful tool to make genetic change for a wide array of production traits. An EPD has not been developed for every economically important trait, but the list is expanding and every area of production has at least minimal EPD representation. Even though EPDs give cattlemen a great tool for making genetic change in production traits, they ignore economic considerations. It has been up to the individual cattleman to determine the economic impact of each trait and try to formulate that information into a multi-trait selection scheme. Without an organized, systematic approach to this complicated endeavor, the results are likely less than desirable. Unfortunately, this has led to an overemphasis on selection for increased outputs

without due consideration to the traits affecting costs. It is important to remember that income does not equal profitability; PROFITABILITY = INCOME – COSTS. The solution to this was the development of economic selection indices, which many breed associations and some private companies have developed and published starting in 2004. This technology was developed in 1940s (Hazel, 1943), and has been used extensively in other livestock industries, but has not seen widespread use in beef until recently. In Weaber's (2014) summary he stated "Selection indices provide a single value, usually reported in dollars, for the selection of breeding stock that optimizes selection on a number of traits the define profit in a particular production scenario. Selection indexes simplify selection by weighting EPDs by appropriate economic values to estimate the net merit of a selection candidate under a predefined breeding objective or goal". The Beef Improvement Federation has presented information on the development and advancement of this technology (Crews, 2005; Spangler, 2010, Brigham, 2011; Ochsner, 2016); however, the purpose of this paper is to address increased adoption.

Why Selection Indices?

In order to make wise selection decisions cattlemen are encouraged to define breeding objectives based on their management and market. Factors such as when and how the cattle will be marketed, retention of replacement heifers, feed quality, availability and cost, and other management practices all play a role in determining breeding objectives. Breeding objectives give cattlemen a target to shoot for with their selection program.

Economic selection indices are a means of making selection decisions based on the economic impact of several traits simultaneously and make genetic progress towards increased profitability. In some cases, it allows for the selection of animals based on a single number that reflects the genetic contribution to its offspring's economic potential. In the best-case scenario, all of the EPDs of economic importance to the specific management and marketing scheme are included in the index. If profitability is the goal in the beef industry, then the authors argue that economic selection indices are the best selection tool available to achieve this end.

What is Available?

Many breeds and some private genetic evaluation companies are currently computing and publishing selection indices. These indices sort into three basic groups; Terminal (Table 1), Weaning/Replacement (Table 2) and All Purpose (Table 3).

Terminal Index

In general, these indices focus on a marketing endpoint of selling carcasses on a Quality and Yield Grade basis. The assumption is that no replacement females will be retained from this mating. Typically, these indices assume that primarily mature cows will be mated and therefore do not place much, if any, emphasis on calving ease. An important component of profitability in a terminal index is feed intake in relation to gain (feed efficiency). There is increasing information available on feed intake, but this trait is still unavailable for several of the indices.

Target: These indices are typically used to select bulls for commercial use when all calves are planned to be marketed as finished cattle or carcasses. No replacement females will be kept. Little to no emphasis is placed on calving ease, so awareness of the Calving Ease Direct EPD is advised, particularly if heifers are to be bred.

Weaning/Replacement Index

For many commercial cattlemen, weaning or yearling is when their cattle are marketed. In addition, a high percentage of these producers keep their own replacement heifers. Currently, few indices are designed to specifically fit this production scheme even though it represents the largest segment of the beef industry. Some All-Purpose indices may meet this need, particularly if the index places a strong emphasis on reproduction traits. If that is the case, then commercial cow/calf producers could effectively use the all-purpose index to effectively select bulls that would satisfy their cost/revenue streams while placing some emphasis on feedlot and carcass traits that will benefit the industry.

Target: These indices are for cow/calf cattleman that sell weaned or backgrounded calves and keep replacement heifers. Calving ease is considered in these indices, but if a large portion of the females to be mated are heifers then additional attention to calving ease may be warranted.

All-Purpose Index

The all-purpose indices assume a marketing endpoint of selling carcasses; however, with this index the management scheme assumes that replacement females will be retained. The indices have varying levels of emphasis on calving ease, but all include both Calving Ease Direct and Calving Ease Maternal. All indices include some measure of female fertility and carcass merit. Feed efficiency or feed intake are absent in most of the indices. Since the all-purpose indices include the entire production system, and include the greatest number of traits, the risk is spread out making these indices the most stable and robust.

Target: These indices take into consideration the entire production model from conception to carcass. These indices work best for cattlemen that plan to market steers and the majority of heifers as carcasses, but plan to retain replacement females from the mating. Seedstock producers that are targeting balance in their breeding program also use these indices.

Keys to Successful Implementation

The first key to successfully implementing an effective breeding program utilizing selection indices is to develop and define your breeding objectives. Selection causes change to the herd; most are intentional, but some are consequences. It is critical to know what traits are important to your management and marketing scheme, but also how selection for those traits affects other traits of economic importance. For example, if a selection scheme was implemented to maximize calf weaning weights and replacements are to be retained, it might be tempting to select for maximum weaning weight direct and weaning weight milk EPDs. The result of this system would be large weaned calves, but there may be other consequences. Because of genetic

correlations, this mating scheme would also result in large, heavy milking cows that require greater nutritional demands; if those demands are not met then reproductive failure is a likely result. When these traits are included in a selection index then proper economic weighting is placed on these traits to balance the costs and returns to maximize profit. When used properly, selection indices allow you to focus on your target while minimizing negative consequences based on a profitability model.

Selection indices do a great job of economically balancing the traits that are included in the index, but there may be traits of economic/convenience/quality of life value to your cattle business that are not in the index of choice. When this occurs, you need to use the index in tandem with the additional trait(s) of importance. A good example would be selecting for improved temperament in conjunction with improved carcass traits. In this scenario, it would be beneficial to select based on a combination of the Terminal Index and the Docility EPD. Another example would be a seedstock producer that wants to market bulls with large scrotal circumferences, with the expectation of improved bull fertility (Rusk, et. al, 2002), and desirable hair shedding ability in addition to good index values, a combined selection scheme would need to be implemented.

Most selection indices assume that traits have a linear relationship with profitability, which is not always the case. Calving Ease Direct is a good example; there is a certain level of calving ease that when reached no more incidences of dystocia will occur. At this point, increases in Calving Ease Direct EPD will not add to increased profitability of the bull, but larger values will continue to increase the index value. This will give the appearance of greater profitability than will be realized. Another trait that may not function in a linear manner is milking ability. Indices do account for the fact that milk contributes to both increased costs and increased revenue and balances the effects. However, at extreme values the consequences may not be reflected in a linear model. Extreme milk levels in a herd with limited resources may have devastating consequences in reproduction, and thus profitability, that the model cannot account for. From a practical standpoint, it makes sense to look at the individual EPD values of bulls that are being considered and avoid those with extreme values in traits of concern.

Some common reasons that cattlemen do not use selection indices is that they may not perfectly fit the management and marketing plan or they are concerned that prices change so the index being used for selection today may be different in the future. Within reason, these issues should have little impact on the genetic progress made by using selection indices (VandePitte and Hazel, 1977). As long as there is a value line for most or all of the traits in the index then the bulls that rise to the top will likely be the same bulls under slightly different circumstances.

What Does the Future Hold?

Selection Indices are a great tool, but there is still room for improvement. Some of the issues that need to be addressed are:
- Limited number of Economically Relevant Traits (ERT) for some areas that play a large role in profitability
- Limited indices specifically targeted to commercial cow/calf producers

- Gathering accurate commercial herd data in proper contemporary groups can enhance the accuracy of traits like stayability relative to commercial cow/calf selection
- Multi-breed indices that can incorporate heterosis information
- Accuracy values for indices similar to BIF accuracies for EPDs

Many of these concerns can be eliminated with minimal additional inputs, but others will require considerable work.

Work is currently underway to enhance the suite of ERTs in areas such as health, reproduction and feed efficiency/cow maintenance. All of these traits have significant impact on profitability, but EPDs in these areas are still limited. DNA/molecular technology will assist in improving the availability and accuracy of many of these traits, but large quantities of phenotypic data are still needed to make this happen.

Expanding the indices that would benefit commercial cow/calf producers that do not retain ownership should be extremely easy. Indices that have a marketing endpoint of weaning or after backgrounding and retained heifers would be of great benefit to a large segment of the beef industry and would require minimal resources. More information is needed on the effectiveness of using an all-purpose index in this segment of the industry. If it can be shown that genetic progress toward increased profitability is not significantly diminished, with the added benefit of improve feedlot and carcass performance, then this would be a great alternative that is also beneficial to the entire beef industry.

Developing selection indices that are multi-breed, with heterosis incorporated, are not impossible tasks, but will require considerable effort to implement. The USDA Meat Animal Research Center is our greatest resource for estimating heterosis values and have provided them for many traits; however, there are still gaps for some economically important traits. Work continues to develop heterosis values for the more difficult traits that influence profitability and when available it will facilitate the development of multi-breed indices.

Accuracy values associated with EPDs are a risk management tool; cattlemen know that lower accuracies means increased risk for a larger change in the genetic merit estimate of the animal. Unfortunately, there is not an accuracy value associated with selection indices at this time and thus no measure of risk associated with them.

As demand for selection indices increases, there will likely be an expansion in the number computed and improvements in their effectiveness. Part of this improvement will come in the increased accuracy in computing EPDs with molecular information. Additional improvements will come as new ERTs are developed and improved. The good news is that a tool that is very useful today will be even better in the future.

Conclusion

Selection indices provide cattlemen with a simple, effective tool to make multi-trait selection decisions that are profit driven. It is prudent to know what traits are included in a prospective index to ensure that individual management and marketing needs are being met and that undue influence is not coming from a trait that does not have a cost/revenue stream. Traits of importance that are not included in the index, heterosis considerations, convenience/personal preference traits, visual appraisal and other factors specific to your cattle business must remain a

part of your overall breeding program, but a well-matched selection index will aid in simplifying the selection process.

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Table 1: Traits included in Terminal Index based on published indices. Terminal – Feedlot and/or Carcass/No Replacements

Index	CED	BW	WW	YW	Intake	PWG	CW	Quality	Yield
Angus									
$Feedlot			X	X	X				
$Grid							X	X^j	$X^{o,p}$
$Beef			X	X	X		X	X^j	$X^{o,p}$
Beefmaster									
Terminal			X	X				X^k	X^p
Charolais									
Terminal Sire Profitability		X	X	X			X	X^j	$X^{o,p}$
Gelbvieh									
FPI	X		X		X	X	X	X^j	X^m
EPI				X	X	X			
Hereford									
Certified Hereford Beef[1]	X		X	X			X	X^k	$X^{o,p}$
Limousin									
Mainstream Terminal			X	X			X	X^j	$X^{o,p}$
Red Angus									
GridMaster			X	X			X	X^j	$X^{o,p}$
Simmental									
Terminal	X		X		X	X	X	X^j	X^m
Shorthorn									
Feedlot	X		X	X			X	X^j	$X^{o,p}$
Industry Indices									
Method QPI						X	X	X^j	X^p

CED = Calving Ease Direct, BW = Birth Weight, WW = Weaning Weight Direct, YW = Yearling Weight, PWG = Post-weaning Gain (see below), FE = CW = Hot Carcass Weight, Quality = Carcass Quality (see below), Yield = Carcass Yield (see below)

Quality = Marbling[j], Intramuscular Fat[k]

Yield = Yield Grade[m], Fat[o], Ribeye Area[p]

[1]Dry Matter Intake with be included starting summer 2017

Table 2: Traits included in Weaning/Replacement Index based on published indices. Feeder – Replacements/No Feedlot/No Carcass

Index	CED	BW	CEM	WW	YW	Milk	HP	SC	Mat
Angus									
$Wean		X		X		X			X
Beefmaster									
Maternal				X	X	X		X	
Shorthorn									
$CEZ	X				X				
Industry									
Method MPI	X		X	X		X	X		X

CED = Calving Ease Direct, BW = Birth Weight, CEM = Calving Ease Maternal, WW = Weaning Weight Direct, YW = Yearling Weight, Milk = Weaning Weight Maternal, HP = Heifer Pregnancy, SC = Scrotal Circumference, Mat = Mature Cow Size

Table 3: Traits included in All Purpose Index based on published indices. All Purpose – Replacement/Feedlot/Carcass

Index	CED	CEM	WW	Milk	Fert	PWG	FE	Mat	CW	Qual	Yield
Gelbvieh											
$Cow	X	X	X	X	X[a,b]	X[h]	X	X		X[j]	X[m]
Hereford											
Baldy Maternal[1]	X	X	X	X	X[c]	X[g]			X	X[k]	X[p]
Calving Ease[1]	X	X	X		X[c]				X	X[k]	X[p]
Brahman Influince[1]	X	X	X		X[c]				X	X[k]	X[p]
Red Angus											
HerdBuilder	X	X	X	X	X[a,b]	X[g]			X	X[j]	X[m]
Simmental											
All Purpose	X	X	X	X	X[a]	X[h]	X	X	X	X[j]	X[m]
Shorthorn											
$BMI	X	X	X	X		X[g]			X	X[j]	X[o,p]
Industry Indices											
Method ROI	X	X	X		X[b]	X[h]		X	X	X[j]	X[p]
Dollar Profit	X	X	X	X	X[d]	X[g]	X	X	X	X[j]	X[n,p]

CED = Calving Ease Direct, CEM = Calving Ease Maternal, WW = Weaning Weight Direct, Milk = Weaning Weight Maternal, Fert = Fertility (see below), PWG = Post-weaning Gain (see below), FE = Feedlot Feed Efficiency, Mat = Mature Cow Size, CW = Hot Carcass Weight, Qual = Carcass Quality (see below), Yield = Carcass Yield (see below)

Fertility = Stayability[a], Heifer Pregnancy[b], Scrotal Circumference[c], Days to Conception[d]

Post Weaning Gain = Yearling Weight[g], Feedlot Gain[h]

Quality = Marbling[j], Intramuscular Fat[k]

Yield = Yield Grade[m], % Retail Product[n], Fat[o], Ribeye Area[p]

[1]Dry Matter Intake, Sustained Cow Fertility and Heifer Calving Rate will be included starting summer 2017

Investing in the Future: Heifer Development for Longevity
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Selection and development of replacement heifers has, rightfully so, garnered considerable attention in research, educational programming, and popular press for many years. While the basic concepts have not changed for decades, new technologies, changes in market dynamics, and leveraging improved genetics has enabled producers to become more efficient with the dollars and time they invest in replacements.

Options for Procuring Replacement Heifers

There are three basic options for obtaining bred replacement heifers. The most common, but not necessarily the best, method is to retain heifers from each calf crop to develop and breed on-farm. Selling all the heifers in a calf crop and purchasing bred replacements or open heifers to breed is another option. The third option, and seemingly least used in beef cattle production, is to retain heifers from the calf crop and have them custom developed by someone else. Nuances develop in these three basic methods depending on geographical and individual farm/ranch influences. Several factors that impact this decision include economics, available resources, experience, genetic improvement, and convenience. The financial concerns of developing replacement heifers are related to diverting cash flow and resources. Consider purchasing replacements if higher returns can be generated by an alternative use for the proceeds from feeder calf sales.

Farm or ranch resources will also direct this decision. If forage or feed supplies are already maximized or overextended by the mature cow herd, then purchasing replacement heifers would be an obvious choice. Proper development of heifers takes a certain amount of knowledge and experience that differs from management of a mature cow herd. Opportunity costs are often overlooked when making management decisions. The convenience of having someone else raise replacements is a valid consideration, especially when the cattle operation is not the primary source of income or operator time or labor is limiting. Custom heifer development centers have become a support-business of the cow-calf sector. Consigning heifers to a custom developer is the best way to retain herd genetics while not using limited environmental resources from the cow herd to raise heifers.

Timeline and Objectives

The period of time most often indicated by the term "heifer development" is from weaning to confirmed pregnant after the first breeding season. For this discussion, that term refers to the period of time from weaning until confirmed pregnant as a two-year-old after the second breeding season. There are several factors that influence development and longevity prior to birth and between birth and weaning. Those factors are usually accounted for during selection or result in early culling during development.

In addition to the significant cash cost for retaining/purchasing and developing heifers, there is a tremendous amount of opportunity cost and time invested. Consider the time from a mating that

results in a retained heifer until that heifer is confirmed pregnant the second time as a two-year-old (Figure 1). That adds up to well over three years and one season of lost cash flow from the heifer's dam. It is easy for cattlemen to lose track of this investment because it is masked by the everyday tasks of maintaining the herd. But, losing that investment when a young cow is culled and average longevity reduced, adds up to enormous losses of sunk costs. Herein lies the importance of selecting, developing, and breeding heifers with longevity in mind.

Time Period	Days
Sixty day breeding season	60
Gestation period for brood cow	285
Birth to weaning	210
Weaning to breeding	240
Gestation period for heifer	280
Calving until re-breeding	80
Rebreeding until pregnancy exam	45
Total time in days	1200 Days
Total time in months	40 Months

Table 1: Time investment from mating that results in a retained heifer until it is confirmed pregnant the second time as a 2-year-old.

To help safeguard the time and resource investments, basic heifer development objectives that help ensure longevity include:
- Reach puberty prior to the first breeding season
- Breed early in the first breeding season (ideally in the first 20 days)
- Minimize calving difficulty
- Breed early in the second breeding season
- Improve genetics for production goals

Puberty and the First Postpartum Interval

Anestrus (not having estrous cycles) has long been recognized as the primary factor reducing reproductive efficiency in beef cow-calf operations (Short, 1990). Unfortunately, anestrus occurs annually in productive females; heifers are anestrus prior to puberty and cows undergo a period of anestrus after each calving. The length of the anestrous period is governed by many factors including presence of a calf, nutritional status, cow age, and degree of calving difficulty. First-calf heifers normally experience a longer postpartum anestrus than mature cows because they have the additional energy requirements of still growing during the first lactation.

To calve at 24 months of age, heifers must reach puberty and conceive by approximately 15 months of age. Several factors influence the age at puberty including breed composition, nutrition, body weight, bull exposure and the environment (Patterson et al., 1992). Lifetime productivity of a female is affected by age at puberty. Heifers that conceive early in the first breeding season are more likely to conceive early in subsequent seasons and thus become more productive cows (Lesmeister et al., 1973).

Similar to postpartum anestrous in cows, the proportion of heifers that are pubertal at the beginning of the breeding season influences reproductive rate. Patterson and coworkers (1992) indicated that approximately 35% of heifers were prepubertal at the onset of the breeding season. In more recent studies, 88% (Larson et al., 2004), 83% (Lamb et al., 2004), and 57% (Lucy et al., 2001) were prepubertal on the first day of the breeding season.

Anestrus, whether prepubertal or postpartum, greatly influences successful reproduction in beef cow-calf operations. Protocols have been developed that effectively induce a fertile estrus in anestrous females. Incorporation of these protocols and managing heifers with the goal of reducing their first postpartum interval will enable beef cow-calf operations to maximize reproductive potential and longevity.

Selection

Selecting early born heifers has long been the first rule of thumb since older heifers will be more likely to attain puberty prior to the first breeding season. A less aggressive nutritional program may be used for heavier weaning heifers and possibly reduce feed costs. However, genetically superior heifers born later in the calving season can be managed to reach proper target weights by breeding and could be considered as replcements over older heifers with less performance potential. Realize that selecting only the largest heifers at weaning can result in larger mature cows that are less efficient.

Temperament should be another key selection criterion. Many beef producers have adopted a "chute scoring" method to keep temperament records. When heifers are restrained in the working chute, they can be assigned a score from 1 to 4 (1 = calm; 2 = restless shifting; 3 = squirming; 4 = twisting and rearing). Temperament is a heritable trait and removing temperamental heifers from the herd will improve farm safety. Furthermore, temperament can negatively affect feeding behavior and reproductive performance of not only the individual heifer but the group it is fed with as well (Cooke et al., 2012).

All heifers selected for development as breeding females should be structurally sound. Hoof structure should be closely evaluated as the heifers mature and can be guided earlier in selection by knowledge of hoof structure of the sire and dam. Udder conformation is key to longevity but requires as much evaluation of the heifer's dam, paternal grand dam, sibs, and half-sibs, as evaluation of the heifer itself. Heifers that do not fit ranch specifications for breeding females will be better suited for post-weaning programs that ultimately result in harvest prior to advanced maturity.

Genetic selection for Seedstock producers is generally guided by EPDs, sometimes gnomically-enhanced, of individual heifers mated for specific goals. Even though Seedstock producers tend to more aggressively improve genetics year-over-year and voluntarily market cows at a younger average age, longevity should still be a primary driver of selection with their commercial clientele in mind. Technologies for genomic selection in commercial herds have made considerable advances in recent years. The market is quickly finding the most appropriate use for including genomic analysis in more traditional benchmarking and indexing tools for commercial herds. Carcass ultrasound is a useful tool for improving carcass merit selection in purebred and commercial herds and is important for validating genomic tools in replacement heifers that will not be harvested as fed cattle.

With all the tools and technologies available to aid heifer selection, the most important phenotypic trait for replacement heifers is pregnancy. In that light, retaining all the heifers from a calf crop, which meet minimum basic requirements, to be exposed to either a single timed AI or one cycle (roughly 20-30 days) with natural service sires is a great option where resources permit. Then, pregnancy is diagnosed early via ultrasonography or blood-based testing and open heifers marketed or retained as heavy feeders. This method ensures selection based on the most important criterion but, it might not be feasible for smaller herds.

Nutritional Management

The traditional approach to feeding replacement heifers has been the "target weight" method (Varner et al., 1977). For heifers to breed at 13 to 15 months of age and calve for the first time as two-year-olds, they should achieve approximately 65 to 70 percent of their mature weight by the start of the breeding season. This helps ensure that the metabolic signals are in place to trigger puberty before the start of the breeding season.

As reviewed by Endecott et al. (2014), more recent reports have suggested that the "target weight" system for developing heifers has become outdated and costly. As beef cattle producers switched from calving heifers as three-year-olds to calving as two-year-olds, more emphasis has been placed on selecting heifers that reach puberty at an earlier age and lighter weight in relation to their expected weight as a mature cow. In support of this idea, field trials have demonstrated that heifers developed to lighter weights relative to their mature weight achieved similar pregnancy rates and longevity in the herd over four years compared to traditionally fed heifers (Funston and Deutscher, 2004 and Mulliniks et al., 2012).

When designing a nutritional program to develop heifers to target breeding weights, evaluate pasture/hay quality and supplies ahead of time. Supplemental feed requirements can be determined by examining weight gains needed to reach target breeding weights, animal nutrient requirements, and forage program deficiencies. The plane of nutrition for reaching the target weight can be altered to match forage availability or feed cost. For instance, if forage is abundant or supplemental feed is relatively inexpensive early in the development period, heifers can be fed to maintain a high ADG early and reach the target weight faster. Then, when forage or supplemental feed availability declines, they can be maintained on a maintenance (or slightly above maintenance) diet until breeding. On the other hand, if forage is limited and supplemental feed cost is high during early development, heifers can be maintained on a low ADG and then

pushed to reach the target weight as forage becomes available or supplemental feed cost decreases. If supplemental feed and forage availability are not a concern, a steady ADG can be maintained.

Regardless of the nutritional program used, it is important to remember that the heifers should not be allowed to lose weight ("back up") or become too fat during the developmental period. Losing weight can alter the age at puberty even if the target weight is reached at the desired time. If heifers are overfed, fat accumulation in the udder will inhibit milk production as a first-calf-heifer and mature cow. Furthermore, multiple feeding groups should be used because individual heifers will require different nutritional inputs.

When cost of production outpaces revenue, developing heifers to a lighter target weight may be appropriate. Using the flushing affect (increasing plane of nutrition approaching the breeding season) seems to be a key component of reproductive success in this system. However, even if the heifers breed well, they should still be managed to calve with additional condition to ensure a shorter postpartum interval. Management practices should not be changed suddenly and implementation of low-input development should be done with careful attention to detail and when genetic potential of the specific group of heifers is known.

Some feed additives or specific feed ingredients can be used to improve heifer development and reproductive performance. Heifers fed an ionophore during development will likely reach puberty at an earlier age and lighter weight. The effect of an ionophore is most obvious in less intensively managed herds. Dietary fat supplementation increases the energy density of the diet and can help improve reproductive function. Additionally, fat supplementation seems to have a direct impact on reproduction independent of the added energy. Additional starch (corn, for example) not only adds energy to the ration but might also shit to a more favorable type of energy from the rumen that advances puberty.

Reproductive and Health Management

Puberty in heifers can be characterized as the first estrus (standing heat). Keep in mind the silent ovulation mentioned in the section above on attainment of puberty and the postpartum interval. A long-held acceptance has been that heifer fertility increases approximately 20 percent from the first to third estrus after puberty (Byerly et al., 1987). However, more recent reports indicate that the magnitude of that improvement is less in modern beef heifers (Robets et al., 2013). Nevertheless, nutrition still plays a large role in the attainment of puberty for heifers. If the nutritional management outlined in the previous section is practiced with adjustments based on input costs relative to benefit, heifers should display estrus prior to the breeding season.

Breed differences, sire and dam effect within breed, and heterosis (hybrid vigor) all contribute to heifer age at puberty and should be considered when selecting heifers at weaning or when making breeding decisions for cows that will potentially produce replacements. Crossbred heifers with less than 75 percent of one breed have a significantly reduced age at puberty compared to purebred heifers. Additionally, overall fertility is increased in crossbred heifers.

Three management practices to be completed one month before the breeding season begins:

1. Pelvic area measurements
2. Reproductive tract scores
3. Vaccination and parasite control

Pelvic area measurements are simply a measurement of the size of the birth canal (Deutscher, 1987). The original use of pelvic area measurements was to relate the size of heifer, size of pelvic area, and potential size of an easily deliverable calf. Because the ratios used to determine size of a deliverable calf are only approximately 80 percent accurate, most heifer development programs set a minimum threshold ("cutoff") to cull heifers with a pelvic area too small to allow delivery of a 70- to 75-pound calf. For example, an 800-pound long yearling heifer with a pelvic area of less than 160 square centimeters would be culled to reduce the opportunity for calving difficulties to high-accuracy, low birthweight sires.

Reproductive tract scores are used to determine a heifer's sexual maturity (Anderson et al., 1991). This procedure was developed because directly measuring puberty in a group of heifers is time consuming and labor intensive. The score can range from 1 (immature) to 5 (cycling). It is simply an estimate of sexual maturity based on ovarian follicular development and palpable size and tone of the reproductive tract. It is critical to use an experienced, reliable technician for reproductive tract scoring. This measurement is usually taken at the same time pelvic area is assessed. If estrus synchronization is not going to be used, consider culling heifers with a reproductive tract score less than three, especially if the genetic value is marginal. If estrus will be synchronized by using melengestrol acetate (MGA) or a Controlled Intervaginal Drug Releasing device (CIDR), heifers with a tract score of 2 could be retained.

The third practice to be completed one month prior to the breeding season is vaccination. Heifers should be vaccinated against *Vibrio fetus*, Leptospirosis, and a respiratory complex that includes Parainfluenza Type 3 (PI_3), Bovine Respiratory Syncytial Virus (BRSV), Bovine Viral Diarrhea (BVD), and Infectious Bovine Rhinotracheitis (IBR). A modified-live vaccine is generally considered to stimulate a better immune response. However, that assertion has been challenged recently (Daly, 2016). It is also suggested to test each heifer for persistently-infected bovine viral diarrhea virus (BVD-PI). Heifers should also be dewormed at this time and effective fly control used as needed.

The next step in heifer development is breeding. Using estrus synchronization and/or artificial insemination (AI) present advantages. The advantage of using estrus synchronization is increased pregnancy rates, a more uniform calf crop at weaning, and increased labor efficiency at breeding and calving. The major benefit offered by AI is access to proven calving ease sires with superior growth and carcass performance genetics. Because most calving problems occur when heifers calve for the first time, special attention should be given to make sure the sire has a desirable and high-accuracy calving ease and/or birth weight EPD. Calving ease should also be considered when selecting a "clean-up" or natural service sire to be used for the remainder of the breeding season after AI. Choosing an estrus synchronization protocol that uses some form of progestin (MGA or CIDR) can stimulate heifers that are on the threshold of puberty to begin to cycle and have a better chance to breed within the breeding season (Anderson et al., 1996).

Pregnancy detection should be performed as early as possible after the end of the breeding season; transrectal ultrasonography and blood-based pregnancy tests are ideal options for early

detection. This will enable a quicker and more informed decision for obtaining salvage value from non-pregnant ("open") heifers. If performed early enough, open heifers can be sold as heavy feeder cattle or moved to a finishing phase. A tremendous amount of revenue potential is lost when open heifers are maintained through the first calving season without producing a calf. They consume more resources and cash and are marketed as non-feds at a much lower value.

If the number of bred heifers exceeds the required replacements, market those bred late in the breeding season. Search for a beef cattle producer that uses a later calving season to market these heifers at a larger profit than heavy open heifers. Further culling should be based on performance data and genetic potential. Keep heifers that grew well and were more efficient during the development phase or that have a dam and/or sire with proven valuable EPDs, genomic analysis results, and/or performance records.

Post-breeding Heifer Management

Management of heifers from the end of the breeding season until calving often receives less attention and fewer resources than development from weaning to breeding. Yet, it is as important to longevity as any other time period in the development phase. Nutritional management, conformation of pregnancy, and calving should be the focus.

If the initial pregnancy diagnosis was performed at less than 60 days post-breeding, late embryonic and early fetal loss can still be significant. Pregnancy loss carries a greater negative economic impact the later it occurs because more resources are consumed without return beyond salvage value of the heifer itself. Technologies that predict the probability of pregnancy loss are in development but have not yet reached full application and market potential. Continue to look for those capabilities and implement them as soon as they are economically feasible to reduce the number of pregnancies lost in the second and third trimesters.

Cows and heifers use energy for maintenance, growth, lactation and reproduction; in that order. A heifer's energy needs for maintenance, growth and lactation must be met before energy is used to begin normal estrous cycles after calving. Adequate nutrition is critical during the last two months of gestation since much of the fetal growth occurs during this time. Separating heifers from the mature cow herd limits competition for bunk space and allows them to be placed on a separate nutritional program that better meets their requirements. Reproduction is regulated by nutrition. Having cattle in proper body condition at calving will positively impact rebreeding rates. Cows and heifers in thin body condition at calving time are slower to rebreed, produce less desirable colostrum, and are less likely to wean a live calf seven to eight months later.

Body condition scoring (BCS) is useful in evaluating heifer nutritional status as calving approaches. It can be easily evaluated in the pasture. Heifers are still growing and have higher nutrient requirements than mature cows, so they should be managed to calve at a body condition score of 6 (where 1 = extremely thin and 9= extremely fat). In addition, calves born to heifers with a BCS of five or six stand sooner after birth than calves out of heifers with a BCS of three or four (. Ideally, heifers should not lose more than one BCS after calving.

While BCS is an important tool, realize that it is an evaluation of nutritional status at the point it is taken and does not indicate plane of nutrition unless it is evaluated at multiple points over time. For example, a heifer losing weight just before calving might appear to be in good

condition at a given point in time. But, it will biologically perceive that its environment if not favorable for quickly establishing another pregnancy after calving; consequently extending the postpartum period.

Conclusions

Both selection and development of replacement heifers impact eventual longevity and productivity as mature cows. Even when all the tools for selection have been effectively implemented, management from weaning to breeding and then rebreeding as a first-calf heifer can negate many of those positive genotypic and phenotypic traits. The basic principles of management that make a good heifer into a productive cow remain the same – breeding early as a virgin heifer and rebreeding in the second season. New technologies and improved genetics have enabled different approaches to replacement heifer development. Staying current with these new concepts will allow progressive cattlemen to stay true to those basic principles more efficiently.

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Lessons Learned from 32 Years of Retained Ownership – TCSCF Summary

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Tri-County Steer Carcass Futurity (TCSCF) was started by Pottawattamie, Cass and Shelby County Cattleman's Association in 1982. The nine member board wanted to know "what was the most profitable steer to feed?" In 2002, the SW Iowa cow-calf consigners utilizing the TCSCF program formed a service cooperative. The current 10 member board has 7 cow-calf producers, two allied industry representatives and one veterinarian.

Cow-calf producers who retain ownership are financially responsible for the genetics, health and management of their calves. Common traits of TCSCF consignors are 1 – early adopters of genetic evaluation tools, 2 – utilize a team of advisors to adopt available technologies to improve calf health and performance, 3 – tired of someone else benefiting from their efforts in genetics, health and management, 4 – believe in working together and sharing information with other producers.

The TCSCF program is about beef producers working together to identify problems they have control over, evaluating alternatives, selecting the best alternative, collecting and analyzing data, and sharing the results to become better beef producers each and every day. The TCSCF Board and consignors have worked with many Extension workers across the US and Canada and partnered with Certified Angus Beef, Iowa Beef Center, Igenity, Pfizer, Fort Dodge Animal Health, Boehringer-Ingelheim, Iowa Beef Industry Council and National Cattleman's Beef Association.

Consignors are able to utilize growth, health and carcass data to make changes in their cowherd. Comparing 1 year and 4 or more years of participation, steers had higher ADG (2.98 vs. 3.25), with lower standard deviations (.62 vs. .24), respectively. Non-weaned calves were 3.4 times more likely to experience BRD than weaned calves, independent of differences in age, test center, or vaccine status. Calves vaccinated with killed vaccines were 2.2 times more likely to experience BRD than calves vaccinated with MLV vaccines, independent of other factors.

Calves not treated compared to calves treated two or more times gained better (3.21 vs. 2.93 lb/day), produced more Choice carcasses (52% vs. 42%), and were more profitable ($52.45 vs. -$137.30/hd). Calves with evidence of lung adhesions after harvest had higher health treatment costs ($12.23 vs. $5.29), poorer ADG (3.01 vs. 3.19), lighter final live weight (1160 vs. 1176) and hot carcass weight (723 vs. 725), lower marbling scores (SM 10 vs. SM 27) and made less money ($1.65 vs. $45.27) than those without lung adhesions. Untreated calves at the feedyard produced carcasses that had lower Warner-Bratzler shear values (0.46 ± .18 lb) compared to treated calves.

The heritability estimate of BRD incidence and the number of treatments were 0.07 ± 0.04 and 0.05 ± 0.04, respectively. Because of the high economic cost associated with BRD incidence, even these modest estimates for heritability of BRD resistance should be considered for incorporation into beef cattle breeding programs.

Southeast calves compared to Midwest calves were older on feedlot arrival (320 vs. 255) had fewer pulls (15.81% vs. 22.11%) and higher CAB acceptance rates (18.43% vs. 16.91%). Midwest calves compared to Southeast calves produced heavy carcasses (725 vs. 723), larger ribeye areas (12.46 vs. 12.33) and higher % Choice – (52.93% vs.50.32%). When considering feedlot and carcass traits and all associated costs including trucking to the feedlot, the Southeast calves had a profit/head of $37.34 versus $23.79 for Midwest calves.

Docile cattle compared to aggressive cattle gain less in the feedlot (3.17 vs. 2.91), produce fewer Choice carcasses (72.4% vs. 58.1%), more Select carcasses (23.3% vs. 36.2%) and the black hided cattle produce a higher percentage CAB carcasses (29.1% vs. 14.3%). Morbidity rates are similar across disposition scores but death loss increases significantly as disposition scores increases. Non-replacement heifers have higher disposition scores than steer mates, as cow-calf producers select for more docile replacement heifers. Average profit for docile cattle was $46.63/head compared to $7.62/head for aggressive cattle.

Marbling score remains the most important variable over the range of feed and carcass prices considered when evaluating factors impacting net return. Feed to gain, placement weight and hot carcass weight are the most sensitive variables to changes in feed costs. Placement weight and hot carcass weight are more important with lower feed costs and feed to gain is more important with higher feed costs. Hot carcass weight is the only variable to show much change due to a change in base price. It is more important at higher prices and less important at lower prices.

Lots consisting of heifers had higher (P<.05) low Choice and above rates than lots of steers or mixed-sex pens. The greater the amount of Angus influence in the cattle, the higher the low Choice and above rate (P<.0001). An inverse relationship existed between feedlot in-weight and lot low Choice and above rate; those cattle with lighter feedlot arrival weights had higher % Choice and above rates (P=.0007). Cattle with lower disposition scores (calmer cattle) had higher % Choice and above rates (P=.0496). Low Choice and above rate increased as cattle became less efficient in converting feed to gain (P=.0027). An inverse relationship existed between cost of gain and low Choice and above rate; those cattle with lower cost of gain had higher low Choice and above rates (P=.0043). Lot low Choice and above rate increased as average daily gain increased (P=.0094).

Comparison of Profit Groups by Year from 2002 - 2013
(77,717 hd of Steers and Heifers)

	Least Profitable	5th Most Profitable	4th Most Profitable	3rd Most Profitable	2nd Most Profitable	Most Profitable
Number of cattle	12,954	12,951	12,952	12,955	12,952	12,953
Profit $/Hd	-$120.42	-$23.59	$26.58	$71.92	$123.40	$216.63
Delivery Wt., lb.	679[f]	677[e]	661[d]	656[c]	651[b]	662[a]
Market Value $/cwt	$104.44	$101.05	$99.17	$97.42	$95.64	$91.47
Market Value $/hd	$709.36	$674.31	$655.12	$639.27	$623.00	$605.35

Warm up ADG, lb.	3.13[f]	3.38[e]	3.47[d]	3.52[c]	3.60[b]	3.72[a]
Warm up ADG Ratio	90[f]	98[e]	100[d]	101[c]	104[b]	107[a]
% Not Treated	69.7%	80.2%	82.8%	85.3%	87.0%	87.6%
% Treated 2 or More Times	12.0%	5.7%	4.4%	3.3%	2.5%	2.1%
Individual Treatment Cost $/Hd	$13.39	$6.96	$5.15	$4.49	$3.67	$3.13
Final Wt., lb.	1179[f]	1185[e]	1192[d]	1199[c]	1204[b]	1231[a]
Overall ADG, lb.	3.06[f]	3.20[e]	3.26[d]	3.29[c]	3.34[b]	3.46[a]
Feed to Gain	7.21[f]	6.97[e]	6.85[d]	6.77[c]	6.70[b]	6.66[a]
Days of Age at Harvest	469.2[bc]	466.2[c]	467.2[bc]	467.4[bc]	469.4[b]	477.1[a]
Hot Carcass Wt., lb.	713.2[f]	722.4[e]	729.2[d]	735.7[c]	741.4[b]	761.7[a]
Fat Cover, in.	0.464[c]	0.455[ab]	0.455[b]	0.453[ab]	0.451[ab]	0.451[a]
Ribeye Area, sq. in.	12.14[f]	12.31[e]	12.40[d]	12.50[c]	12.59[b]	12.83[a]
REA/cwt. of Hot Carcass Wt.	1.710[c]	1.709[c]	1.705[bc]	1.703[b]	1.702[b]	1.688[a]
% YG 1&2	52.4%	53.0%	53.6%	54.3%	56.4%	59.2%
% YG 4&5	10.9%	4.4%	2.7%	1.8%	1.4%	0.8%
Marbling Score	SL 94[f]	SM 15[e]	SM 28[d]	SM 35[c]	SM 44[b]	SM 58[a]
% low Choice or Higher	43.8%	59.4%	67.5%	73.6%	78.2%	82.6%
% CAB of Black Hided Cattle	7.3%	12.1%	14.8%	18.3%	22.0%	28.4%
Carcass Price $/cwt	$142.01	$146.83	$149.50	$152.17	$155.54	$160.97
Gross Income $/Hd	$1,012.82	$1,060.70	$1,090.15	$1,119.51	$1,153.17	$1,226.11
Retail Value /Day on Test	$3.21	$3.48	$3.61	$3.71	$3.84	$4.12
Profit $/Hd	-$120.42	-$23.59	$26.58	$71.92	$123.40	$216.63
Difference in Profit/Hd from the Least Profitable	$0.00	$96.83	$147.00	$192.34	$243.82	$337.05
True Value on Delivery, $/cwt	$87.93	$98.32	$103.96	$108.88	$114.71	$124.14

Individual animal records for each year were sorted from most profitable to least profitable and divided into six groups of equal size. Values within a factor without a common superscript differ (P<0.05). All categories with $ amounts differ by P < 0.05.

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Economic Risk Analysis of Embryo Transfer Programs through Stochastic Simulation

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ABSTRACT

To accomplish the objective of creating an economic risk analysis tool for user-defined embryo transfer (ET) programs, a circumstantial, stochastic prediction model utilizing @Risk© software to generate comparable economic values as an aid in the ET decision making process has been created. More realistic than the use of means in deterministic models, distributions defining the biological uncertainty for a multitude of reproductive outcomes are estimated through extensive literature review and limited industry sources. Applying the Latin Hypercube variation of Monte Carlo simulation, a sample value from the descriptive distribution associated with each stochastic variable is included in an iteration of the simulation. Through large numbers of iterations with dynamic combinations of variables, the process culminates in a distribution of possible values for the net present value (NPV), annuity equivalent net present value (ANPV), and return on investment (ROI) associated with the model described scenario of in-vivo derived (IVD) or in-vitro produced (IVP) embryos. Finally, using the distributions of NPV, ANPV, and ROI a decision maker can assess the economic risk linked to a user-defined ET program.

Cattle producers are presented with a choice between two primary methods of ET: Multiple Ovulation Embryo Transfer (MOET) and IVP. Encompassed within the two methods of ET exist several different sub-techniques, including the use of unsorted or sex-sorted semen in both methods and the exception or inclusion of follicular synchronization and/or stimulation before ovum pick-up (OPU) in IVP procedures. Even more recently, the commercial application of pre-transfer embryo biopsy has entered the marketplace. Ultimately, operators must decide whether ET programs, of any type, serve as an economically viable means to increase rate of genetic improvement or take advantage of marketing opportunities. Ample opportunity exists for the commercial application of in-depth, alternative ET scenario assessment afforded through stochastic simulation methodology that the ET industry has not yet fully exploited.

1. Introduction

Dynamic environments, varying production practices, and biological uncertainty associated with bovine reproduction make informed, strategic decision making regarding implementation of bovine reproductive technology a great challenge for producers. Profitability of an ET program depends on marketability of the end-products (embryos, pregnant recipients, progeny, etc.) and expenses required to produce them. Aherin (2017) describes in detail the many sources of production and economic variation.

Although several economic value predictors for ET programs already exist (Beltrame et al. 2010), the opportunity remains to create more applicable models for *Bos taurus* beef production and varying marketing avenues in the U.S. The host of stochastic factors, decision points, and interactions among them that affect the success of an ET program motivated development of a simulation model for their joint consideration in assessing the economic feasibility of alternative programs.

2. Model

2.1. Model Outline
The model allows for the comparison and analysis of the production and economic factors of ten primary ET protocols.
1. MOET: Unsorted Semen
2. MOET: Sex-Sorted Semen
3. MOET: Frozen Biopsied Embryos
4. MOET: Frozen Non-Biopsied Embryos
5. IVP: No Ovarian Stimulation (NS), Random OPU Interval, Unsorted Semen
6. IVP: No Ovarian Stimulation (NS), 3-4 d or 14 d OPU Interval, Unsorted Semen
7. IVP: Follicular Synchronization and Ovarian Stimulation (SS), Unsorted Semen
8. IVP: NS, Random OPU Interval, Sex-Sorted Semen
9. IVP: NS, 3-4 d or 14 d OPU Interval, Sex-Sorted Semen
10. IVP: SS, Sex-Sorted Semen

2.2. Economic Values
NPV, ANPV, and ROI are used to measure ET program profitability. Each simulation replication for a particular ET protocol produces a value for the NPV, ANPV, and ROI. Since multiple replications are performed, the result is a probability distribution for NPV, ANPV, and ROI under each protocol.

2.3. Assumptions

2.3.1. General Model Assumptions
*   No correlation between traits/measurements
*   All recipients enter the system as purchased opens
*   All purchases occur on d 1 of fiscal year
*   All calves weaned same day
*   If calf lives to weaning, it lives through development

2.3.2. Reproductive Model Assumptions
*   Healthy donors, recipients, and bulls
*   21 d estrous cycles
*   ET on d 7 following the onset of estrus
*   Recipients synchronized within 24 h of donor
*   Normally cycling donors and recipients
*   ET program is seasonal, not continuous
*   MOET IVD is limited to 3 flushes/breeding season

2.3.3. Embryo Production Model Assumptions
- Recipients that return to estrus on d 21 reenter available recipient population, depending on ET round and time interval between flush/OPU.
- ET recipients that experience pregnancy loss between 21 d and 60 d of pregnancy are eligible for natural service, depending on interval between transfers and length of bull turnout.
- ET bred recipients that experience pregnancy loss between d 60 and term are not eligible for natural service.
- Natural service bred recipients that experience pregnancy loss at any point after d 21 of gestation are not eligible for another natural service conception.

2.3.4. Revenue Model Assumptions
- Bred recipients are sold carrying a minimum 60 d pregnancy with no calf at side.
- Calf development revenue occurs in same fiscal year that calves are born.

2.3.5. Expense Model Assumptions
- Expenses not included:
    - Overhead or whole ranch costs
    - Facilities
    - Non-ET veterinary costs (pulling calves, emergencies, etc)
    - Labor when not applied to ET program
    - Equipment Expense
    - Taxes

2.4. Distributions of Biological Uncertainties
@Risk© is an Excel© add-in that allows for probability distributions to be built into an Excel© workbook and values drawn from said distributions through the simulation of an Excel©-based model. The model includes stochastic variables describing donor superovulation response, embryo production, oocyte production, blastocyst rate, recipient synchrony, pregnancy rates, pregnancy failures, calf survival, and progeny revenue according to each respective ET methodology and/or marketing scenario. Aherin (2017) describes the distributions generated for each of the stochastic variables in further detail.

2.9. Deterministic Variables
Accompanying the stochastic variables characterized by the distributions previously described are user-defined deterministic variables. Deterministic elements include variables describing ET production management strategy and protocols, anticipated calf performance, costs associated with specific factors, and several end-product marketing values (Aherin, 2017).

2.10. Model Simulation
To demonstrate the capability of the stochastic model, analysis for a select few scenarios is presented here. For the scenarios, 100,000 replications of the simulation model are performed using the parameters described previously. The use of 100,000 iterations balances a high confidence in output, while still allowing for a reasonably short simulation run-time. Sections of the model where the numerical outcome is influenced by an estimation of the true probability

associated with a binary outcome (i.e., pregnancy rate) are determined using a binomial distribution with *n* number of trials and success probability, *p*. As the true probability of success for such traits is unknown, a sample value from the distribution describing the potential value of the true probability is selected per LHS for each iteration/replication of the model. The distributions describing the range of values for stochastic variables with non-binary outcomes are sampled per LHS without the need for a complementary binomial distribution. The LHS variation of Monte Carlo simulation (Iman and Shortencarier, 1984) culminates in a distribution of possible outcome values through large numbers of iterations with dynamic combinations of variables.

The model may be used to analyze numerous scenarios utilizing sex-sorted or unsorted semen with variations in ownership of donors and recipients and alternative marketing avenues compared simultaneously. The intent of the selected scenarios is to illustrate these possibilities, not to provide a means for industry wide assessment of a specific reproductive technology application or the profitability of a given marketing strategy, in general.

Scenario 1:
- Embryo Production Method: MOET using unsorted semen.

Scenario 2:
- Embryo Production Method: IVP NS, 14 d OPU interval using unsorted semen.

Scenario 3:
- Embryo Production Method: IVP SS using unsorted semen.

All Scenarios:
- Ownership: Own donors and own recipients.
- Marketing: Sell developed bulls and females per the pricing distribution described in the previous chapter. Sell all cull progeny and naturally sired calves by weight, as feeder cattle, per the feeder calf pricing index. Market excess embryos using the user-defined price disclosed in the preceding chapter. Open females are sold at the conclusion of the breeding season, with the corresponding value of an open female.

2.11. Statistical Analysis

Statistical analysis was performed using StatTools 7.5 ©. Using the individual results generated from each simulation replication, a standardized, stepwise regression analysis was executed for each scenario with each stochastic variable serving as an independent variable and ROI as the dependent variable (Iman et al., 1985). Adjusted R-squared values were determined for each regression model (Mendenhall and Sincich, 2012). The assumptions of multivariate linear regression were tested by analyzing the distribution of residuals.

3. Results: Scenario: Unsorted Semen- Owned Donors- Owned Recipients- Market Developed Bulls and Heifers

Figure 1 through Figure 9 and Table 1 display the results of the simulation model according to the example scenario, in terms of ROI.

3.1. Scenario 1: MOET

Figure 1. Probability distribution of the ROI resulting from the scenario of MOET- unsorted semen- owned donors- owned recipients- market developed bulls and heifers.

Figure 2. Standardized stepwise regression coefficients for the stochastic variables influencing the scenario of MOET- unsorted semen- owned donors- owned recipients- market developed bulls and heifers.
Num of Embry per Col (number of transferable embryos per collection). Preg Rate (pregnancy rate at 21 days post-ovulation).

Figure 3. Cumulative distribution of the R-squared value associated with the stochastic variables influencing the scenario of MOET- unsorted semen- owned donors- owned recipients- market developed bulls and heifers.
Num of Embry per Col (number of transferable embryos per collection). Preg Rate (pregnancy rate at 21 days post-ovulation).
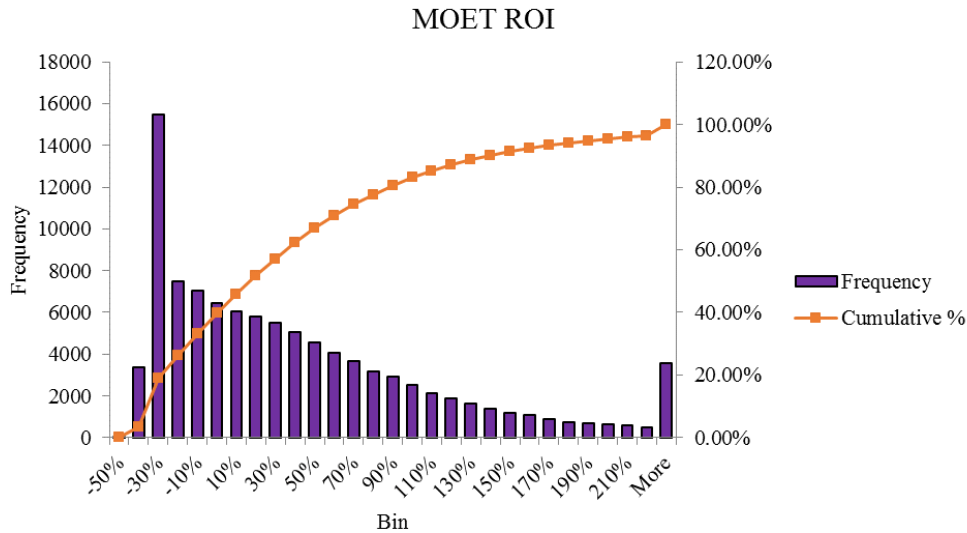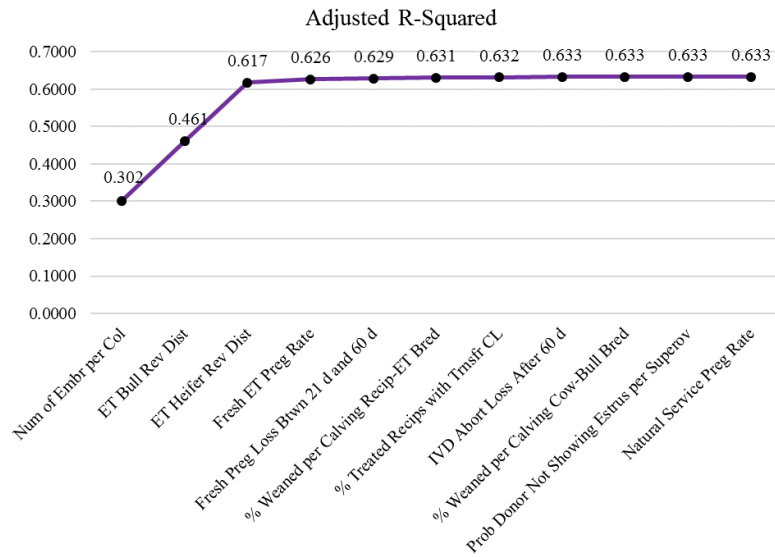
3.2. Scenario 2: IVP NS

Figure 4. Probability distribution of the ROI resulting from the scenario of IVP NS- unsorted semen- owned donors- owned recipients- market developed bulls and heifers.

Figure 5. Standardized stepwise regression coefficients for the stochastic variables influencing the scenario of IVP NS- unsorted semen- owned donors- owned recipients- market developed bulls and heifers.

Preg Rate (pregnancy rate 21 d post-ovulation). Blast Rate (blastocyst rate). COCs Per OPU (number of cultured oocytes per OPU).

Figure 6. Cumulative distribution of the R-squared value associated with the stochastic variables influencing the scenario of IVP NS- unsorted semen- owned donors- owned recipients- market developed bulls and heifers.

Preg Rate (pregnancy rate 21 d post-ovulation). Blast Rate (blastocyst rate). COCs Per OPU (number of cultured oocytes per OPU).
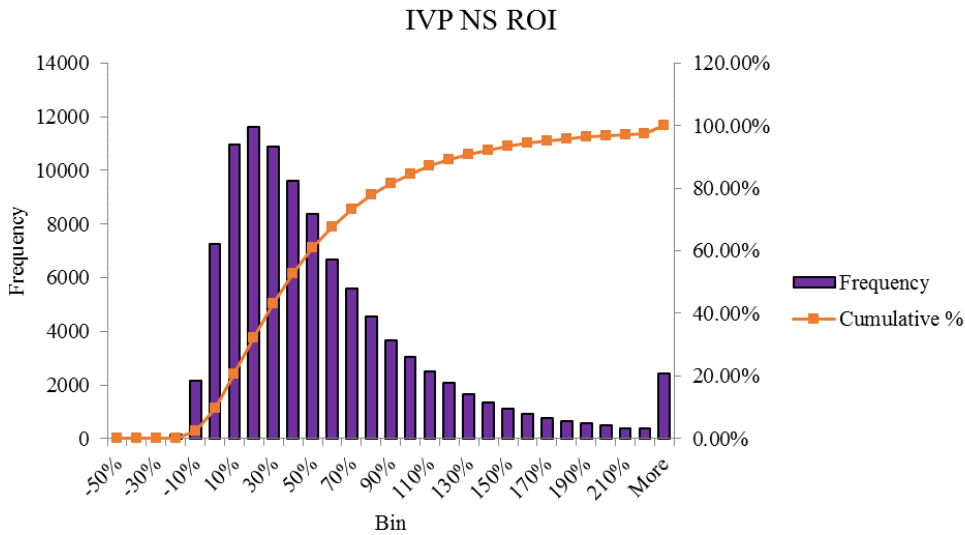
3.3. Scenario 3: IVP SS
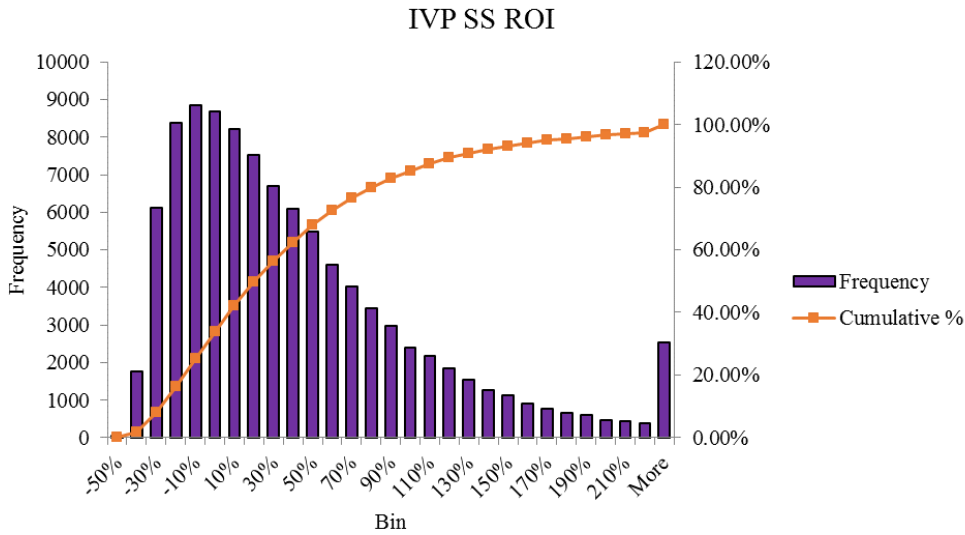
Figure 7. Probability distribution of the ROI resulting from the scenario of IVP SS- unsorted semen- owned donors- owned recipients- market developed bulls and heifers.
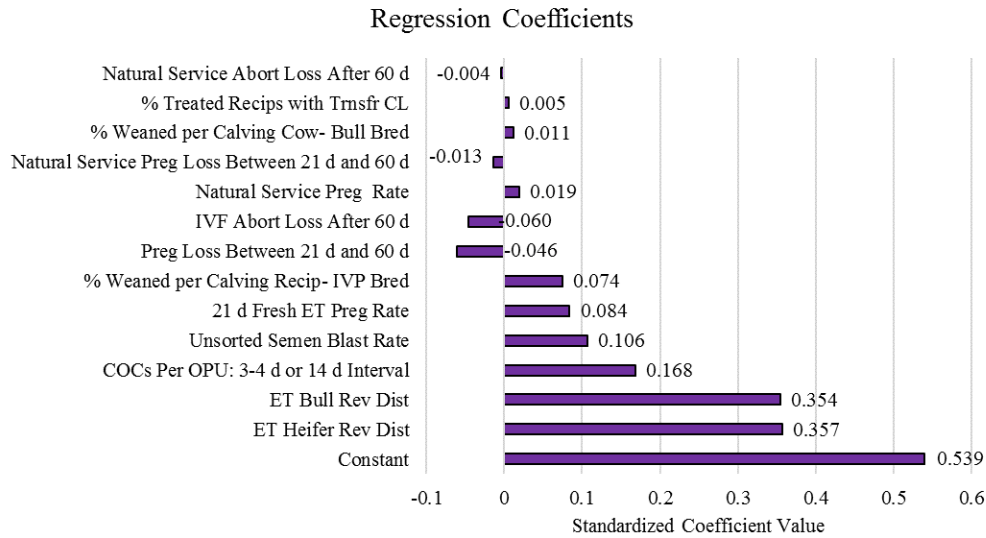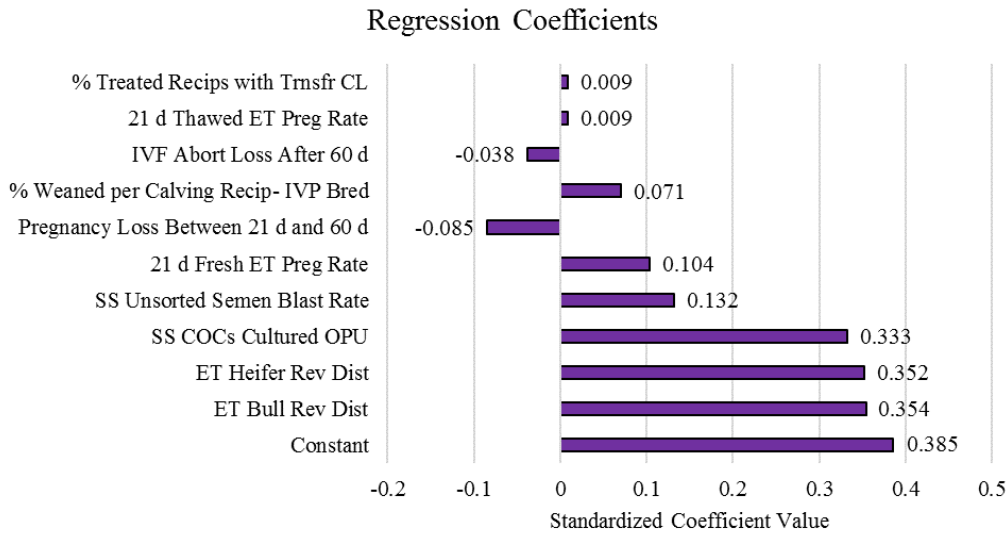

Figure 8. Standardized stepwise regression coefficients for the stochastic variables influencing the scenario of IVP SS- unsorted semen- owned donors- owned recipients- market developed bulls and heifers.
Preg Rate (pregnancy rate 21 d post-ovulation). Blast Rate (blastocyst rate). SS COCs Cultured OPU (number of cultured oocytes per OPU).
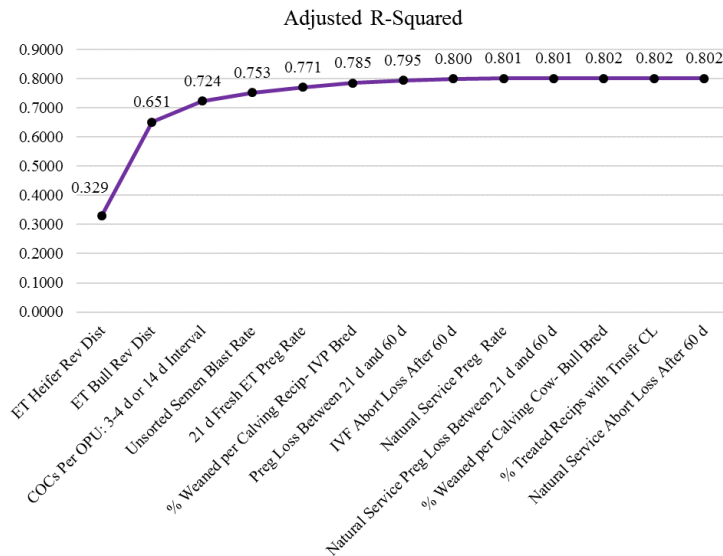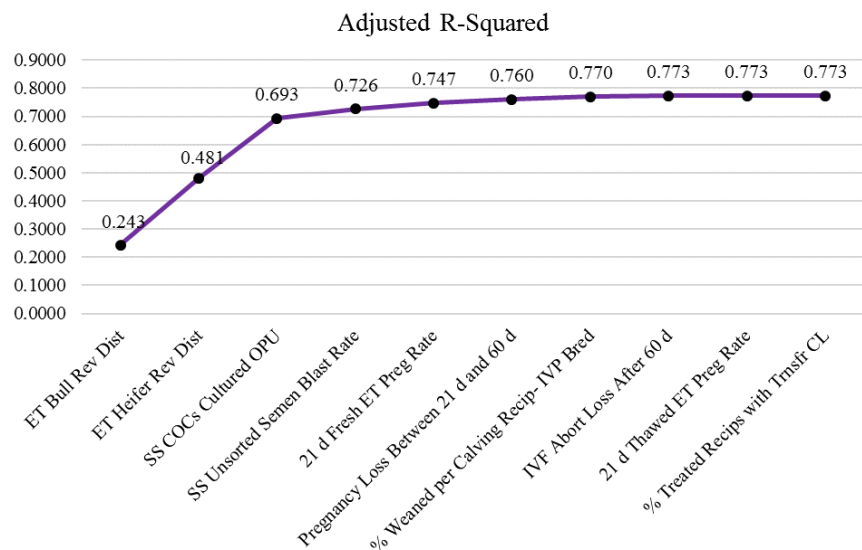
Figure 9. Cumulative distribution of the R-squared value associated with the stochastic variables influencing the scenario of IVP SS- unsorted semen- owned donors- owned recipients- market developed bulls and heifers.

Preg Rate (pregnancy rate 21 d post-ovulation). Blast Rate (blastocyst rate). SS COCs Cultured OPU (number of cultured oocytes per OPU).

| ROI (%)	MOET	IVP NS	IVP SS
Mode	-37.4	13.5	-16.3
5%	-39.0	-5.5	-34.3
25%	-22.0	13.9	-10.2
Median	16.9	37.1	20.5
75%	71.3	74.1	66.0
95%	194.5	166.9	169.8
Mean ± 90% C.I.	38.6± 0.437	53.7 ± 0.326	38.4± 0.374
SD	84.0	62.6	71.8
Probability of Negative Return	40.0	9.6	34.0

Table 1. Mode, 5th percentile, 25th percentile, median, 75th percentile, 95th percentile, mean, and standard deviation of the ROI resulting from the scenario of unsorted semen- owned donors- owned recipients- market developed bulls and heifers.

4. Discussion

A strength of the proposed simulation approach is that is makes it possible to examine the range of potential outcomes for a given production strategy with a combination of expediency, negligible resource use, and number of trials that could not be replicated in the field. Mean values of economic and production measures are important, but the distributions of biological uncertainties embedded within the model cause many output distributions to vary greatly in shape, often straying far from a normal distribution. Thus, it is possible for distribution means and most likely outcomes to diverge from one another substantially. Therefore, equal, if not greater, attention should be paid to the percentiles and probabilities associated with each output

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distribution. Furthermore, a deeper investigation into the varying production outputs that cause differences between the economic outputs of the scenarios in question is feasible, although not described in the scope of this paper.

The mean ROI for MOET, 38.6%, and IVP SS, 38.4%, were not significantly different at 90% confidence (Table 1). Mean ROI for IVP NS, 53.7%, was significantly greater than the mean ROI for both MOET and IVP SS at 90% confidence (Table 1). Besides the differences in output means, there is also a noticeable difference in the standard deviations of means (Table 1).

Along with noting the standard deviation of output means, an effective method of risk appraisal is an analysis of the probability distribution associated with each economic and production output. When considering ROI, the most likely outcomes for MOET, IVP NS, and IVP SS are -37.4%, 13.5%, and -16.3%, respectively (Table 1). The medians for each respective ROI distribution are 16.9%, 37.1%, and 20.5% (Table 1). Perhaps the greatest measurement of financial risk is the probability of negative return. Regarding this measurement, MOET, IVP NS, and IVP SS had probabilities of 40.0%, 9.6%, and 34.0% (Table 1), respectively. It seems rational that IVP NS has the lowest probability of negative return, because IVP NS is less influenced by the success or failure of expensive human intervention (no exogenous hormone protocols for synchronization or stimulation of donors) than either MOET or IVP SS.

Although each individual firm may consider risk differently, using the most likely outcome and probability of negative return, one can argue that for the given scenario both the MOET and IVP SS programs are in contention for the economically riskiest methods of ET. Alternatively, if one defines risk as an uncertainty of outcome, MOET also has the greatest standard deviation of ROI, at 84.0% (Table 1). Not surprisingly, considering many risk-reward trade-offs, MOET also has the greatest ROI at the 95th percentile (Table 1). Depending on a firm's risk aversion, IVP NS could be an attractive method under the given scenario, as it boasts the, the lowest probability of negative return, the greatest most likely return, and the smallest standard deviation around the mean. Simultaneously, the 95th percentile ROI of IVP NS, 166.9%, rivals that of IVP SS, 169.8% (Table 1).

The statistical results are shown in Figure 2 and 3, Figure 5 and 6, and Figure 8 and 9. For Scenario 1, the three largest regression values are the number of transferable embryos per collection, the revenue distribution for heifers, and the revenue distribution for bulls. For Scenario 2 and Scenario 3, the three largest regression coefficient values are the revenue distribution for heifers, the revenue distribution for bulls, and the number of oocytes incubated per OPU. According to the R-squared values, the regression model for each of the scenarios does not completely explain the outcome of the scenario. This is, in part, because of the incorporation of binomial distributions, which are not included in the regression analysis, as a method of implementing the stochastic variables that represent a mean probability, such as pregnancy rate. It is likely that the results of the binomial distributions account for a large proportion of the variation that the model utilizing only stochastic variables cannot explain.

5. Conclusions

Inherent to the identity of the beef industry is the variation of environment, cattle type, and management practices between operations. Thus, a critical aspect of the stochastic model described and applied in the preceding pages is the ability to incorporate user-defined variable values, specific to an individual operation, as parameters for the program in question. The stochastic elements of the model create a more realistic outlook than the use of means in deterministic models, as distributions defining the biological uncertainty for a multitude of

reproductive outcomes are incorporated into the model. The core function of this model should be as a consultative tool using the generated distributions of NPV, ANPV, and ROI as an aid in the assessment of the economic risk linked to a user-defined MOET or IVP program.

This model does not account for the increased magnitude and rate of genetic gain that is possible through ET and the potential long-term impact those genetic improvements may have on a breeding program. Accounting for the long-term economic impact of accumulated improvements or changes in production efficiency is a potential next step in analyzing the economics of ET. This model could serve as a foundational template for that opportunity.

The pace of change in the IVP industry is rapid enough that many advances are not reported in the scientific literature before being implemented in industry. Furthermore, it is likely that IVP companies may regard technological advancements as trade secrets that yield a competitive advantage in the marketplace. Thus, a challenge in the application of this model is creating and maintaining an accurate representation of expected production outcomes from the most current ET practices.

The numerical and logical analysis afforded through the stochastic simulation of alternative scenarios through this model allows for in-depth assessment of ET programs not previously available. The caveat is that any model, no matter how robust, will never be completely accurate, as all are a simplified version of a complicated reality. That said, there is ample opportunity for the commercial application of this stochastic model to complement the deterministic, instinctive, and experience based elements of the decision-making process pertaining to the prediction of the economic outcome of an ET program, through methodology that the ET industry has not fully exploited.

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MEAN EPDs REPORTED BY DIFFERENT BREEDS

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

It is useful for producers to compare the EPDs of potential breeding animals with their breed average. The current EPDs from the most recent genetic evaluations of 26 breeds are presented in this report. Mean EPDs for growth traits are shown in Table 1 (26 breeds), for other production traits in Table 2 (21 breeds), and for carcass and composition traits in Table 3 (21 breeds). Several breeds also have EPDs and indices that are unique to their breed; these EPDs are presented in Table 4.

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

This list is likely incomplete; evaluations for some breeds are not widely reported. We are aware of recent EPD evaluations for the Blonde d'Aquitaine, North American Piedmontese, American Pinzgauer, and American Waygu breeds but their EPDs do not appear to have been updated in the last year. If you see a breed missing and would like to report the average EPDs for that breed, please contact Larry (Larry.Kuehn@ars.usda.gov) or Mark (Mark.Thallman@ars.usda.gov).

Table 1. Birth year 2014 average EPDs from 2016 evaluations for growth traits

Breed	Birth Weight (lb)	Weaning Weight (lb)	Yearling Weight (lb)	Maternal Milk (lb)	Total Maternal (lb)
Angus	1.2	49	87	24	
Black Hereford	2.8	44.6	75.7	21.8	44.1
Hereford	3.2	48.9	79.4	21.0	45.5
Murray Grey	3.8	24	37	4	16
Red Angus	-1.4	58	88	21	
Red Poll	1.7	15	24	6	
Shorthorn	1.9	51	59.3	17.1	42.6
South Devon	2.2	45	83	25	48
Beefmaster	0.5	23	42	9	21
Braford	1.1	14	21	4	11
Brahman	1.9	16.8	26.8	5.5	
Brangus	1.1	25.3	47.2	9.3	22.0
Red Brangus	1.6	11.9	19.2	5.4	11.3
Santa Gertrudis	0.2	4.2	6.2	0.7	
Senepol	0.6	8.3	9.6	3.8	8.0
Simbrah	3.6	60.0	81.3	21.1	50.8
American Akaushi	0.1	25.6	46.1	27.0	39.8
Braunvieh	2.5	44.0	68.0	34.7	56.0
Charolais	0.4	26.8	49.3	8.8	22.2
Chianina	2.2	40.1	57.2	15.8	35.7
Gelbvieh	0.5	68.7	99.8	27.6	62.0
Limousin	1.2	61.9	90.4	26.0	57.0
Maine-Anjou	1.5	44.6	57.2	18.3	40.5
Salers	1.5	43.8	83.4	19.7	41.6
Simmental	1.8	62.6	91.3	21.1	52.4
Tarentaise	0.5	14.6	26.9	0.3	

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

Breed	Calving Ease Direct (%)	Calving Ease Maternal (%)	Scrotal Circ. (cm)	Docil. Score	Mature Weight (lb)	Heifer Pregnancy (%)	Stayability (%)
Angus	6	8	0.81	15	27	11.5	
Hereford	1.2	1.4	0.9		88		
Murray Grey	-0.5	-0.1	0.2		56		
Red Angus	5	4				11	10
Shorthorn	5.1	1.1					
South Devon			0.1				
Beefmaster			0.3				
Brahman			0.2	0.0			
Brangus	3.8	4.1	0.48				
Santa Gertrudis			-0.01				
Simbrah	2.9	6.0		8.8			7.6
American Akaushi	3.7	5.0					
Braunvieh	5.9	0.9	-0.09				
Charolais	3.1	3.2	0.78				
Chianina	4.7	-2.1					
Gelbvieh	10.8	6.5				3.8	6.0
Limousin	8.0	6.4	0.74	20.1			7.8
Maine Anjou	7.4	1.7					
Salers	0.4	0.4	0.3	8.6			23.8
Simmental	9.3	8.7		10.8			11.6
Tarentaise	0.6	0.5					

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

Breed	Carcass Wt (lb)	Retail Product (%)	Yield Grade	Marbling Score	Carcass Ribeye Area (in^2)	Fat Thickness (in)	Rump fat (in)	WBSF (lb)
Angus	35.0			0.59	0.57	0.018		
Hereford	61			0.09	0.34	0.005		
Murray Grey	33	0.5		0.0[a]	0.11[a]	0.00[a]	0.00[a]	
Red Angus	21		0.00	0.43	0.14	-0.005		
Shorthorn	7.4			0.05	0.01	-0.042		
South Devon	29.0	0.8		0.4	0.23	0.01		
Beefmaster				0.00[a]	-0.17[a]	-0.03[a]		
Braford	7			0.02	0.06	0.012		
Brahman	1.8	-0.01		0.01	0.01	0.00		0.03
Brangus				0.02[a]	0.36[a]	-0.040[a]		
Santa Gertrudis	4.0			-0.01	0.04	0.002		
Simbrah	23.3		-0.23	-0.06	0.46	-0.058		-0.11
American Akaushi				0.74[a]	0.16[a]	0.055[a]		
Braunvieh	22.6			0.60	0.34	-0.089		
Charolais	16.8			0.04	0.34	0.005		
Chianina	8.8		-0.24	0.06	0.38	-0.049		
Gelbvieh	29.6		-0.29	0.12	0.45	-0.040		
Limousin	25.0		-0.19	-0.02	0.46	-0.044		
Maine-Anjou	6.2	0.53		-0.03	0.31	-0.050		
Salers	22.9	0		0.2	0.04	0.000		
Simmental	26.8		-0.33	0.14	0.80	-0.055		-0.32

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

Table 4. Birth year 2014 average EPDs from 2016 evaluations for other traits unique to individual breeds

Angus	Residual Avg Daily Gain (lb)	Dry Matter Intake (lb)	Mature Height (in)	Yearling Height (in)	Cow Energy Value ($)	Weaned Calf Value ($)	Feedlot Value ($)	Grid Value ($)	Beef Value ($)
	0.22	0.20	0.3	0.5	-3.15	47.38	42.56	35.91	117.44

Hereford	Baldy Maternal Index ($)	Brahman Influence Index ($)	Certified Hereford Beef Index ($)	Calving Ease Index ($)	Udder Score	Teat Score
	18.15	15.84	23.58	15.5	1.18	1.12

Red Angus	Mature Cow Maintenance (Mcal/mo)	Murray Grey	600-d wt (lb)	Gestational Length (d)	Days to Calving (d)
	0		55	-0.2	-0.8

Shorthorn	$ Calving Ease	$ Feedlot	$ British Maternal Index
	20.4	51.01	110.1

Beefmaster	Terminal Index ($)	Maternal Index ($)
	71.06	15.31

Gelbvieh	30-Month Pregnancy	DMI (lb/d)	ADG (lb/d)	RFI (lb/d)	$ Cow ($)	Efficiency Profit Index ($)	Feeder Profit Index ($)
	1.2	0.017	0.005	-0.015	65.27	113.07	71.56

Limousin	Mainstream Terminal Index ($)	Gestation Length (d)
	49.48	-2.8

Simmental	All Purpose Index ($)	Terminal Index ($)	ADG (lb/d)	Simbrah	All Purpose Index ($)	Terminal Index ($)
	121.9	67.6	0.18		79.9	51.6

ACROSS-BREED EPD TABLES FOR THE YEAR 2017 ADJUSTED TO BREED DIFFERENCES FOR BIRTH YEAR OF 2015

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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 2017 EPD. Older or newer EPD may be computed on different bases and, therefore, could produce misleading results. When the base of a breed changes from year to year, its adjustment factor (Column 6) changes in the opposite direction and by about the same amount.

Breed differences change over time as breeds put selection emphasis on different traits and their genetic trends differ accordingly. Therefore, it is necessary to qualify the point in time at which breed differences are represented. Column 5 of Tables 1-8 contains estimates of the differences between the averages of calves from sires of each breed born in year 2015. 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 2015) 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 2017 update of estimates of sire breed means from data of the Germplasm Evaluation (GPE) project at USMARC adjusted to a year 2015 basis using EPD from the most recent national cattle evaluations. The 2015 basis year is chosen because yearling records for weight and carcass traits should have been accounted for in EPDs for progeny born in 2015 in the Spring 2017 EPD national genetic evaluations. Factors to adjust Spring 2017 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, 2017)

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 2016 (Kuehn and Thallman, 2016):

New samplings of sires in the USMARC GPE program continued to increase progeny records for all of the breeds. The GPE program has entered a new phase in which more progeny are produced from breeds with higher numbers of registrations. Breeds with large increases in progeny numbers as a percentage of total progeny included South Devon and Tarentaise (especially for yearling weight, carcass traits, and maternal milk) and Santa Gertrudis and Chiangus (especially for maternal milk). However, all of the breeds continue to produce progeny in the project and sires continue to be sampled on a continuous basis for each of the 18 breeds in the across-breed EPD program.

Several breed associations are adapting to genomic information being included in their national cattle evaluations. In some cases, new statistical models and computer programs are being implemented to improve the accuracy of breeding value predictions. Sires sampled for the GPE in recent years are most affected by the influx of genomic predictions and, possibly, more subject to small changes from year to year as these new prediction models are implemented. We expect small changes to the mean breed and USMARC EPD (Columns 1 and 2 in Tables 1-8) as these new genetic evaluation systems come on line. These changes may affect the breed differences and adjustment factors in these tables (Columns 5 and 6).

We are in the process of evaluating the release of these factors at different intervals during the year to service spring and fall bull buying seasons and timing of genetic evaluations in the industry. This potential change will be discussed at the 2017 Beef Improvement Federation meeting.

Materials and Methods

All calculations were as outlined in the 2016 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 (2012-2016). Estimates of variance components, regression coefficients, and breed effects were obtained using the MTDFREML package (Boldman et al., 1995). All breed solutions are reported as differences from Angus. The table values of adjustment factors to add to within-breed EPD are relative to Angus.

Models for Analysis of USMARC Records

An animal model with breed effects represented as genetic groups was fitted to the GPE data set (Arnold et al., 1992; Westell et al., 1988). In the analysis, all AI sires (sires used via

artificial insemination) were assigned a genetic group according to their breed of origin. Due to lack of pedigree and different selection histories, dams mated to the AI sires and natural service bulls mated to F_1 females were also assigned to separate genetic groups (i.e., Hereford dams were assigned to different genetic groups than Hereford AI sires). Cows from Hereford selection lines (Koch et al., 1994) were used in Cycle IV of GPE and assigned into their own genetic groups. Through Cycle VIII, most dams were from Hereford, Angus, or MARCIII (1/4 Angus, 1/4 Hereford, 1/4 Pinzgauer, 1/4 Red Poll) composite lines. In order to be considered in the analysis, sires had to have an EPD for the trait of interest. All AI sires were considered unrelated for the analysis in order to adjust resulting genetic group effects to the average EPD of the sires.

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

For the carcass traits (MAR, REA, FAT, and CWT), breed (fitted as genetic groups), sex (heifer, steer) and slaughter date by any treatment combination where applicable were included in the model as fixed effects. Fixed covariates included slaughter age and heterosis. Random effects were animal and residual error. To be included, breeds had to report carcass EPD on a carcass (vs. ultrasound) basis using age-adjusted endpoints, as suggested in the 2016 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. Also, composite breeds were considered to be composed of their fractional composition to derived heterosis. 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):

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

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

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

where,

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

EPD(i)$_{YY}$ is the average within-breed 2017 EPD for breed i for animals born in the base year (YY, which is two years before the update; e.g., YY = 2015 for the 2017 update),

EPD(i)$_{USMARC}$ is the weighted (by total relationship of descendants with records at USMARC) average of 2017 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 2017: 1.18, 0.80, 0.96, and 1.05 BWT, WWT, YWT, and MILK, respectively; 1.00 was applied to MAR, REA, FAT, and CWT data),

i denotes sire breed i, and

x denotes the base breed, which is Angus in this report.

Results

Heterosis

Heterosis was included in the statistical model as a covariate for all traits. Maternal heterosis was also fit as a covariate in the analysis of weaning weight. Resulting estimates were 1.73 lb, 15.53 lb, 25.58 lb, -0.06 marbling score units (i.e. 4.00 = Sl^{00}, 5.00 = Sm^{00}), 0.26 in^2, 0.030 in, and 31.21 lb in for BWT, WWT, YWT, MAR, REA, FAT, and CWT respectively. These estimates are interpreted as the amount by which the performance of an F$_1$ is expected to exceed that of its parental breeds. The estimate of maternal heterosis for WWT was 9.36 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 2015 birth year basis. The column labeled 6 of each table corresponds to the Across-breed EPD Adjustment Factor for that trait. Table 4 summarizes the analysis of MILK. Tables 5, 6, 7, and 8 summarize data from the carcass traits (MAR, REA, FAT, and CWT). Because of the accuracy of sire carcass EPDs and the greatest percentage of data being added to carcass traits, sire effects and adjustment factors are more likely to change for carcass traits in the future.

Column 5 of each table represents the best estimates of sire breed differences for calves born in 2015 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 2015) 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 2012 through 2016 at USMARC (Column 4) to make these differences more interpretable to producers on scales they are accustomed to.

Figures 1-8 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 weaning weight for a Shorthorn bull is +63.0 (which is above the birth year 2015 average of 51.0 for Shorthorn) and for a Simmental bull is +55.0 (which is below the birth year 2015 average of 62.6 for Simmental). The across-breed adjustment factors in the last column of Table 3 are -32.3 for Shorthorn and -9.5 for Simmental. Then the adjusted EPD for the Shorthorn bull is 63.0 + (-32.3) = 30.7 and for the Simmental bull is 55.0 + (-9.5) = 45.5. The expected weaning weight difference when both are mated to another breed of cow, e.g., Hereford, would be 30.7 – 45.5 = -14.8 lb. Thus the difference in true breeding value of -14.8 lb between the two bulls was dramatically changed from the difference in their within-breed EPDs (+8 lb) due to differences in the breed means and genetic base from which those within-breed EPDs are deviated.

Birth Weight

The range in estimated breed of sire differences relative to Angus for BWT (Table 1, column 5) ranged from -0.1 lb for Red Angus to 6.9 lb for Charolais and 10.9 lb for Brahman. Red Angus had the lowest estimated sire effect for birth weight (Table 1, column 5). The relatively heavy birth weights of Brahman-sired progeny would be expected to be offset by favorable maternal effects reducing birth weight if progeny were from Brahman or Brahman cross dams which would be an important consideration in crossbreeding programs involving Brahman cross females. Changes in breed of sire effects were small (1.0 lb or less) for all breeds relative to last year's update (Kuehn and Thallman, 2016).

Weaning Weight

All of the 17 breed differences (Table 2, column 5) were within 5 lb of the values reported by Kuehn and Thallman (2016). Otherwise, changes in breed effects for all 18 breeds seem to be stabilizing since continuous sampling started in 2007, with most minor year-to-year

changes coming from greater genetic trend in Angus (increases in the mean EPD each year).

Yearling Weight

Breed of sire effects for yearling weight were also similar to Kuehn and Thallman (2016) in general. There was some suggestion that the mean may have shifted for Angus in this year's evaluation, possibly due to changes in their genetic evaluation model with genomic information. Thus there was no consistent trend in breed differences from Angus (Table 3, column 5) relative to Kuehn and Thallman (2016). All changes in these differences were less than 8 lb.

Maternal Milk

Changes to the maternal milk breed of sire differences (Table 4, column 5) were generally small. All changes were less than 3 lb different from those reported in 2016. However, the breed solution estimates (Table 4, column 3) are expected to change the most in future updates as GPE heifers from each of the 18 breeds being continuously sampled are developed and bred. Females from newly sampled South Devon or Tarentaise sires have continued to add progeny in this update; difference from Angus changed very little in these breeds. We would expect their solutions to change the most in future reports.

Marbling, Ribeye Area, Fat Thickness and Carcass Weight

Most changes to breed of sire differences were minor for each of these carcass traits. The largest changes from the 2016 report (Kuehn and Thallman, 2016) were observed in carcass weight differences from Angus. Much of this change can be attributed to heavy selection for carcass weight (directly and using indices) in the Angus breed as shown in Figure 8.

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 along with the numbers of sires sampled 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 0.54, 0.17, 0.44, and 0.15, respectively. Heritability estimates for MAR, REA, FAT, and CWT were 0.52, 0.47, 0.42, 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 1.18 for BWT, 0.80 for WWT, and 0.96 for YWT were used to adjust breed of sire solutions to the base year of 2015. 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 1.05 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 2015 base and factors to adjust within breed EPD to an Angus equivalent – BIRTH WEIGHT (lb)

Breed	Number AI Sires	Number Direct Progeny	Ave. Base EPD Breed 2015 (1)	Ave. Base EPD USMARC Bulls (2)	Breed Soln at USMARC (vs Ang) (3)	BY 2015 Sire Breed Average (4)	BY 2015 Sire Breed Difference[a] (5)	Factor to adjust EPD To Angus (6)
Angus	211	2418	1.2	1.6	0.0	86.0	0.0	0.0
Hereford	194	2671	3.2	2.4	3.5	90.2	4.1	2.1
Red Angus	74	873	-1.4	-1.4	-0.6	85.9	-0.1	2.5
Shorthorn	64	644	1.9	2.5	6.6	91.4	5.3	4.6
South Devon	30	251	2.2	2.0	4.1	90.1	4.0	3.0
Beefmaster	58	606	0.5	1.2	5.0	90.0	3.9	4.6
Brahman	64	726	1.9	0.9	11.2	96.9	10.9	10.2
Brangus	62	606	1.1	0.9	3.2	89.3	3.2	3.3
Santa Gertrudis	32	357	0.2	0.6	4.7	90.1	4.0	5.0
Braunvieh	37	502	2.5	4.1	5.3	89.3	3.3	2.0
Charolais	129	1352	0.4	0.2	7.4	92.9	6.9	7.7
Chiangus	34	380	2.2	2.2	4.4	90.2	4.1	3.1
Gelbvieh	95	1214	0.5	2.2	3.9	88.1	2.1	2.8
Limousin	88	1308	1.2	1.3	2.4	88.3	2.3	2.3
Maine Anjou	50	567	1.5	2.2	5.1	90.1	4.0	3.7
Salers	60	532	1.5	2.4	3.0	88.0	2.0	1.7
Simmental	119	1415	1.8	3.1	5.4	89.7	3.6	3.0
Tarentaise	17	300	0.5	2.1	4.3	88.4	2.4	3.1

Calculations:
(4) = (3) / b + [(1) − (2)] + (Recent Raw Angus Mean: 86.4 lb) with b = 1.18
(5) = (4) − (4, Angus)
(6) = (5) − (5, Angus) − [(1) − (1, Angus)]
[a]The breed difference estimates represent half the differences that would be expected between purebreds of the two breeds.

Table 2. Breed of sire solutions from USMARC, mean breed and USMARC EPD used to adjust for genetic trend to the year 2015 base and factors to adjust within breed EPD to an Angus equivalent – WEANING WEIGHT (lb)

	Number		Ave. Base EPD		Breed Soln	BY 2015	BY 2015	Factor to
			Breed	USMARC	at USMARC	Sire Breed	Sire Breed	adjust EPD
	AI	Direct	2015	Bulls	(vs Ang)	Average	Difference[a]	To Angus
Breed	Sires	Progeny	(1)	(2)	(3)	(4)	(5)	(6)
Angus	211	2239	49.0	27.9	0.0	574.6	0.0	0.0
Hereford	192	2473	48.9	30.6	-5.2	565.3	-9.3	-9.2
Red Angus	74	835	58.0	53.7	-5.6	550.8	-23.8	-32.8
Shorthorn	64	607	51.0	52.7	-6.0	544.3	-30.3	-32.3
South Devon	30	229	45.0	28.9	-8.7	558.7	-15.9	-11.9
Beefmaster	58	569	23.0	23.1	10.9	566.9	-7.7	18.3
Brahman	61	627	16.8	8.1	20.8	588.1	13.5	45.7
Brangus	61	573	25.3	21.4	3.6	561.9	-12.7	11.0
Santa Gertrudis	32	337	4.2	6.2	10.7	564.8	-9.8	35.0
Braunvieh	37	466	44.0	45.1	-6.1	544.7	-29.9	-24.9
Charolais	128	1235	26.8	15.9	17.5	586.3	11.7	33.9
Chiangus	34	341	40.1	42.1	-6.3	543.7	-30.9	-22.0
Gelbvieh	94	1138	68.7	59.2	6.7	571.3	-3.3	-23.0
Limousin	88	1206	61.9	44.0	0.6	572.1	-2.5	-15.4
Maine Anjou	50	524	44.6	44.7	-11.4	539.1	-35.5	-31.1
Salers	60	506	43.8	35.8	-2.2	558.7	-15.9	-10.7
Simmental	118	1298	62.6	56.8	15.6	578.7	4.1	-9.5
Tarentaise	17	290	14.6	0.8	-0.3	567.0	-7.6	26.8

Calculations:

(4) = (3) / b + [(1) − (2)] + (Raw Angus Mean: 553.5 lb) with b = 0.80

(5) = (4) − (4, Angus)

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

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

Table 3. Breed of sire solutions from USMARC, mean breed and USMARC EPD used to adjust for genetic trend to the year 2015 base and factors to adjust within breed EPD to an Angus equivalent − YEARLING WEIGHT (lb)

Breed	Number AI Sires	Number Direct Progeny	Ave. Base EPD Breed 2015 (1)	Ave. Base EPD USMARC Bulls (2)	Breed Soln at USMARC (vs Ang) (3)	BY 2015 Sire Breed Average (4)	BY 2015 Sire Breed Difference[a] (5)	Factor to adjust EPD To Angus (6)
Angus	196	2000	87.0	48.7	0.0	1077.0	0.0	0.0
Hereford	181	2278	79.4	50.7	-31.1	1035.0	-41.9	-34.3
Red Angus	69	768	88.0	76.5	-15.5	1034.0	-42.9	-43.9
Shorthorn	61	559	59.3	59.2	-8.0	1030.4	-46.6	-18.9
South Devon	29	218	83.0	58.9	-19.7	1042.3	-34.7	-30.7
Beefmaster	58	472	42.0	43.0	-13.4	1023.8	-53.2	-8.2
Brahman	58	571	26.8	14.1	-32.1	1018.0	-59.0	1.2
Brangus	59	470	47.2	38.8	-11.2	1035.5	-41.5	-1.7
Santa Gertrudis	29	311	6.2	9.5	-7.8	1027.3	-49.7	31.1
Braunvieh	36	452	68.0	69.7	-33.3	1002.3	-74.7	-55.7
Charolais	123	1120	49.3	30.8	15.6	1073.4	-3.6	34.1
Chiangus	30	312	57.2	60.8	-23.8	1010.3	-66.6	-36.8
Gelbvieh	90	1082	99.8	77.8	-5.5	1054.9	-22.0	-34.8
Limousin	86	1116	90.4	58.4	-31.3	1038.2	-38.8	-42.2
Maine Anjou	48	496	57.2	58.1	-34.3	1002.0	-74.9	-45.1
Salers	58	484	83.4	68.6	-13.8	1039.2	-37.8	-34.2
Simmental	109	1147	91.3	83.5	17.2	1064.4	-12.6	-16.9
Tarentaise	17	279	26.9	6.3	-37.4	1020.4	-56.6	3.5

Calculations:

(4) = (3) / b + [(1) − (2)] + (Raw Angus Mean: 1038.7 lb) with b = 0.96

(5) = (4) − (4, Angus)

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

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

Table 4. Breed of maternal grandsire solutions from USMARC, mean breed and USMARC EPD used to adjust for genetic trend to the year 2015 base and factors to adjust within breed EPD to an Angus equivalent – MILK (lb)

Breed	AI Sires	Number Direct Gpr	Direct Progeny	Ave. Base EPD Breed 2015 (1)	Ave. Base EPD USMARC Bulls (2)	Breed Soln at USMARC (vs Ang) (3)	BY 2015 Sire Breed Average (4)	BY 2015 Sire Breed Difference[a] (5)	Factor to adjust EPD To Angus (6)
Angus	153	3287	806	24.0	16.7	0.0	560.8	0.0	0.0
Hereford	147	3932	976	21.0	11.4	-24.5	539.8	-21.0	-18.0
Red Angus	54	1111	307	21.0	18.1	4.5	560.7	-0.1	2.9
Shorthorn	54	584	205	17.1	19.6	7.8	558.5	-2.3	4.6
South Devon	26	394	100	25.0	20.7	7.3	564.7	3.9	2.9
Beefmaster	50	496	154	9.0	9.2	-1.1	552.3	-8.5	6.5
Brahman	56	897	259	5.5	6.7	14.4	565.9	5.1	23.6
Brangus	51	478	147	9.3	7.0	-0.7	555.2	-5.6	9.1
Santa Gertrudis	23	324	123	0.7	-1.2	-2.3	553.2	-7.6	15.7
Braunvieh	30	757	193	34.7	33.9	18.4	571.8	11.0	0.3
Charolais	102	1904	500	8.8	6.2	-3.3	552.9	-7.9	7.3
Chiangus	26	314	126	15.8	13.5	-4.1	551.9	-8.9	-0.7
Gelbvieh	78	1782	425	27.6	29.0	17.2	568.5	7.7	4.1
Limousin	70	2038	461	26.0	24.5	-5.9	549.4	-11.4	-13.4
Maine Anjou	44	702	199	18.3	17.2	-3.4	551.3	-9.5	-3.8
Salers	47	680	209	19.7	18.8	8.7	562.7	1.9	6.2
Simmental	87	2051	510	21.1	25.7	12.9	561.2	0.4	3.3
Tarentaise	15	390	107	0.3	4.2	10.9	560.0	-0.8	22.9

Calculations:

(4) = (3) / b + [(1) − (2)] + (Raw Angus Mean: 553.5 lb) with b = 1.05

(5) = (4) − (4, Angus)

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

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

Table 5. Breed of sire solutions from USMARC, mean breed and USMARC EPD used to adjust for genetic trend to the year 2015 base and factors to adjust within breed EPD to an Angus equivalent – MARBLING (marbling score units[a])

Breed	Number AI Sires	Number Direct Progeny	Ave. Base EPD Breed 2015 (1)	Ave. Base EPD USMARC Bulls (2)	Breed Soln at USMARC (vs Ang) (3)	BY 2015 Sire Breed Average (4)	BY 2015 Sire Breed Difference[b] (5)	Factor to adjust EPD To Angus (6)
Angus	177	914	0.59	0.26	0.00	5.83	0.00	0.00
Hereford	172	1061	0.09	0.02	-0.53	5.03	-0.80	-0.30
Red Angus	63	301	0.43	0.42	-0.06	5.44	-0.39	-0.23
Shorthorn	58	284	0.05	0.02	-0.34	5.18	-0.65	-0.11
South Devon	25	77	0.40	-0.04	-0.37	5.56	-0.27	-0.08
Brahman	56	236	0.00	-0.01	-1.02	4.49	-1.34	-0.75
Santa Gertrudis	28	150	-0.01	-0.02	-0.83	4.67	-1.16	-0.56
Braunvieh	35	211	0.60	0.49	-0.43	5.17	-0.66	-0.67
Charolais	117	531	0.04	-0.01	-0.62	4.93	-0.90	-0.35
Chiangus	29	146	0.06	0.03	-0.46	5.06	-0.77	-0.24
Gelbvieh	87	482	0.12	-0.20	-0.75	5.07	-0.76	-0.29
Limousin	80	454	-0.02	-0.26	-0.90	4.83	-1.00	-0.39
Maine Anjou	48	247	-0.03	-0.02	-0.79	4.70	-1.13	-0.51
Salers	52	237	0.20	-0.39	-0.68	5.41	-0.42	-0.03
Simmental	103	528	0.14	0.01	-0.58	5.04	-0.79	-0.34

Calculations:

(4) = (3) / b + [(1) – (2)] + (Raw Angus Mean: 5.50) with b = 1.00

(5) = (4) – (4, Angus)

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

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

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

Table 6. Breed of sire solutions from USMARC, mean breed and USMARC EPD used to adjust for genetic trend to the year 2015 base and factors to adjust within breed EPD to an Angus equivalent – RIBEYE AREA (in^2)

Breed	Number		Ave. Base EPD		Breed Soln at USMARC	BY 2015 Sire Breed	BY 2015 Sire Breed	Factor to adjust EPD
	AI Sires	Direct Progeny	Breed 2015	USMARC Bulls	(vs Ang)	Average	Difference[a]	To Angus
			(1)	(2)	(3)	(4)	(5)	(6)
Angus	177	915	0.57	0.13	0.00	13.88	0.00	0.00
Hereford	172	1061	0.34	0.01	-0.20	13.57	-0.31	-0.08
Red Angus	63	301	0.14	-0.04	-0.23	13.39	-0.49	-0.06
Shorthorn	58	284	0.01	-0.08	0.16	13.69	-0.18	0.38
South Devon	25	77	0.23	0.22	0.40	13.84	-0.04	0.30
Brahman	56	241	0.01	0.04	-0.13	13.28	-0.59	-0.03
Santa Gertrudis	28	151	0.04	0.00	-0.23	13.24	-0.63	-0.10
Braunvieh	35	211	0.34	0.29	0.99	14.48	0.61	0.84
Charolais	117	535	0.34	0.12	1.16	14.82	0.94	1.17
Chiangus	29	147	0.38	0.15	0.45	14.12	0.24	0.43
Gelbvieh	87	484	0.45	0.36	0.98	14.52	0.64	0.76
Limousin	80	455	0.46	0.37	1.24	14.77	0.90	1.01
Maine Anjou	48	247	0.31	0.26	1.03	14.52	0.64	0.90
Salers	52	238	0.04	0.03	0.82	14.27	0.39	0.92
Simmental	103	529	0.80	0.59	0.94	14.59	0.71	0.48

Calculations:

(4) = (3) / b + [(1) − (2)] + (Raw Angus Mean: 13.44 in^2) with b = 1.00

(5) = (4) − (4, Angus)

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

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

Table 7. Breed of sire solutions from USMARC, mean breed and USMARC EPD used to adjust for genetic trend to the year 2015 base and factors to adjust within breed EPD to an Angus equivalent – FAT THICKNESS (in)

Breed	Number AI Sires	Number Direct Progeny	Ave. Base EPD Breed 2015 (1)	Ave. Base EPD USMARC Bulls (2)	Breed Soln at USMARC (vs Ang) (3)	BY 2015 Sire Breed Average (4)	BY 2015 Sire Breed Difference[a] (5)	Factor to adjust EPD To Angus (6)
Angus	177	915	0.018	0.004	0.000	0.667	0.000	0.000
Hereford	172	1060	0.005	-0.002	-0.062	0.598	-0.069	-0.056
Red Angus	63	299	-0.005	-0.011	-0.029	0.630	-0.037	-0.014
Shorthorn	58	284	-0.042	-0.034	-0.131	0.514	-0.154	-0.094
South Devon	25	77	0.010	0.009	-0.127	0.527	-0.141	-0.133
Brahman	56	241	0.000	-0.002	-0.146	0.509	-0.158	-0.140
Santa Gertrudis	28	151	0.002	0.003	-0.082	0.570	-0.097	-0.081
Braunvieh	35	210	-0.089	-0.090	-0.184	0.469	-0.198	-0.091
Charolais	117	534	0.005	0.005	-0.207	0.446	-0.221	-0.208
Chiangus	29	146	-0.049	-0.030	-0.125	0.509	-0.158	-0.091
Gelbvieh	87	482	-0.040	-0.075	-0.188	0.500	-0.167	-0.109
Limousin	80	454	-0.044	-0.075	-0.192	0.493	-0.174	-0.112
Maine Anjou	48	247	-0.050	-0.039	-0.215	0.427	-0.240	-0.172
Salers	52	238	0.000	-0.007	-0.197	0.464	-0.204	-0.186
Simmental	103	529	-0.055	-0.053	-0.176	0.474	-0.193	-0.120

Calculations:

(4) = (3) / b + [(1) – (2)] + (Raw Angus Mean: 0. 663 in) with b = 1.00

(5) = (4) – (4, Angus)

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

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

Table 8. Breed of sire solutions from USMARC, mean breed and USMARC EPD used to adjust for genetic trend to the year 2015 base and factors to adjust within breed EPD to an Angus equivalent – CARCASS WEIGHT (lb)

Breed	Number AI Sires	Number Direct Progeny	Ave. Base EPD Breed 2015 (1)	Ave. Base EPD USMARC Bulls (2)	Breed Soln at USMARC (vs Ang) (3)	BY 2015 Sire Breed Average (4)	BY 2015 Sire Breed Difference[a] (5)	Factor to adjust EPD To Angus (6)
Angus	177	915	35.0	15.7	0.0	936.1	0.0	0.0
Hereford	172	1061	61.0	43.6	-33.6	900.6	-35.5	-61.5
Red Angus	63	301	21.0	13.9	-16.3	907.6	-28.5	-14.5
Shorthorn	58	284	7.4	8.5	-14.1	901.7	-34.5	-6.9
South Devon	25	77	29.0	16.3	-24.0	905.5	-30.6	-24.6
Brahman	56	242	1.8	0.9	-43.7	874.0	-62.1	-28.9
Santa Gertrudis	28	151	4.0	5.3	-15.8	899.7	-36.4	-5.4
Braunvieh	35	212	22.6	21.0	-42.1	876.3	-59.8	-47.4
Charolais	117	535	16.8	8.0	9.7	935.3	-0.8	17.4
Chiangus	29	147	8.8	9.4	-21.2	895.1	-41.1	-14.9
Gelbvieh	87	484	29.6	18.5	-13.6	914.3	-21.8	-16.4
Limousin	80	455	25.0	5.7	-20.8	915.3	-20.9	-10.9
Maine Anjou	48	247	6.2	8.1	-27.0	887.9	-48.3	-19.5
Salers	52	239	22.9	16.4	-28.0	895.4	-40.7	-28.6
Simmental	103	529	26.8	22.3	9.4	930.6	-5.5	2.7

Calculations:

(4) = (3) / b + [(1) − (2)] + (Raw Angus Mean: 916.8 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	0.83	0.80	0.76	0.76	0.56	0.56	0.54	0.54
Hereford	0.70	0.66	0.65	0.62	0.34	0.45	0.37	0.57
Red Angus	0.92	0.91	0.91	0.89	0.71	0.69	0.70	0.60
Shorthorn	0.83	0.82	0.81	0.81	0.49	0.48	0.49	0.57
South Devon	0.47	0.51	0.46	0.52	0.08	0.10	0.11	0.34
Beefmaster	0.89	0.90	0.82	0.69				
Brahman	0.55	0.52	0.46	0.35	0.12	0.15	0.12	0.30
Brangus	0.89	0.83	0.73	0.74				
Santa Gertrudis	0.72	0.69	0.55	0.56	0.40	0.39	0.49	0.43
Braunvieh	0.64	0.57	0.32	0.51	0.12	0.19	0.10	0.19
Charolais	0.82	0.77	0.70	0.71	0.35	0.39	0.33	0.36
Chiangus	0.80	0.78	0.78	0.74	0.33	0.31	0.33	0.56
Gelbvieh	0.86	0.85	0.84	0.83	0.63	0.58	0.60	0.56
Limousin	0.93	0.92	0.92	0.92	0.64	0.63	0.65	0.60
Maine Anjou	0.79	0.77	0.77	0.78	0.24	0.23	0.27	0.54
Salers	0.82	0.82	0.76	0.79	0.28	0.31	0.36	0.60
Simmental	0.94	0.94	0.94	0.93	0.73	0.71	0.72	0.60
Tarentaise	0.92	0.90	0.88	0.86				

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

Table 10. Estimates of variance components (lb^2) for birth weight (BWT), weaning weight (WWT), yearling weight (YWT), and maternal weaning weight (MWWT) and for marbling (MAR; marbling score units^2), ribeye area (REA; in^4), fat thickness (FAT; in^2), and carcass weight (CWT; lb) from mixed model analyses of USMARC data

Analysis	BWT	WWT[a]	YWT
Animal within breed (18 breeds)	68.64	501.36	3674.23
Maternal genetic within breed (18 breeds)		444.60	
Maternal permanent environment		703.53	
Residual	58.76	1323.70	4617.04

Carcass Direct	MAR	REA	FAT	CWT
Animal within breed (15 breeds)	0.282	0.687	0.0103	2344.82
Residual	0.256	0.770	0.0143	2266.19

[a]Estimated direct maternal covariance for weaning weight was -35.51 lb^2

Table 11. Pooled and within-breed regression coefficients (lb/lb) for weights at birth (BWT), 205 days (WWT), and 365 days (YWT) of F_1 progeny and for calf weights (205 d) of F_1 dams (MILK) on sire expected progeny difference and by sire breed

	BWT	WWT	YWT	MILK
Pooled	1.18 + 0.03	0.80 + 0.03	0.96 + 0.03	1.05 + 0.06
Sire breed				
Angus	1.12 + 0.09	0.85 + 0.06	1.14 + 0.06	1.08 + 0.14
Hereford	1.20 + 0.07	0.68 + 0.05	0.95 + 0.05	1.07 + 0.14
Red Angus	1.00 + 0.13	0.73 + 0.13	0.62 + 0.14	1.05 + 0.22
Shorthorn	0.74 + 0.18	0.53 + 0.14	0.48 + 0.17	0.56 + 0.39
South Devon	0.21 + 0.37	0.98 + 0.25	0.72 + 0.26	1.08 + 0.95
Beefmaster	1.88 + 0.26	0.56 + 0.19	0.30 + 0.28	3.30 + 0.80
Brahman	1.89 + 0.21	1.19 + 0.17	1.32 + 0.20	0.53 + 0.56
Brangus	1.57 + 0.21	0.87 + 0.18	0.84 + 0.16	0.63 + 0.49
Santa Gertrudis	3.20 + 0.62	1.17 + 0.23	1.21 + 0.28	0.57 + 0.96
Braunvieh	0.78 + 0.27	0.61 + 0.28	0.38 + 0.26	1.42 + 0.62
Charolais	1.05 + 0.11	0.88 + 0.10	0.83 + 0.11	1.00 + 0.19
Chiangus	1.35 + 0.22	0.38 + 0.24	0.61 + 0.27	0.29 + 0.41
Gelbvieh	1.13 + 0.13	0.86 + 0.10	1.11 + 0.11	0.82 + 0.22
Limousin	1.14 + 0.12	0.79 + 0.07	0.83 + 0.08	1.24 + 0.20
Maine Anjou	1.61 + 0.18	1.04 + 0.19	1.05 + 0.26	1.87 + 0.37
Salers	1.31 + 0.22	0.68 + 0.24	0.70 + 0.23	1.77 + 0.34
Simmental	1.08 + 0.12	1.40 + 0.12	1.30 + 0.11	0.95 + 0.26
Tarentaise	0.99 + 0.47	1.06 + 0.21	1.58 + 0.29	1.12 + 0.71

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

	MAR	REA	FAT	CWT
Pooled	0.52 + 0.03	0.84 + 0.05	0.84 + 0.07	0.99 + 0.05
Sire breed				
Angus	0.76 + 0.07	0.68 + 0.11	0.70 + 0.11	0.98 + 0.09
Hereford	0.60 + 0.12	0.66 + 0.11	1.01 + 0.15	1.02 + 0.10
Red Angus	1.11 + 0.14	1.18 + 0.17	1.01 + 0.29	1.01 + 0.21
Shorthorn	1.19 + 0.19	0.57 + 0.32	1.23 + 0.36	0.49 + 0.28
South Devon	-0.09 + 0.17	1.77 + 2.18	2.96 + 1.66	0.08 + 0.69
Brahman	1.86 + 0.85	1.03 + 0.31	0.70 + 0.49	0.59 + 0.23
Santa Gertrudis	0.79 + 0.61	0.73 + 0.46	1.32 + 0.82	1.35 + 0.44
Braunvieh	0.25 + 0.29	0.86 + 0.31	-0.53 + 0.47	0.27 + 0.37
Charolais	0.98 + 0.17	0.88 + 0.15	1.27 + 0.31	1.06 + 0.22
Chiangus	0.51 + 0.13	0.59 + 0.43	1.49 + 0.46	0.79 + 0.43
Gelbvieh	1.04 + 0.17	1.25 + 0.15	1.70 + 0.24	1.49 + 0.18
Limousin	0.72 + 0.21	0.89 + 0.12	1.63 + 0.26	0.86 + 0.12
Maine Anjou	-0.35 + 0.42	-0.53 + 0.40	0.02 + 0.21	1.75 + 0.35
Salers	0.04 + 0.06	1.31 + 0.51	0.48 + 0.44	0.62 + 0.42
Simmental	0.98 + 0.14	0.85 + 0.13	0.20 + 0.25	1.51 + 0.19

Figure 1. Relative genetic trends for birth weight (lb) of the seven most highly used beef breeds (1a) and all breeds that submitted 2017 trends (1b) adjusted for birth year 2015 using the 2017 across-breed EPD adjustment factors.
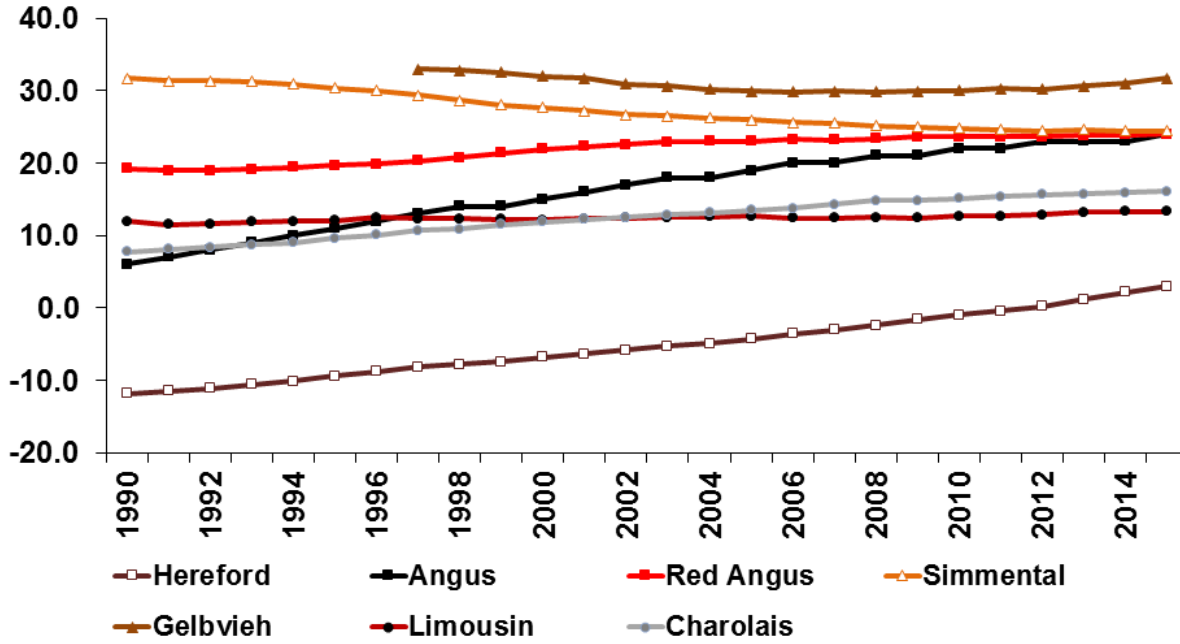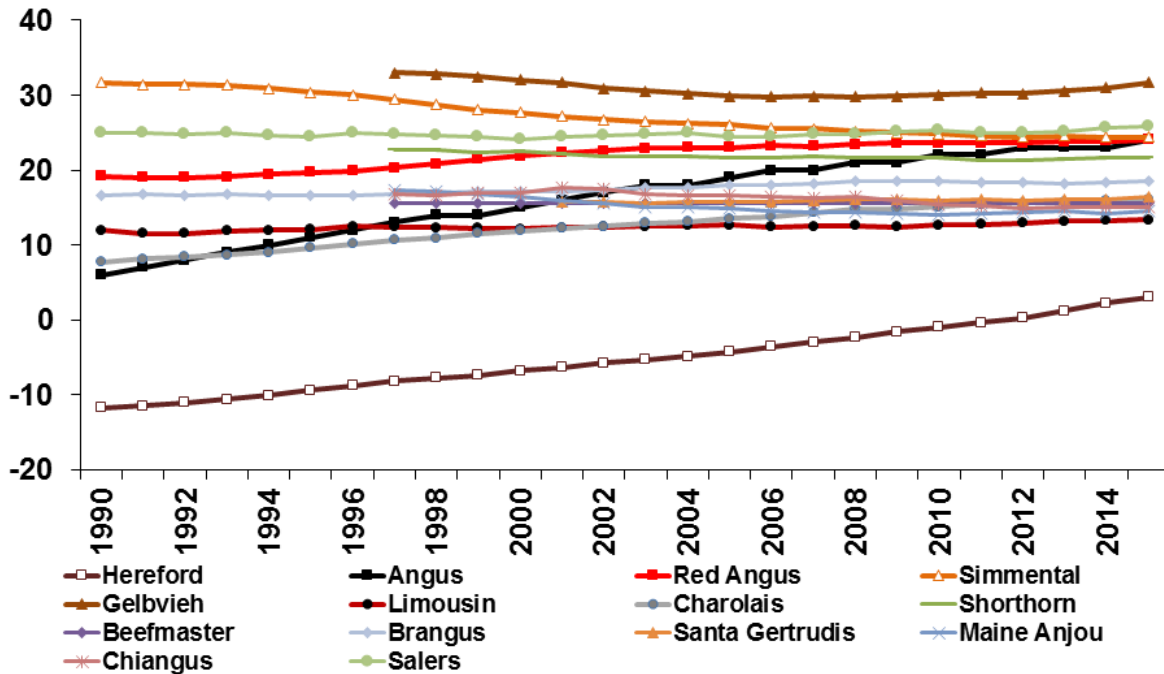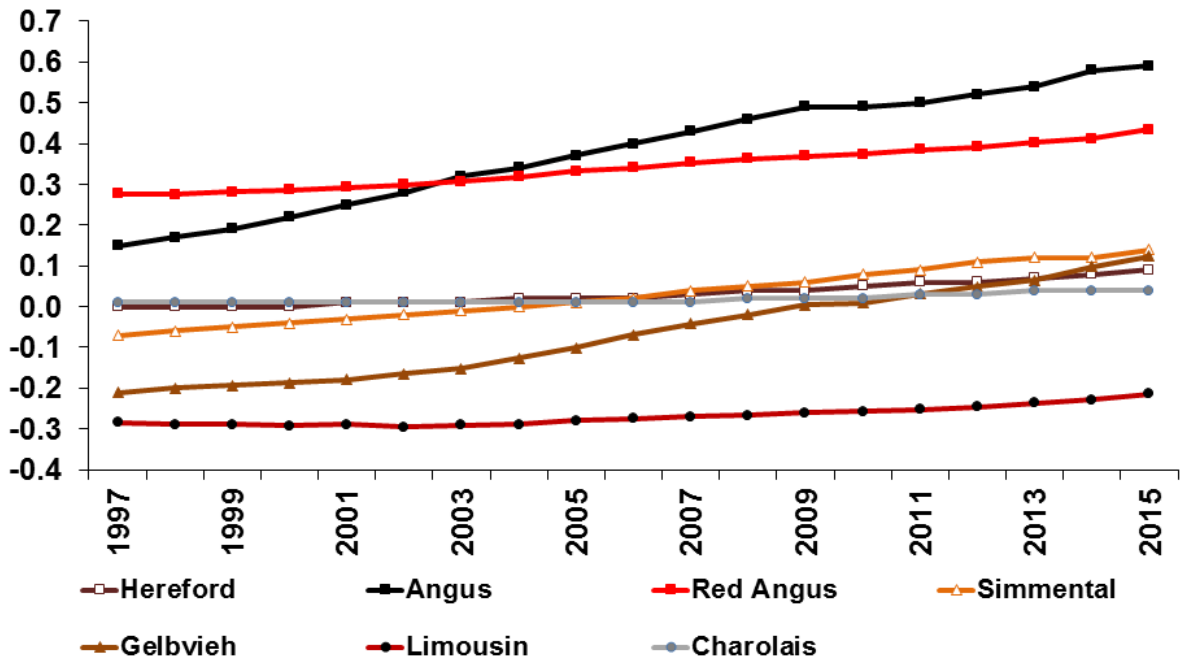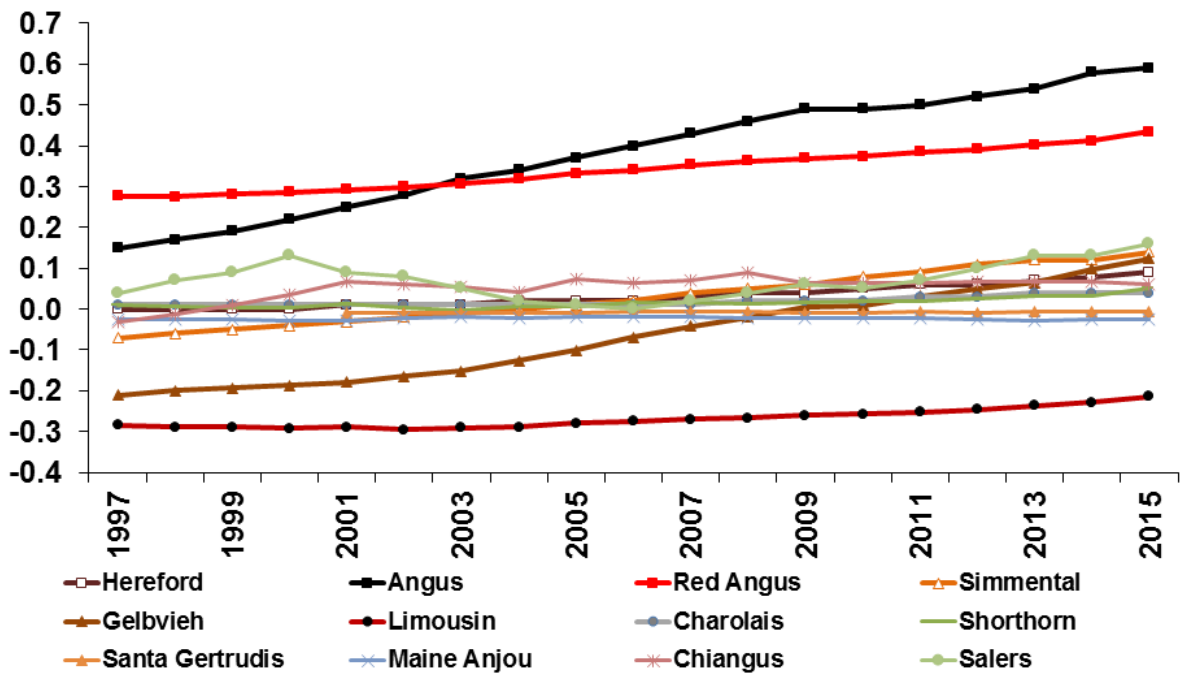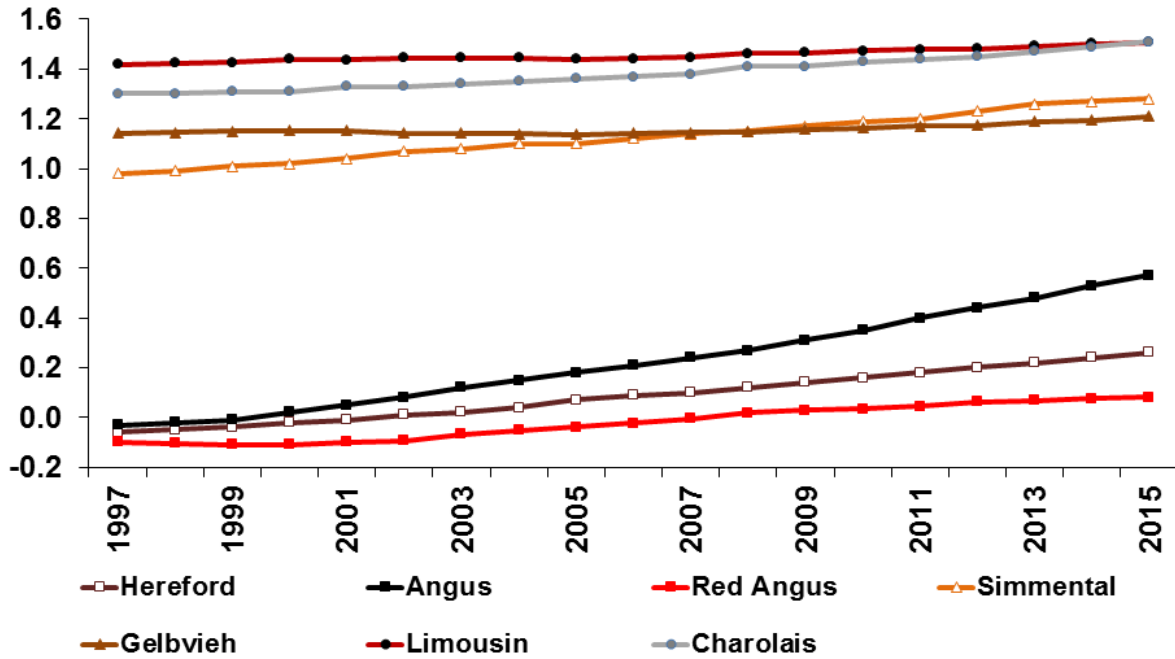
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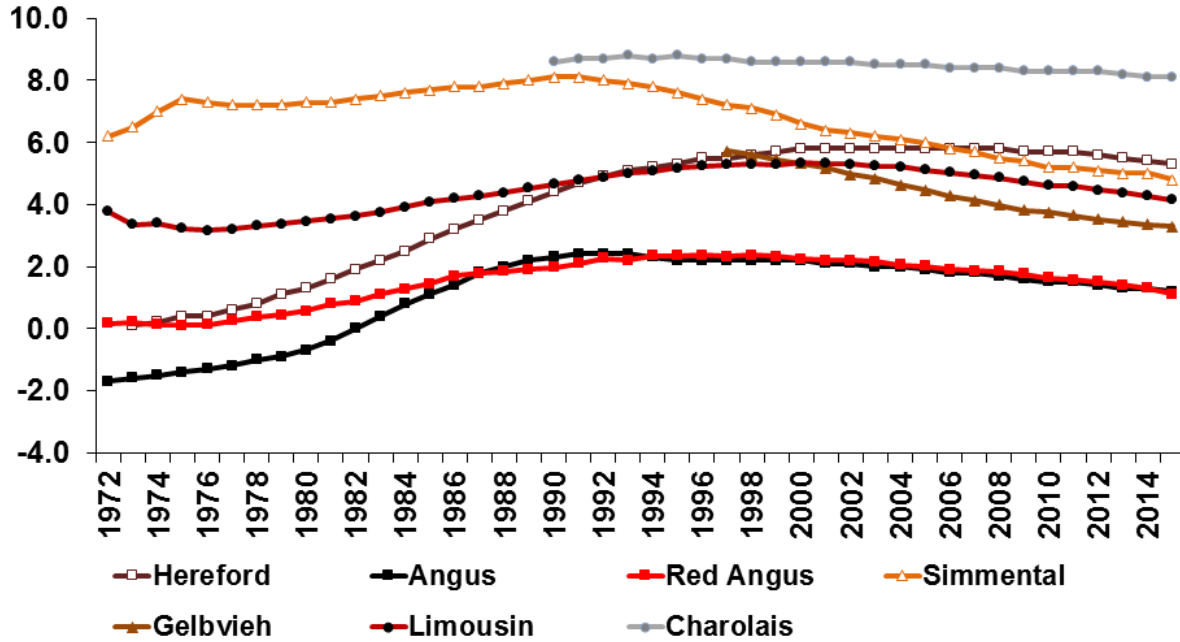
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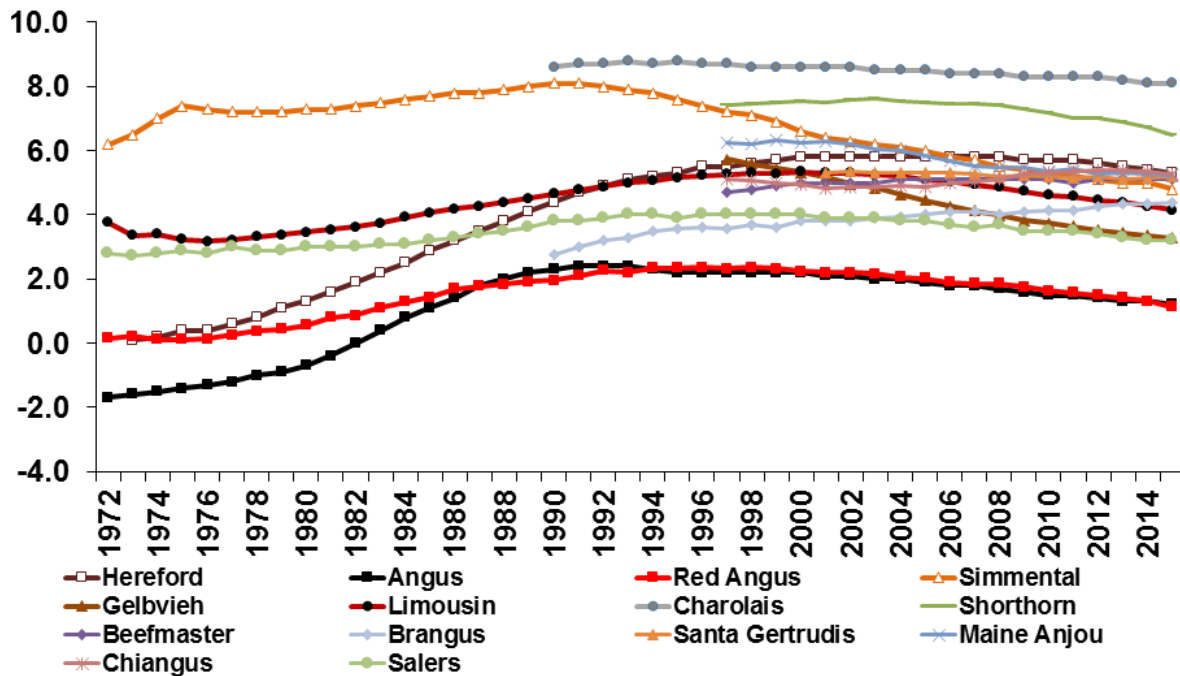
Figure 2. Relative genetic trends for weaning weight (lb) of the seven most highly used beef breeds (2a) and all breeds that submitted 2017 trends (2b) adjusted for birth year 2015 using the 2017 across-breed EPD adjustment factors.
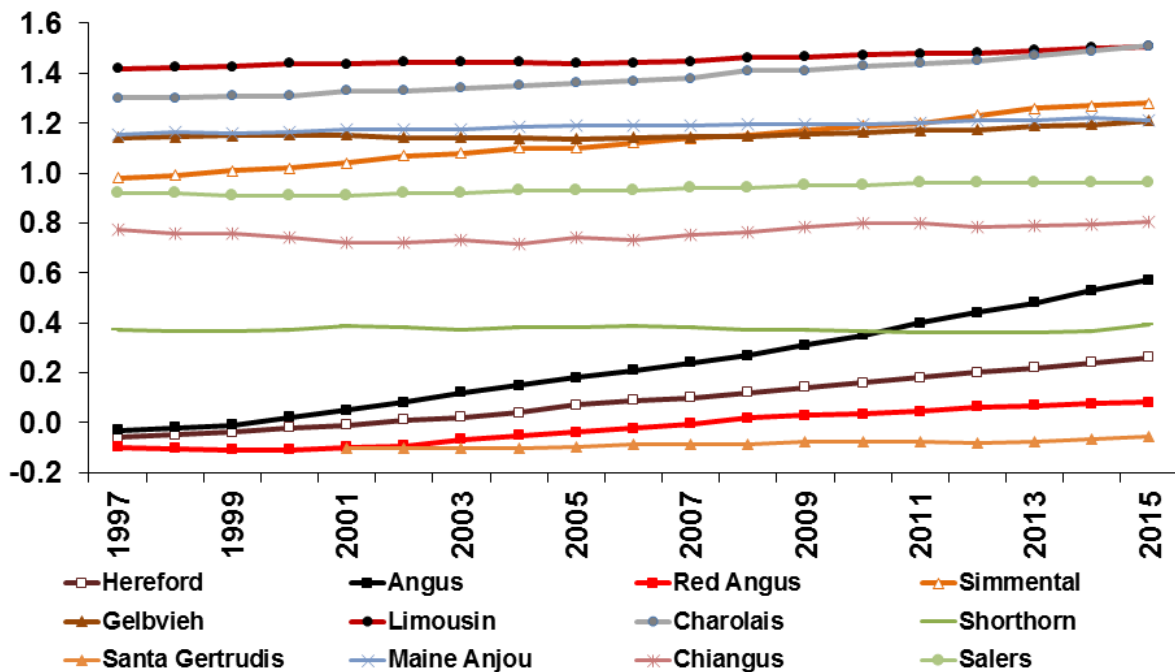
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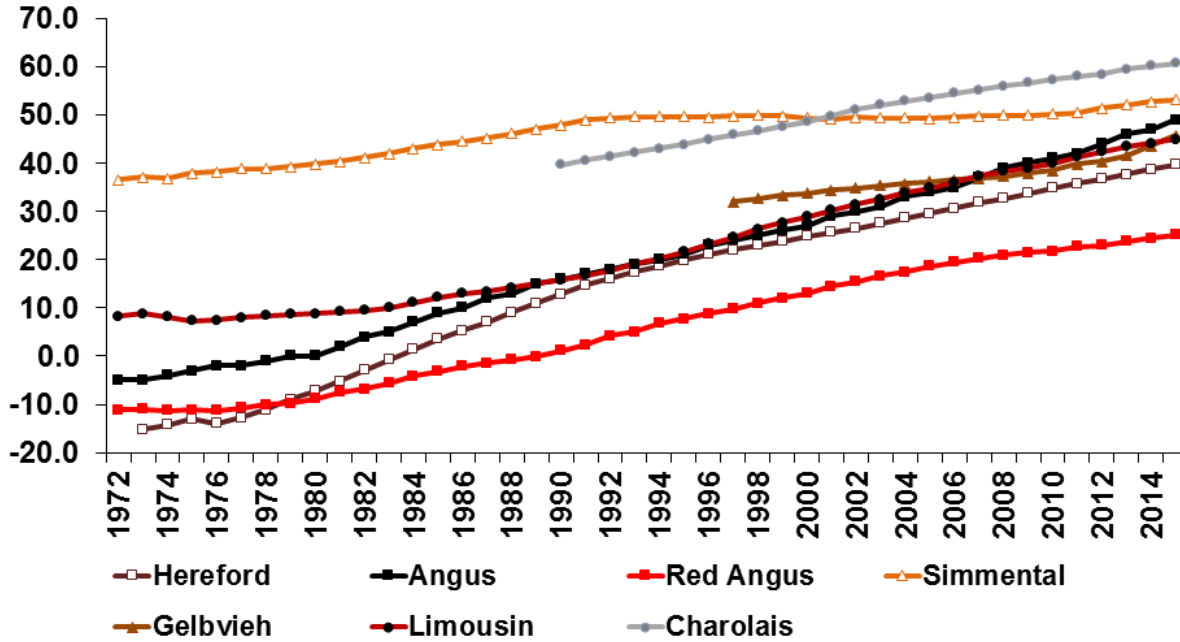
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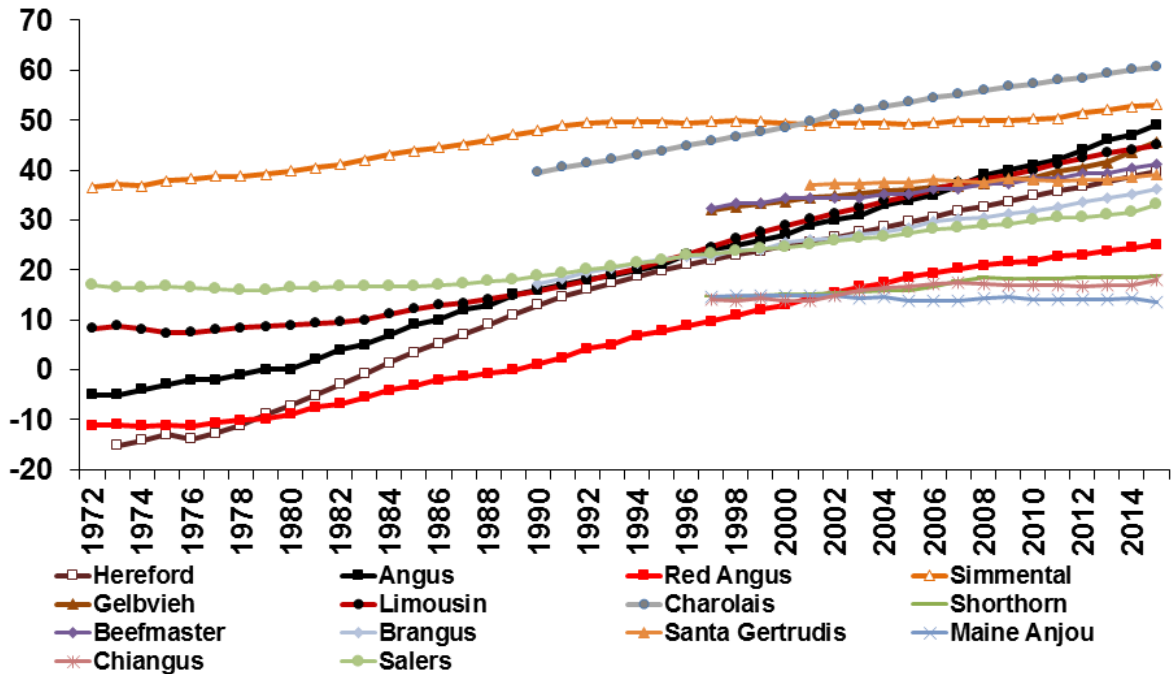
Figure 3. Relative genetic trends for yearling weight (lb) of the seven most highly used beef breeds (3a) and all breeds that submitted 2017 trends (3b) adjusted for birth year 2015 using the 2017 across-breed EPD adjustment factors.
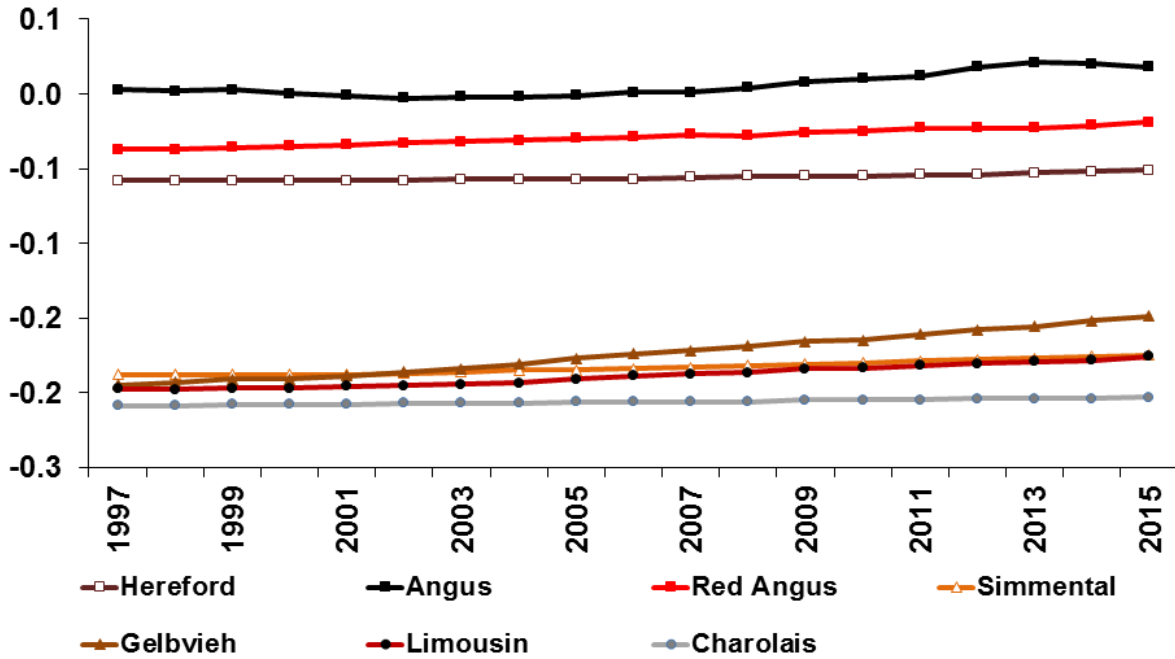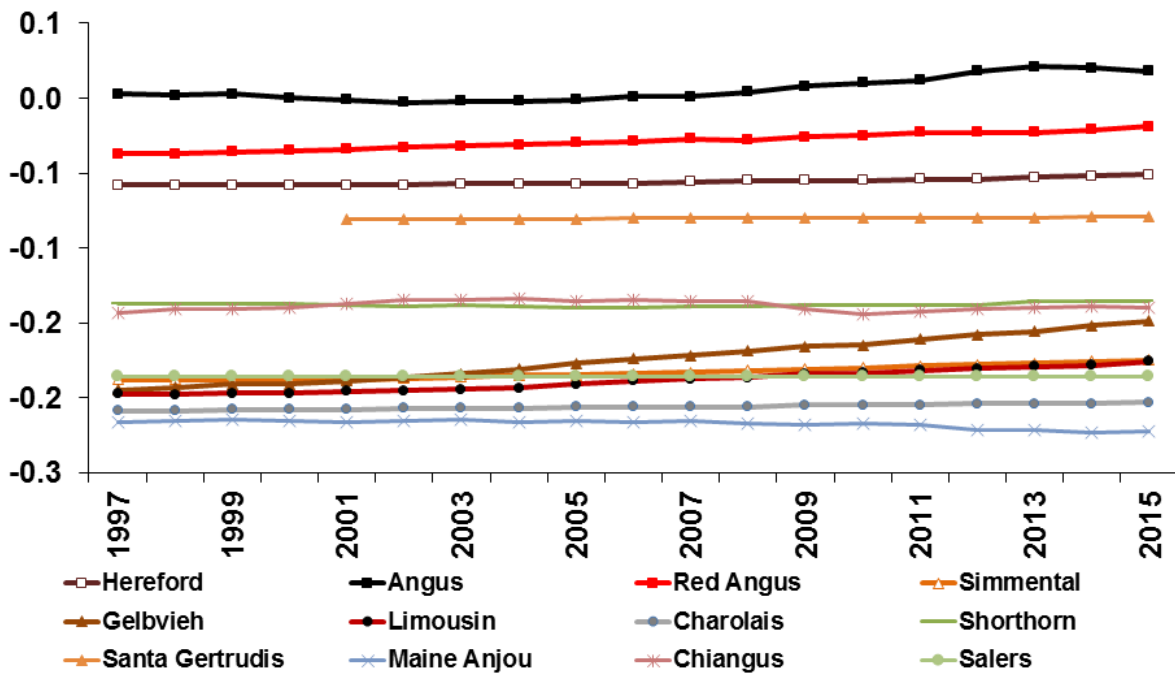
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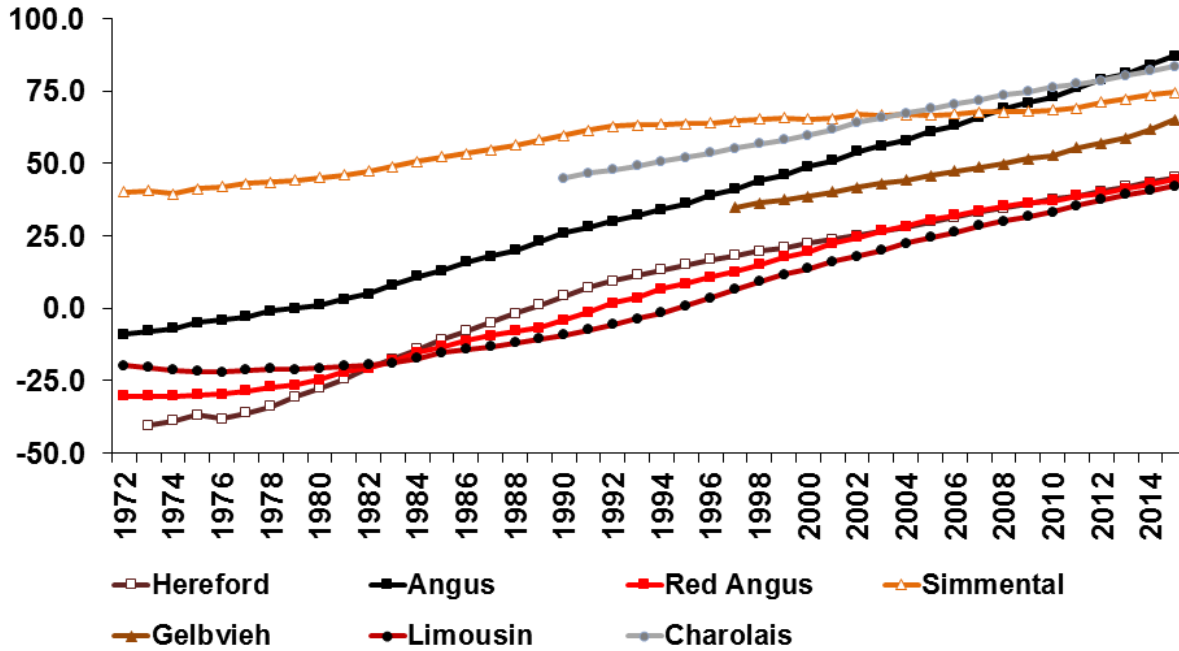
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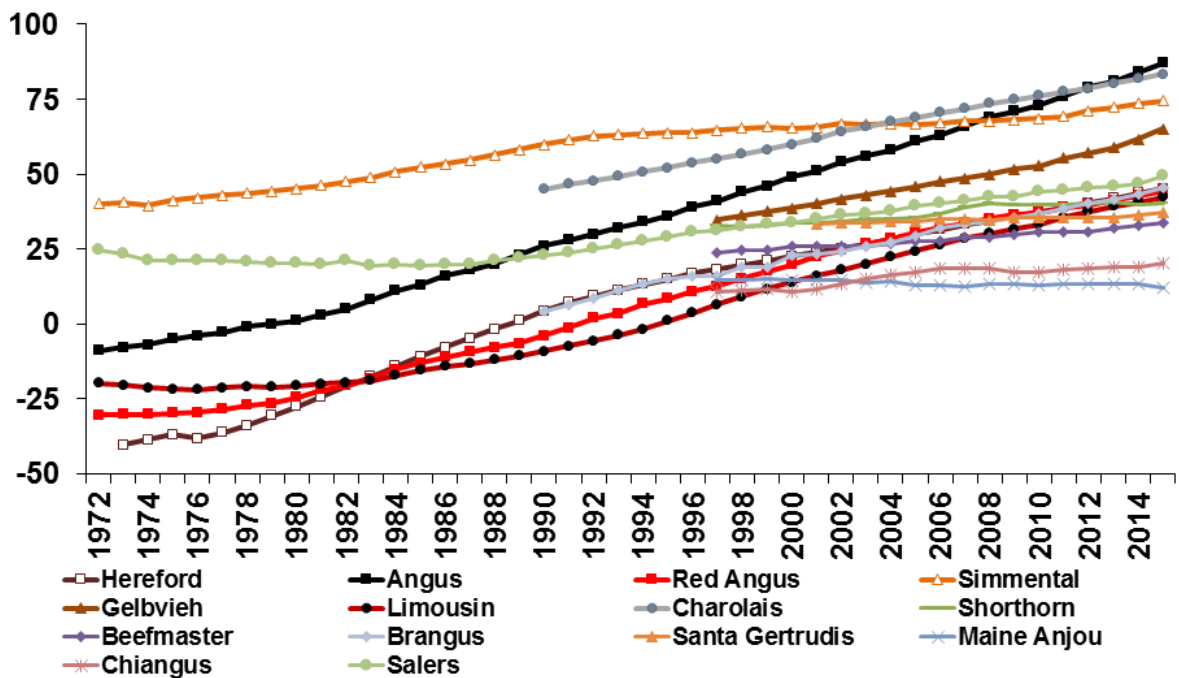
Figure 4. Relative genetic trends for maternal milk (lb) of the seven most highly used beef breeds (4a) and all breeds that submitted 2017 trends (4b) adjusted for birth year 2015 using the 2017 across-breed EPD adjustment factors.

4a.

4b.

Figure 5. Relative genetic trends for marbling score (marbling score units; $4.00 = Sl^{00}$, $5.00 = Sm^{00}$) of the seven most highly used beef breeds (5a) and all breeds that submitted 2017 trends (5b) adjusted for birth year 2015 using the 2017 across-breed EPD adjustment factors.

5a.

5b.

Figure 6. Relative genetic trends for maternal milk (lb) of the seven most highly used beef breeds (6a) and all breeds that submitted 2017 trends (6b) adjusted for birth year 2015 using the 2017 across-breed EPD adjustment factors.

6a.

6b.

Figure 7. Relative genetic trends for backfat depth (in) of the seven most highly used beef breeds (7a) and all breeds that submitted 2017 trends (7b) adjusted for birth year 2015 using the 2017 across-breed EPD adjustment factors.

7a.

7b.

Figure 8. Relative genetic trends for maternal milk (lb) of the seven most highly used beef breeds
(8a) and all breeds that submitted 2017 trends (8b) adjusted for birth year 2015 using the 2017
across-breed EPD adjustment factors.

8a.
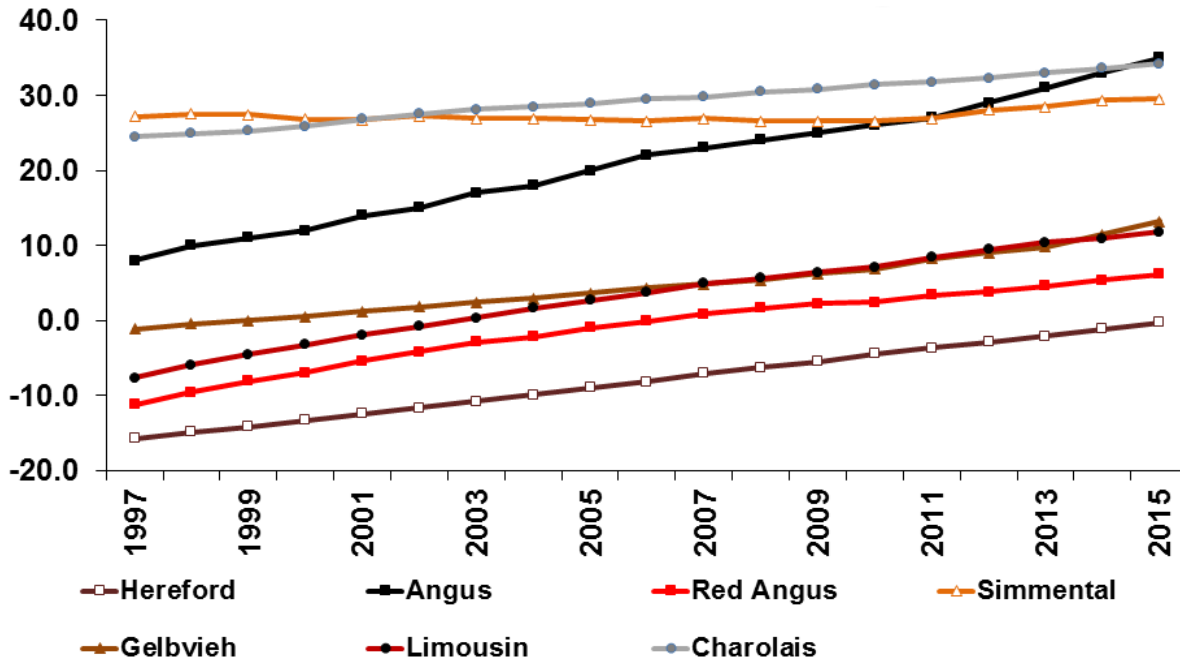
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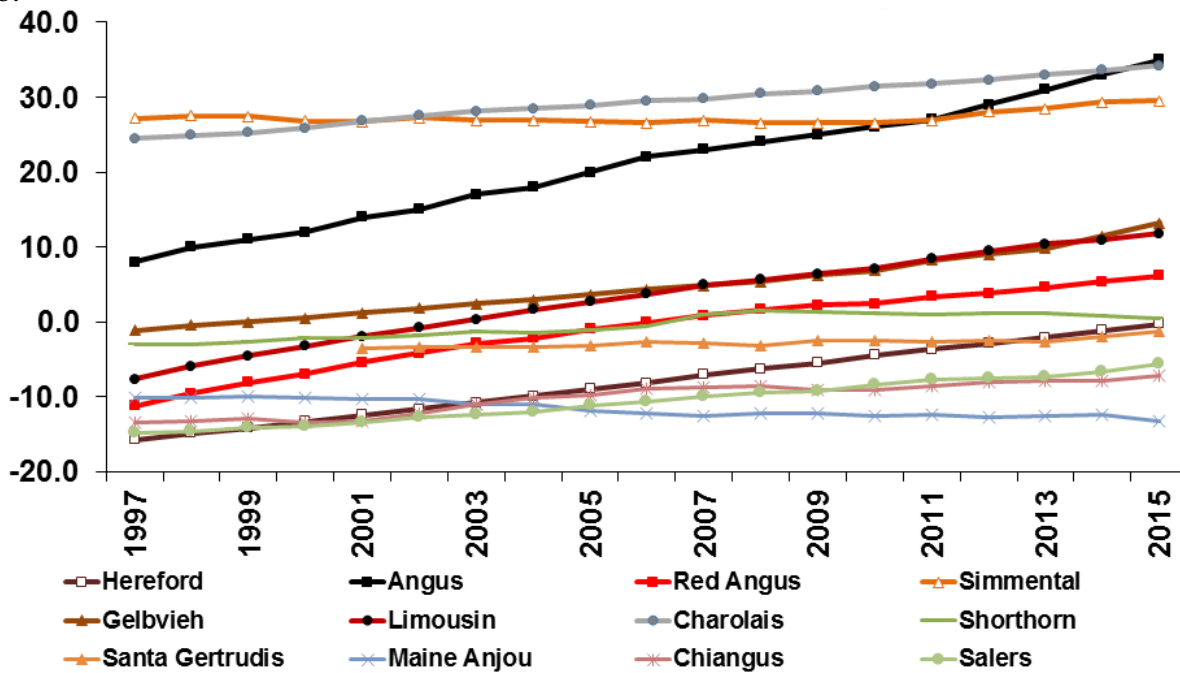
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