

54TH ANNUAL

BEEF IMPROVEMENT FEDERATION RESEARCH SYMPOSIUM & CONVENTION

JUNE 1-3 | LAS CRUCES, NEW MEXICO





**54TH ANNUAL
BEEF IMPROVEMENT FEDERATION
RESEARCH SYMPOSIUM & CONVENTION**

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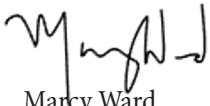
Welcome to Las Cruces

On behalf of New Mexico State University, we would like to welcome you to the 2022 Beef Improvement Federation Annual Meeting and Research Symposium. This is the first time the symposium has come to New Mexico, and we are honored and grateful for the opportunity.

The next three days will provide a unique perspective of ranching in arid environments, sustainability, and global trade. The symposium will kick off Wednesday June 1st, with an opportunity to visit the country's largest livestock crossing between Mexico and North America, located in Santa Teresa, NM. This tour will provide a real time perspective of global trade and all that is involved in bringing cattle into the United States. Thursday's general session will focus on the impacts of sustainability efforts on beef production, which will conclude with a panel of producers providing their perspective. The afternoon breakouts will allow attendees to learn the latest in genomic research, practical application, and the progress of genetic efficiency.

For Friday, the topics go global with discussions on where genetics are headed worldwide, and will conclude with a topic that will tie sustainability and genetic selection together. The final set of breakout sessions for the symposium will cover EBVs and trait development, carcass evaluation, nutrition, and cross breeding systems.

Regards,



Marcy Ward

ACES-CES Extension Livestock Specialist

2022 BIF Organizing Committee Chair



2022-23 BIF President Joe Epperly thanks Marcy Ward for her leadership planning the 2022 BIF Symposium.



Schedule of Events

Wednesday, June 1, 2022

Young Producer Symposium/Pre-Tour – Santa Teresa Livestock Crossing

- 12:00 p.m.... Depart from the Las Cruces Convention Center and El Paso International Airport
- 1:00 p.m..... Arrive in Santa Teresa (lunch served upon arrival)
- 1:15 p.m..... Santa Teresa Livestock Auction introduction/cattle marketing from Mexico to the United States
Tito Medina, STLA Manager/Auctioneer
- 1:30 p.m..... Breeding strategies in Mexico
Dr. Moises Montaño-Bermúdez, INIFAP
- 2:00 p.m..... Tour of Santa Teresa Livestock Crossing
Daniel Manzanarez, STBC Manager
- 4:00 p.m..... Depart Santa Teresa for Las Cruces
- 5:00 p.m..... Opening reception
Dina Chacón-Rietzel, New Mexico Beef Council

Thursday, June 2, 2022

General Session I

Sustainability: Rhetoric vs. Reality – Exhibit Hall 2

- 8:00 a.m..... Opening comments and welcome
Dr. Rolando A. Flores, College of ACES Dean, New Mexico State University
- 8:15 a.m..... Sustainability: Rhetoric vs. Reality
Ruaraidh Petre, Executive Director, Global Roundtable for Sustainable Beef
- 9:00 a.m..... Fitting Environmental Impacts into Economic Selection Indexes
Dr. John Crowley, AbacusBio
- 9:30 a.m..... Climate Neutral Beef: Where Do We Go from Here
Dr. Jason Sawyer, Associate Professor & Research Scientist, King Ranch® Institute for Ranch Management
- 10:00 a.m..... Break
- 10:30 a.m.... Strategies for Sustainability at the Ranch Producer Panel
Dr. Clay Mathis, Executive Director, King Ranch® Institute for Ranch Management
- Featuring speakers: CS Ranch, Cimarron, New Mexico; Decky Spiller, Silver Spur LLC, Kiowa County, Colorado; Dr. Trey Patterson, Chief Executive Officer, Padlock Ranch; and Erik Jakobsen, Vice President, Cattle for AgReserves*
- 11:30 a.m..... What I Heard
Dr. Clay Mathis, Executive Director, King Ranch® Institute for Ranch Management

Noon Awards Luncheon – Ballroom 1

Presentation of BIF Commercial Producer, Continuing Service and Ambassador Awards, and Roy Wallace Scholarship

- 2:00 p.m..... Technical breakouts

Advancements in Genomics and Genetic Prediction – Meeting Room 718

Chair: Dr. Warren Snelling, U.S. Meat Animal Research Center

- 2:00 p.m. Sequencing as the Foundation for a Modern Agrigenomics
Dr. Jesse Hoff, Gencove
- 2:30 p.m..... Relationship Between Mitochondrial DNA and Growth Carcass Traits in Beef Cattle
Dr. Leticia Sanglard, University of Nebraska-Lincoln
- 3:00 p.m..... Break

- 3:20 p.m..... The Bovine Pangenome Consortium: Developing Resources to Replace the Single Animal Reference Genome
Dr. Ben Rosen, USDA-ARS Animal Genomics and Improvement Laboratory

- 3:50 p.m..... Considerations and Strategies for Imputation Reference Panel Construction
Dr. Troy Rowan, University of Tennessee, Knoxville

- 4:20 p.m. Panel discussion

Advancements in Producer Applications – Meeting Room 3A/B

- Chair: Dr. Darrh Bullock, University of Kentucky**
- 2:00 p.m..... Can you Afford to Avoid Crossbreeding?
Dr. Jennifer Minick Bormann, Kansas State University

- 2:40 p.m.... Hitting the Bullseye: Factors Driving Bull Management and Bull Purchasing Decisions in the Southwest
Dr. Craig Gifford, New Mexico State University

- 3:20 p.m..... Break
- 3:30 p.m..... iGENDEC – Next Generation Decision Support
Dr. Matt Spangler, University of Nebraska-Lincoln

- 4:20 p.m..... Targeting Bull Selection to Match Your Management, Environment and Market
Dr. Mark Enns, Colorado State University

Advancements in Efficiency and Adaptability – Meeting Room 9/10

- Chair: Dr. Mark Enns, Colorado State University**
- 2:00 p.m..... Feedlot Heart Disease: Relationships between Heart Score and Performance
Dr. Scott E. Speidel, Colorado State University

- 2:40 p.m.... Impact of Arid Environments on Beef Cow Resiliency
Dr. Eric Scholljegerdes, New Mexico State University

- 3:20 p.m..... Break
- 3:30 p.m.... Assessing the Use of Partial Body Weight Measures for Liveweight Prediction
Dr. John Crowley, AbacusBio, Limited

- 4:10 p.m.... Development of a Genetic Selection Program for Beef Cattle Grazing Distribution: An Update
Dr. Derek Bailey, New Mexico State University

- 5:00 p.m. Busses depart to Farm and Ranch Heritage Museum

Friday, June 3, 2022

General Session II

Global Perspectives on Adaptation and Genetic Prediction – Exhibit Hall 2

- 7:45 am..... Announcements
- 8:00 a.m.... U.S. Genetic Exports: Where Are They Going and How Are They Doing?
Tony Clayton, Clayton Agri-Marketing

- 10:00 a.m. Global Sourcing of Beef Genetics to Meet a Vertically Coordinated Breeding Objective
Dr. Phil George, Miratorg Agribusiness Holding Production Director, Beef & Lamb Operations, Moscow, Russia

- 10:30 a.m. ... Harnessing Genetic x Environment Interactions – Are They Important in Production
Dr. Milton G. Thomas

- 11:15 a.m. BIF Board of Directors Caucuses and Elections

Noon Awards Luncheon – Ballroom 1

Presentation of BIF Pioneer and Seedstock Producer awards, Frank Baker and Larry Cundiff Scholarships, retiring president’s comments, introduction of newly elected BIF Board of Directors and invitation to BIF 2022

2:00 p.m..... Technical breakouts

Advancements in Emerging Technology – Meeting Room 3A/B

Chair: Dr. Megan Rolf, Kansas State University

2:30 p.m..... Across Country Genetic Evaluations
Dr. Andre Garcia, Angus Genetics, Inc.

3:05 p.m..... Title TBD
Dr. Jason Sawyer, Texas A&M-Kingsville, King Ranch® Institute for Ranch Management

3:40 p.m.....Break

3:50 p.m..... Feedlot Heart Disease: New Trait Development and Validation of Packing Plant Heart Score
Dr. Milton G. Thomas, Colorado State University

4:25 p.m.PrimeOne – An Animal Breeding Project That Began with The End
Dr. Ty Lawrence, West Texas A&M University

Advancements in End Product Improvement – Meeting Room 7/8

Chair: Dr. Tommy Perkins, West Texas A&M University

2:00 p.m..... Ultrasound Guidelines Council Update
Dr. Tommy Perkins, West Texas A&M University

2:30 p.m.....The Effect of Growth-Promoting Implants and Feeding Duration on Growth Performance, Feeding Behavior, Carcass Yields and Empty Body Composition of Serially-Harvested Charolais X Angus Steers
Dr. Ty Lawrence, West Texas A&M University

3:15 p.m.....Break

3:45 p.m.....Impact of Cow Nutrition on Final Body Composition Endpoints in Their Calves
Dr. Eric Scholljegerdes, New Mexico State University

4:15 p.m..... Body Composition Impacts Due to the Transcriptome in Mature Cows and the F94I Myostatin Gene in Growing Beef Heifers
Dr. Kristin Hales, Texas Tech University

Advancements in Selection Decisions – Meeting Room 9/10

Chair: Dr. Matt Spangler, University of Nebraska-Lincoln

2:00 p.m. Building Environmental Sustainability into Selection Indexes
Dr. John Crowley, Abacus Bio

2:40 p.m.....Contemplating Planning Horizon Length in Economically Optimal Selection Indexes
Dr. Matt Spangler, University of Nebraska-Lincoln

3:20 p.m.....Break

3:40 p.m.Breed Complementarity in the Context of Beef x Dairy Decisions
Dr. Bob Weaver, Kansas State University

4:20 p.m.....Across-Breed EPD Adjustments: Progress on Missing Traits and Multi-breed Evaluations
Dr. Larry Kuehn, U.S. Meat Animal Research Center

5:00 p.m..... BIF Board of Directors meeting

6:00 p.m. Dinner on your own



Dina Chacón-Rietzel, New Mexico Beef Council, was the keynote speaker on Wednesday night.



Dr. Rolando A. Flores, NMSU College of ACES Dean, welcomed guests on Thursday morning.

President's Profile: Catalyst for Progress



2021-22 BIF President

Matt Perrier encourages producers to focus on producing efficient, sustainable beef.

Fifth generation cattle rancher Matt Perrier grew up in the picturesque Kansas Flint Hills near Eureka. As part owner and manager of Dalebanks Angus he strives to provide genetics to commercial cow-calf and seedstock producers.

“Dad’s ‘office’ was a desk in our family room, and most of my childhood memories were of him on the phone explaining things like adjusted 205-day weights, contemporary groups and eventually expected progeny differences to our bull customers and counterparts in the seedstock business,” Matt recalls. “Some of the biggest advances in technology came when we were able to move from a mass-balance scale to a digital readout in the 1990s. Then came ultrasound, genomics and other technologies. Right or wrong, my ‘ranch lessons’ were often more about proper contemporary groups and ratios than they were about riding and roping.”

Elected to the Beef Improvement Federation (BIF) board of directors in 2016, Matt has served as BIF president for the past year. He passed the gavel to Vice President Joe Epperly from Albion, Nebraska, during the 2022 BIF Symposium June 3.

“To me, BIF is a catalyst for progress in the beef cattle industry,” Matt explains. “That progress isn’t always immediate, polished or perfect, but BIF has a good track record for being the place where industry change is often initiated.”

Matt’s path back to the ranch

Matt earned his bachelor’s degree in Animal Sciences and Industry from Kansas State University. While at K-State he was a member of the meat and livestock judging teams, FarmHouse fraternity and was active in several other campus groups.

After college, he worked for the American Angus Association as a regional manager and later director of commercial and industry relations. “Working in these roles opened my eyes to the various ways that performance information and genetic predictions are viewed and utilized,” he explains.

Bill Bowman, Method Genetics manager and Matt’s former American Angus Association co-worker, says, “Matt was a solution-driven leader with a passion to improve the beef industry. Matt had a thirst to always learn and consider the future of the American Angus Association during his tenure there, and many of the successful programs today were the result of his futuristic thought process. Matt was very service oriented in a member organization, and that characteristic has also served him well in his leadership role at BIF.

“Matt took his experience in all segments of a very diverse beef industry home to Dalebanks Angus, using his knowledge to create practical, profit-oriented genetics, while providing unmatched customer service to their commercial cow-calf clientele.”

Dalebanks Angus was settled by Matt’s ancestors in 1867. The next generation purchased the first registered Angus in 1904, and they have been raising Angus since then.

“We calve about 450 females in separate spring- and fall-calving herds,” Matt explains. “Cows spend all year on grass and are supplemented protein and limited hay in the winter. All breeding-age females are synchronized and artificially inseminated through two heat cycles, then bulls are turned out for 25-45 days.”

Dalebanks markets roughly 200 bulls annually through a fall sale and spring private treaty. The Perriers have a small farming enterprise of corn, soybeans and wheat that serves to raise feed for the cow herd. “We also grow cover crops on all of our farmed acres, which serves as supplemental forage for pairs during the fall, winter and early spring,” Matt adds.

BIF leadership

“My first contact with BIF was when my parents won the BIF Seedstock Producer Award in 1995. After later attending the Symposia myself in the late 90s and early 2000s as a breed association representative, it’s hard for me to believe that I’m now serving in a leadership role,” Matt explains.

“Some presidents want to ‘leave a legacy’ on the organization that they lead. That hasn’t been my style in past roles, and it certainly wasn’t necessary in this one,” he adds. “Part of BIF’s uniqueness has been its ability to bring hundreds of enormous egos who all believe that their breed, research focus, technology or breeding philosophy are superior; and then put them in a room to listen, share and learn. The ideas that come out of those rooms are often industry-changing and inspiring.

“I consider BIF as a place that brings all segments of beef cattle genetics together to share ideas, debate concepts and methods and then find their own ways to develop and use the information to improve beef production. As president, I didn’t try to improve on that model...I just tried to encourage folks to recognize its unique value and let the model quietly work.”

If you survey Symposium attendees, they’d describe the event as one of the few meetings that draws a balanced representation from the genetic

research, teaching, breed association and producer segments of the beef business. For example, a PhD may give a technical lecture reviewing research that has been ongoing for years or even decades, one straight-shooting cowboy may then ask a pointed question about said research, and most of the academics and association folks in the room will then spend the rest of the night at the bar debating the viewpoint that the guy with manure on his boots brought to light.

“Most folks in BIF meet each other where we are,” Matt describes. “The scientists simplify their language for me, I (try to) elevate my knowledge closer to their level, and we connect curious minds with a dedication to beef cattle breeding so we can share ideas, challenge each other’s thoughts and hopefully improve our ability to profitably produce genetics that meet the needs of our customers and consumers now and in the future.”

But whether it’s a discussion around the board table or during our annual symposium, most BIF folks look forward to the hard questions that challenge the presenter and help attendees find solutions to the complex challenges in the beef cattle industry. Matt says some of the best Symposia and workshops have been the ones where there was lively debate about an issue or two.

“BIF is one of the few organizations I’ve witnessed that encourages questions and challenging viewpoints,” Matt says. “Whether it’s a political party, cattlemen’s association, social media platform or cable news channel, society today drives folks into rigid segments based upon our viewpoints on a few issues. Once we get into that box, questions or dissenting opinions are often considered wrong, uninformed or even hateful.

“As society narrows its philosophical focus and proprietary nature, I believe that BIF serves as important of a role as ever in the beef industry. Carl Jung said, ‘To ask the right question is already half the solution to the problem,’ and I believe that BIF can continue to help our industry find solutions by encouraging this type of open dialogue.”

Matt was elected to the BIF board in 2016. “My tenure on the board would be summarized as one of adaptability,” he says.

Matt says highlights of his tenure have included:

- Thanks to a lot of work by dedicated BIF stakeholders in the academic community, we’ve moved our BIF Guidelines to a Wiki format to better align with today’s technology.
- Due to COVID restrictions, our staff and leadership hosted the first virtual symposium in BIF history in 2020, then used what we learned that year to offer a “hybrid” format (virtual and in-person) Symposium in 2021.
- Last fall, we had a productive strategic planning session with our board and staff members to better position BIF for the next decade of service to the industry. Not only did this help us chart our course, it more importantly gave us the opportunity to look introspectively and determine what our stakeholders truly expect from BIF.
- We vastly increased our communications arm, adding social media platforms, planning a website overhaul, moving the live coverage of our Symposia to our own platforms and distributing

countless press releases about award winners, proceedings and other highlights from BIF events throughout the year.

“Matt’s been an exceptional board member,” explains Bob Weaber, BIF executive director. “His experience as both a seedstock breeder and former association staff member provides a unique perspective on the roles and impact of BIF. Matt has been instrumental in the development of the organization’s strategic plan and fulfillment of its mission. Never afraid to ask the hard questions or seek to answer them, His leadership and passion for our mission has always helped our board and staff stay focused on the opportunities for BIF to positively impact genetic improvement.”

Looking forward

“I believe that we are in the midst of a significant transition within the cow-calf segment today,” Matt says. “A variety of factors are driving significant numbers of cows to market, and much of that land is being converted into farm production, residential real estate or yearling grazing acres.

Marketing and political issues are best left out of BIF discussions, but BIF leadership will be faced with a different landscape in terms of average cow herd size, regional distribution and trait emphasis in the coming decade.”

Matt met his wife, Amy, at K-State and the couple has been married for more than 20 years. They have five children — Ava (18), Lyle (16), Hannah (14), Henry (11) and Hope (3). His mom and dad, Carolyn and Tom Perrier, live down the road from them and are still very active in the family business.

“As much as genetic selection and improvement excite me, I’m even more passionate about improving our land management through planted cover crops, managed grazing and improved soil health,” Matt says. “Working with nature to help sustainably raise forages and allowing cattle to be part of this cycle is an area where I believe that we can reduce our expenses and build consumer trust simultaneously, so it can be a win-win.”

Matt believes in service. He is currently vice-chair of the Kansas Health Institute and is a past president of the Kansas Livestock Association and has served on several other local and state volunteer boards.

“Matt Perrier exemplifies a progressive breeder,” summarizes Joe Epperly, 2022 BIF vice president. “He is always looking for the trend and the cutting-edge technology to grow our ability to produce high-quality beef. In his time on the board, he has been a leader that opens the door to ideas. His ability to foster discussion is second to none and that is what BIF is all about. A forum for the best minds to get in a room and discuss any and all ideas that further our mission of beef improvement.”

SPEAKERS—Wednesday



DINA CHACÓN-REITZEL

Director, New Mexico Beef Council | Regent, New Mexico State University

Dina Chacón-Reitzel is a native of northern New Mexico, hailing from Cebolla in Rio Arriba County, where she grew up on her family's cow-calf ranch, Pināvetal Ranch. She is a graduate of Española High School and now resides in Albuquerque. Dina received two degrees from New Mexico State University, a Bachelor of Science in home economics and business in 1978, then returned to NMSU to earn a Master of Business Administration with an emphasis in marketing and management from the College of Business in 1983.

Chacón-Reitzel started her career as a home economist for NMSU's Cooperative Extension Service, serving for six years in Eddy County and Las Cruces. In 1989, she became the executive director of the New Mexico Beef Council – the marketing, research and education arm of the beef industry in New Mexico. Chacón-Reitzel has also served on other national and regional boards and committees including the National Cattlemen's Beef Association Beef Safety Research Committee, New Mexico 4-H Foundation, Saint Pius High School Foundation and UNM Children's Hospital Foundation.

Throughout her esteemed career, she has maintained close ties to NMSU. For 30 years, she has worked to implement educational programs with the College of Agricultural, Consumer and Environmental Sciences, the Agricultural Experiment Station, the Cooperative Extension Service and 4-H Youth Development. Since 2003, she has served as the NMSU delegate to the Council for Agricultural Research Extension and Teaching. In this role, she advocates for federal funding for NMSU and other land-grant universities across the country. Chacón-Reitzel was also a recipient of the College of Agricultural, Consumer and Environmental Sciences Distinguished Alumni Award in 1996. Regent Chacón-Reitzel serves as chair of the Regents Real Estate Committee and Position Director for Arrowhead Center Incorporated, industry, and her family.

SPEAKERS—Thursday



RUARIDH PETRE

Executive Director, Global Roundtable for Sustainable Beef

Ruairidh (Rory) has been the executive director of GRSB since 2012. His background is in agriculture, specializing in livestock production, and he has an M.Sc. in tropical animal production and health from the University of Edinburgh veterinary faculty. His early career was in commercial livestock and farm management in New Zealand, Australia and Scotland.

Petre went on to work on farming systems and veterinary development in South and Central Asia. Subsequently, he worked on financing of agricultural development projects for a wide range of countries in Africa, Asia and Latin America, and served as regional director for Solidaridad Southern Africa until joining GRSB.

Over the past decade, Ruairidh has overseen the growth of the sustainable beef roundtable network to include 24 countries with a common commitment to making sustainable beef part of a thriving food system. The GRSB released its global goals on reducing climate impact, nature positive production and animal welfare in early July 2021, and is currently working on the MRV framework to report on progress.

JOHN CROWLEY

AbacusBio

John is currently a consultant with AbacusBio Ltd., an agricultural science and business company with headquarters in New Zealand. Until recently, John was based in the Edinburgh office, but with opportunity to grow the North American side of the business, he recently moved back to Alberta where he has spent several years after earning his Ph.D.

Originally from Ireland, John grew up on a mixed dairy and beef operation. He received his Ph.D. in animal breeding and genetics in 2010 from University College Dublin and Teagasc. John's current work focuses on many aspects of genetic improvement across plants and animals, the sustainability of food and fiber production, and the application and evaluation of emerging agri-technologies.





JASON SAWYER

King Ranch® Institute for Ranch Management

Jason Sawyer was raised in and around central Texas, with deep family roots and the family place still in McCulloch County. He received a B.S. degree in rangeland ecology and ranch management from Texas A&M University in 1995 as well as an M.S. in ruminant nutrition (1998), and a Ph.D. in range nutrition and beef cattle management (2000) – both from New Mexico State University.

Dr. Sawyer joined the faculty at the Clayton Livestock Research Center in Clayton, New Mexico with a joint appointment in research and extension as a beef cattle extension specialist. In this role, he developed applied research programs in conjunction with regional producer advisory groups, conducted statewide extension programs, and served in a consulting role for numerous producers. He joined the faculty at Texas A&M University in 2003, with teaching and research roles in beef cattle production, focusing on beef cattle nutrition and stocker cattle production management. In 2008, he assumed the role of superintendent of the McGregor Research Center, overseeing an integrated crop and livestock operation with approximately 1,200 beef cows, stocker and grow yard, all while finishing enterprises and facilitating research programs related to beef cattle production and management. During this time, Jason also continued to teach and conduct research in beef cattle production systems and related areas.

Jason joined the team at the King Ranch® Institute for Ranch Management (KRIRM) in January, 2020 to expand opportunities for the institute to create innovative solutions for ranch management. His primary interests are the development of strategies to enhance the sustainability of beef production systems, the application of nutritional strategies on these systems, and the development of valid indicators of sustainable production. He has authored and co-authored over 75 peer-reviewed publications, over 200 abstracts, proceedings and technical reports, and given presentations at over 100 local, state and national meetings.

Jason and his wife, Alison have three children. They enjoy sports, hunting, fishing, spending time on the family place, and church and community involvement.



ERIK JACOBSEN

Vice President, Cattle, AgReserves

Erik Jacobsen is vice president of the AgReserves cattle division. He is responsible for ranching and feeding operations throughout North America and also oversees long-term land-use planning at Deseret Ranches of Florida. Erik joined AgReserves in 1987 as a cattle foreman at Deseret Ranches of Florida before leaving in 1995 for Smithfield Foods. In 2006, he returned to AgReserves as general manager of Deseret Ranches of Florida. Erik has served as president of the Florida Cattlemen's Association and on various committees of the National Cattlemen's Beef Association. Erik is an animal science graduate of the University of Florida and earned an M.B.A from Brigham Young University. Raised in Lakeland, Florida, Erik and his wife, Renee, live in Provo, Utah, and have six children.



TREY PATTERSON

CEO, Padlock Ranch Inc.

Dr. Trey Patterson received a B.S. and M.S. in animal science from Colorado State University and a Ph.D. in ruminant nutrition from the University of Nebraska. Trey served on faculty as an extension beef specialist for South Dakota State University for five years. In this role, he led statewide extension and research programs in beef cattle nutrition and management. Since 2005, Trey has been with Padlock Ranch Company, a multigenerational and diversified family-owned agribusiness with operations in northern Wyoming and southern Montana. Trey now holds the position of president and CEO. He is a three-time award winner for the Excellence in Applied Animal Science Research award presented by the Western Section American Society of Animal Science. In 2008, he was listed in the top 10 industry leaders under 40 by Cattle Business Weekly. He was recently honored with the 2021 CSU Livestock Leader Award. Trey and his wife Amy have five children and reside near Ranchester, Wyoming.

SPEAKERS — Thursday cont.



CLAY MATHIS

Executive Director, King Ranch® Institute for Ranch Management

Dr. Clay Mathis is the director of the King Ranch® Institute for Ranch Management at Texas A&M University-Kingsville. As director, Dr. Mathis leads KRIRM faculty and staff, and oversees teaching, outreach and innovation efforts of the institute. Graduates of the King Ranch® Institute currently manage over 150,000 cows on more than 7 million acres of ranchland and wildlife habitat in North America.

Dr. Mathis holds a B.S. in animal science and M.S. in the physiology of reproduction from Texas A&M University. He also earned a Ph.D. from Kansas State University in ruminant nutrition. From 1998 to 2010, Dr. Mathis worked as a professor and extension livestock specialist at New Mexico State University. Dr. Mathis and his wife, Rhonda, are the proud parents of Morgan, Miles and Amy Kaye Mathis.

SPEAKERS — Friday



TONY CLAYTON

Clayton Agri-Marketing

Tony Clayton, president of Clayton Agri-Marketing, Inc., has been involved in the international marketing of animal genetics and agricultural products for over 30 years in many different capacities in both the private and government sectors.

Clayton Agri-Marketing, Inc. is one of the largest export companies in the United States that deal in the live animal trade. Tony has exported beef cattle, dairy cattle, goats, horses, sheep, swine and agricultural equipment to 65 different countries.

Before starting his own company in 1996, Tony was employed by an Illinois-based livestock exporting firm as director of market development from 1992 to 1996. He was also employed by the Missouri Department of Agriculture from 1985 to 1992 as coordinator of the international marketing program. He was responsible for the promotion of Missouri's livestock genetic industry to potential buyers around the world.

Tony is a graduate of the University of Central Missouri in Warrensburg, Missouri and has a B.S. degree in agricultural education. He is also a graduate of State Fair Community College in Sedalia, Missouri where he obtained an A.S. degree in agri-business. He is the 2013 recipient of the Small Business Administration (SBA) Exporter of the Year Award for Missouri and Region VII. In 2002, Clayton Agri-Marketing, Inc. received the Agriculture Exporter of the Year Award from the state of Missouri.

Tony is the past president of the U.S. Livestock Exporters Association and past chairman of the United States Livestock Genetic Exports, Inc. (USLGE). He is currently serving his third term on the United States Department of Agriculture (USDA) and U.S. Trade Representative (USTR) Agricultural Technical Advisory Committee (ATAC) for the development of export trade on animals and animal products.

He lives in Jefferson City, Missouri, with his wife, Evann. They have three children and three grandkids.



PHIL GEORGE

Mirotorg Agribusiness Holding Production Director

Phil graduated with a bachelor of science degree in animal science from Kansas State University and earned his Ph.D. in animal nutrition from Cornell University. His first position after his graduate studies was with the University of Illinois' Animal Science Department. His focus of research was investigating the relationship between genetic markers and cattle performance. After leaving the U of I, Phil was hired as general manager of a diverse cattle operation located in northwest Colorado, that also included a sizable sheep herd and large game hunting. Phil then moved to a completely different environment where he managed 8,500 mother cows for the Rollins Ranches in Okeechobee, Florida. Changing environments again, Phil then went on to manage the Pine Valley Ranch located near Halfway, Oregon. Phil and his wife Lynna currently reside on the family's ranch in Kansas which has been in the family for 152 years.



DR. MILTON G. THOMAS

Colorado State University

Dr. Milt Thomas was raised on farms and ranches in Texas and Missouri, and received animal science degrees from the University of Missouri and Texas A&M University. Dr. Thomas progressed through the faculty ranks in the Department of Animal and Range Sciences at New Mexico State University (NMSU; 15 years) and served as the Gerald Thomas Chair in Food Production and Natural Resources from 2010 to 2011. In these years of service at NMSU, Dr. Thomas was involved in breeding Angus, Brangus and Brahman cattle for the Chihuahuan Desert, which was great experience to prepare for breeding Angus cattle for tolerance to high altitude in Colorado and Wyoming. Dr. Thomas joined Colorado State University in December of 2012 as professor and John E. Rouse Chair of Beef Cattle Breeding and Genetics in the Department of Animal Sciences. Dr. Thomas helped market over 1,000 yearling breeding bulls from both state agricultural experiment station breeding programs over the last 25 years. Dr. Thomas was also involved in using such resources to teach undergraduate students interested in learning about breeding and genetics and beef production and management as well as publish over 500 professional articles as abstracts, experiment station reports and extension articles. 115 of these papers were published in peer-reviewed scientific journals with the help of 30 graduate students, postdoctoral trainees, and numerous collaborations with beef industry partners, cooperating ranches and international scientists. On July 1, 2022, Dr. Thomas will return to his Texas roots and move to his family's ranch in Goliad County where he will initiate a new research program in beef cattle systems at the Texas A&M AgriLife Research Center in Beeville.

WEDNESDAY TOUR — Santa Teresa Livestock Crossing



NOMINEES — Seedstock Producer of the Year



Bieber Red Angus — Leola, South Dakota

Owners: Craig & Peggy Bieber

Managers: Craig Bieber

Ron Bieber moved to South Dakota in 1961 and founded Bieber Red Angus as a diversified crop and commercial livestock venture. In 1966, Ron and Lois crossed Hereford/Shorthorn cows with a Red Angus bull and were convinced that Red Angus would be a leading breed in the industry. In 1968, Ron bought registered Red Angus females and officially started a Red Angus seedstock herd.

Biebers hosted their first sale in 1976. Early on, performance data, birth weight, weaning weight, yearling weight and average daily gain were provided as selection tools for buyers.

Today, Bieber Red Angus is operated by Craig and Peggy Bieber. They sell over 500 bulls and 400 females every year and provide performance information including EPD traits on every animal. They calve more than 900 registered Red Angus females and wean additional ET calves. The cow herd runs under range conditions requiring 10+ acres per pair. The operation has a limited crop component producing mainly feed for bull and female development and herd maintenance during winter.

Over time, the Biebers have continued to operate as a family-owned business breeding South Devon, Angus, Simmental and hybrid seedstock into the operation. The Biebers current focus is solely on Red Angus. They remain consistent in their approach to breeding by using technology to improve performance and carcass traits. The operation utilizes EPDs, carcass ultrasound and DNA technology to improve the performance and quality of the genetics they produce. Bieber genetics are a common component to pedigrees in the Red Angus breed worldwide.

Bieber Red Angus was nominated by the Red Angus Association of America



Blythe Family Farms — White City, Kansas

Owners: The Blythe Family

Managers: Duane Blythe, Debbie Lyons-Blythe and Trenton Blythe

Since 1890, Blythe Family Farms has been located near White City, KS, in the Kansas Flint Hills. Debbie and Duane began raising registered Angus cattle in 1989, and Debbie is a lifetime member of the American Angus Association, since 1977.

The cow herd consists of 175 registered Angus and 225 Angus-based crossbred cows and bred heifers. In addition, 350 replacement heifers are developed and bred for sale annually. The Blythes use artificial insemination extensively in their cow herd and heifer program.

Since 2005, more than 4,500 bred heifers have been marketed by private treaty and consignment sales to buyers across the nation. The Blythes have chosen to focus on seedstock from a female perspective, raising and offering herd-building genetics and well-managed females that provide a foundation to many herds. Sixty registered Angus bulls are raised from the herd annually, selecting for predictable calving ease and birth weight, as well as high-quality carcass and maternal traits. They are used in the Heifer Development Program and marketed by private treaty.

Debbie and Duane are working to add their three adult sons to daily labor and management of the ranch, as well as their two daughters to the legacy of Blythe Family Farms.

“Trying to do things better, always” is the motto at Blythe Family Farms. This is lived out through their dedication to the improvement of their cattle, land and resources; diligently working to meet customer needs; and their willingness to go beyond their own ranch gates to advocate for the cattle industry and its future.

Blythe Family Farms was nominated by the Kansas Livestock Association.



B.R. Cutrer, Inc. — Wharton, Texas

Owners: Brandon & Rachel Cutrer Family

Managers: Keaton Dodd, Fransisco Garcia, Harley Wade

Wharton, Texas

BRC Ranch is the USA's most innovative Brahman ranch, while embracing their strong Texas ranching roots. When the Cutrer's married in 2010, they owned 0 acres and 6 head of cattle. Without inheriting a single acre of land or a single head, BRC has shown the world that with great mentors, solid management practices, and a great team, first-generation land-owners and new seedstock brands can be a success.

Brandon and Rachel run 350 head of Brahman cattle and F-1s and stand at the very top of the upper echelon of Brahman breeders worldwide. They are the breeder of six International Champion Grey Brahman females of the last decade (2021, 2020, 2019, 2017, 2016 and 2013), the #1 Brahman AI sire in the USA for the last three years (Noble), and the #1 polled Grey Brahman bull and female of the breed. In 2020, they exported cattle and genetics to 17 countries and 5 continents, including over 30,000 units of semen on their Brahman AI sires.

BRC showcases the beef industry from pasture to plate, with an emphasis on values, work ethic, and entrepreneurship. They blaze a new trail including being the only Brahman breeders in the USA utilizing genomically-enhanced EPDs, and the founders of Brahman Country Beef and FitBeef, both 100% Brahman branded beef programs. BRC is also a strong advocate for climate smart ranching and the role that Brahman cattle will play in keeping beef on the table for future generations.

B.R. Cutrer, Inc. was nominated by the American Brahman Breeders Association.



Express Ranches — Yukon, Oklahoma

Owner: Bob Funk

Manager: Jarold Callahan

Bob Funk was raised in Duvall, Washington, working on a family-owned dairy farm. After graduating high school, he tried to purchase the dairy as it ignited his love for farming and livestock, but his family encouraged him to attend college and pursue a career off the farm.

Following college, Funk went to work for ACME Personnel, a Washington-based staffing company, and was transferred to Oklahoma where he went on to purchase a portion of the company after it went bankrupt. Moving to Oklahoma, surrounded by cattle on pastures far and wide, rekindled his love for cattle. In 1989, he purchased a small group of Limousin cattle and never looked back.

Fast forward to 1996, Funk and Jarold Callahan, his newly hired herd manager, purchased their first Angus herd which immensely impacted the trajectory of Express Ranches. As more cattle were purchased, Funk needed more land, which led to purchasing more cattle – a cycle that continues today. Twenty-five years later, Funk has built one of the largest seedstock operations in the United States while simultaneously being involved in every facet of beef production. The ranch registers an average of 2,000 head of Angus and approximately 400 head of Hereford cattle per year. The operation has several facilities in Oklahoma, a commercial herd in New Mexico and owns one-third of a feedlot in Oklahoma. Additionally, the ranch hosts six production sales a year. Beyond the cattle business, Funk strongly believes in the future of agriculture and more importantly, the youth behind it.

Express Ranches was nominated by the American Angus Association and the American Hereford Association.

2022 Seedstock Producer of Year Nominees



Tennessee River Music Inc. — Fort Payne, Alabama

Owners: Randy & Kelly Owen, Randa Starnes

Managers: John & Randa Starnes

Tennessee River Music, Inc. (TRM), located in Fort Payne, Alabama, is a diversified cattle operation centered on producing quality Hereford and Angus genetics. TRM began with a childhood dream of Randy Owen, whose family farming roots run deep, helping grow crops, raise cattle and being active in 4-H and FFA in northeast Alabama.

Tennessee River Music was formed where his family farmed for generations and was named after the first number one single for his country music band Alabama. The Hereford herd was established in 1981 with an Angus herd being developed in the late 1980s. This year, the 39th female production sale and 9th bull sale will be held. This diversified cattle operation consists of a custom bull collection facility, Lookout Mountain Genetics; the seedstock operation, Tennessee River Music; and an on-farm local meat market, The Market at TRM.

TRM cattle are bred with emphasis on value in all facets, from conception to consumption. With a base in balanced EPD values from proven pedigrees, TRM emphasizes function with moderate size, muscling, easy fleshing, solid maternal, docile, and soundness for longevity in southeastern pastures. Beef quality is also a primary focus for nutritious, high marbling, tender beef products to perform in the market.

TRM is a true family farm with each generation working side-by-side. Randy and Kelly Owen and Roland and Janet Starnes are actively involved in daily ranch duties. John and Randa Starnes serve as managers, with their children by their side, to lead TRM into a brighter future.

Tennessee River Music Inc. was nominated by the Alabama Beef Cattle Improvement Association.

2021 Seedstock Producer of Year



Cow Camp Ranch — 2021 BIF Seedstock Producer of the Year

Pictured (l to r) are: Greg Henderson, Drivers, award sponsor; Kent and Jean Brunner, Cow Camp Ranch; and Joe Mushrush, 2020-21 BIF president.

2022 Seedstock Producer of Year



B.R. Cutrer Inc. — 2022 BIF Seedstock Producer of the Year

Pictured (l to r) are: Matt Perrier, 2021-22 BIF president; and Brandon Cutrer and Keaton Dodd.

2022	B.R. Cutrer Inc.	Texas	1997	Bob and Gloria Thomas	Oregon
2021	Cow Camp Ranch	Kansas	1996	Frank Felton	Missouri
2020	Your Family Farms	South Carolina	1995	Tom and Carolyn Perrier	Kansas
2019	Hinkson Angus Ranch	Kansas	1994	Richard Janssen	Kansas
2018	Van Newkirk Herefords	Nebraska	1993	R.A. "Rob" Brown	Texas
2017	Hunt Limousin Ranch	Nebraska	1993	J. David Nichols	Iowa
2016	Shaw Cattle Company	Idaho	1992	Leonard Wulf & Sons	Minnesota
2015	McCurry Angus Ranch	Kansas	1991	Summitcrest Farms	Ohio
2014	Schuler Red Angus	Nebraska	1990	Douglas and Molly Hoff	South Dakota
2013	Bradley 3 Ranch	Texas	1989	Glynn Debter	Alabama
2012	V8 Ranch	Texas	1988	W.T. "Bill" Bennett	Washington
2011	Mushrush Red Angus	Kansas	1987	Henry Gardiner	Kansas
2010	Sandhill Farms	Kansas	1986	Leonard Lodoen	North Dakota
2009	Harrell Hereford Ranch	Oregon	1985	Ric Hoyt	Oregon
2009	Champion Hill	Ohio	1984	Lee Nichols	Iowa
2008	TC Ranch	Nebraska	1983	Bill Borrer	California
2007	Pelton Simmental Red Angus	Kansas	1982	A.F. "Frankie" Flint	New Mexico
2006	Sauk Valley Angus	Illinois	1981	Bob Dickinson	Kansas
2005	Rishel Angus	Nebraska	1980	Bill Wolfe	Oregon
2004	Camp Cooley Ranch	Texas	1979	Jim Wolf	Nebraska
2003	Moser Ranch	Kansas	1978	James D. Bennett	Virginia
2002	Circle A Ranch	Missouri	1977	Glenn Burrows	New Mexico
2001	Sydenstricker Genetics	Missouri	1976	Jorgenson Brothers	South Dakota
2000	Fink Beef Genetics	Kansas	1975	Leslie J. Holden	Montana
1999	Morven Farms	Virginia	1975	Jack Cooper	Montana
1998	Knoll Crest Farms	Virginia	1974	Carlton Corbin	Oklahoma
1998	Flying H Genetics	Nebraska	1973	Mrs. R. W. Jones, Jr.	Georgia
1997	Wehrmann Angus Ranch	Virginia	1972	John Crowe	California

2022 Commercial Producer of Year Nominees



Parker Farms — Williams, California

Owners/Managers: Doug and Judy Parker

The Parkers are proud to build upon and honor the legacy started by Judy's parents, Bob and Elma Griffith. Doug and Judy as well as their family work to manage a diverse farming and ranching operation in northern California and southern Oregon. Their enterprises include rice, walnut, and livestock production. Their approximately 650 head of Angus and Angus-influenced fall and spring calving herds spend the winter and spring on annual-grass rangeland in the foothills of the Sacramento Valley and the summer and early fall on irrigated pastures on their ranches in Southern Oregon.

The Parkers prioritize genetic improvement in their cow herd. They are devoted to creating uniform, solid cows – without a top or bottom end. They were early adopters of estrus synchronization and artificial insemination in commercial herds. The family has developed their own replacements through the use of AI for many years. Semen is obtained from purchased bulls including some with retained ownership from northern California seedstock producers. This practice allows them to purchase elite genetics economically because they are able to purchase fewer bulls than would otherwise be required. Judy and Doug have strong relationships with the Black Gold and Byrd Bull Sale breeders and purchase bulls that meet phenotypic standards and have trait measures, EPDs, and genomic measures that are in the top 10-20% of the breed. This effort to purchase bulls at the top end of the sale helps to maintain a balanced and moderate cow herd that excels in maternal traits, calving ease, high rates of growth, and outstanding carcass genetics.

Parker Farms was nominated by the California Beef Cattle Improvement Association.

Rezac Land & Livestock — Onaga, Kansas

Owners/Managers: Jay & Stacy Rezac, Lance & Deb Rezac, Russell Rezac, Matthew Rezac, Nicole Harrison and Garrett Rezac

Rezac Land & Livestock, founded by Don and Barbara Rezac, is a diversified ranch located on the northern edge of the Kansas Flint Hills. In 1986, their son, Jay, and his wife, Stacy, and Jay's older brother Lance and his wife, Debra, formed a partnership.

Since that time, the operation has grown substantially and today includes six partners - Jay and Lance; Jay's sons, Russell and Matthew; and Lance's children, Nicole and Garrett. Jay, Russell and his wife, Tiffany, and Matthew and his wife, Alexa, manage the cattle and rangeland near Onaga, KS. Jay's daughter, Jayme, and her husband, Corey Lundberg, live on the Olsburg, KS, division, where Corey manages the cow herd and a starting lot.

The cattle operation consists of 900 Simmental- and Angus-bred spring-calving cows. Once the calves are weaned, they are either sold or shipped to a commercial feedyard or finished in the family-owned feedyard. The cows graze year-round on native grass, stocks and cover crops. By following a strict grazing management plan, the Rezacs are able to maintain their cows with limited supplementation, while also keeping their natural resources in excellent condition.

In addition to their cow herd, they purchase about 5,500 calves each year for their stocker and backgrounding operations. Calves are bought from Missouri to North and South Dakota. The majority are sold as feeder cattle, with the remaining retained for finishing in the family's feedyard.

A clear set of goals and dedication to the management practices needed to meet those goals have made Rezac Land and Livestock a truly progressive commercial cow-calf business.

Rezac Land & Livestock was nominated by the Kansas Livestock Association.





Willis Ranch — Cokeville, Wyoming

Owners/Managers: The Willis Family: Linda; Jordan and Jennie; Jed and Stephanie; and James and Tonya Willis

The Willis Family: Linda; Jordan and Jennie; Jed and Stephanie; and James and Tonya Willis, Cokeville, Wyoming.

Nestled in the valleys of Cokeville, Wyoming, resides a family rooted in the traditional ways of rural life but with a focus on the future. The combination of crops, cattle and kids serves as the foundation of their operation, ensuring the land remains fruitful, the cattle continuously provide profitability and the kids carry on the multi-generational legacy.

Originally from Laketown, Utah, the Willis family bought their current ranch in the early 1950s. About that time, a parcel of what the family still calls the B.Q. Ranch came up for sale and allowed growth across the Wyoming state line. Today, twenty-four pivots cover nearly 3,700 acres of flood-irrigated soil with 1,800 commercial cows surrounding it.

Jordan Willis; his wife, Jennie; and their four children claim the Cowboy State as their own. His mother, Linda, and one brother, Jed; his wife, Stephanie; and their three children, still live in Utah, while oldest brother, James and his wife Tonya, live just up the hill.

Willis Ranch is a diversified operation, committed to producing top-tier commercial Angus cattle, collecting detailed data, irrigating and farming their native lands and raising their family in a wholesome and respectable manner. Their operation holds its roots deep in family ties and the value of hard work.

Willis Ranch was nominated by the American Angus Association.

2021 Commercial Producer of Year



W&S Ranch — 2021 BIF Commercial Producer of the Year

Pictured (l to r) are Philip, Kaylee and Jessica Weltmer of W&S Ranch; and Joe Mushrush, 2020-21 BIF president.

BIF Commercial Producer of the Year



Rezac Land & Livestock — 2022 BIF Commercial Producer of the Year

Pictured (l to r) are Matt Perrier, 2021-22 BIF president; and Russell, Tiffany, Stacy and Jay Rezac.

2022	Rezac Land and Livestock	Kansas	1998	Randy and Judy Mills	Kansas
2021	W&S Ranch, Inc.	Kansas	1997	Merlin and Bonnie Anderson	Kansas
2020	Vest Ranches	Texas	1996	Virgil and Mary Jo Huseman	Kansas
2019	Mershon Cattle LLC	Missouri	1995	Joe and Susan Thielen	Kansas
2018	Woolfolk Ranch	Kansas	1994	Fran and Beth Dobitz	South Dakota
2017	Mundhenke Beef	Kansas	1993	Jon Ferguson	Kansas
2016	Plum Thicket Farms	Nebraska	1992	Kopp Family	Oregon
2015	Woodbury Farms	Kansas	1991	Dave and Sandy Umbarger	Oregon
2014	CB Farms Family Partnership	Kansas	1990	Mike and Diana Hopper	Oregon
2013	Darnall Ranch, Inc.	Nebraska	1989	Jerry Adamson	Nebraska
2012	Maddux Cattle Company	Nebraska	1988	Gary Johnson	Kansas
2011	Quinn Cow Company	Nebraska	1987	Rodney G. Oliphant	Kansas
2010	Downey Ranch	Kansas	1986	Charles Fariss	Virginia
2009	JHL Ranch	Nebraska	1985	Glenn Harvey	Oregon
2008	Kniebel Farms and Cattle Co.	Kansas	1984	Bob and Sharon Beck	Oregon
2007	Broseco Ranch	Colorado	1983	Al Smith	Virginia
2006	Pitchfork Ranch	Illinois	1982	Sam Hands	Kansas
2005	Prather Ranch	California	1981	Henry Gardiner	Kansas
2004	Olsen Ranches, Inc.	Nebraska	1980	Jess Kilgore	Montana
2003	Tailgate Ranch	Kansas	1979	Bert Hawkins	Oregon
2002	Griffith Seedstock	Kansas	1978	Mose Tucker	Alabama
2001	Maxey Farms	Virginia	1977	Mary and Stephen Garst	Iowa
2000	Bill and Claudia Tucker	Virginia	1976	Ron Baker	Oregon
1999	Mossy Creek Farm	Virginia	1975	Gene Gates	Kansas
1999	Giles Family	Kansas	1974	Lloyd Nygard	North Dakota
1998	Mike and Priscilla Kasten	Missouri	1973	Pat Wilson	Florida
			1972	Chan Cooper	Montana

BIF Pioneer Award

The Pioneer Award recognizes individuals who have made lasting contributions to the improvement of beef cattle, honoring those who have had a major role in acceptance of performance reporting and documentation as the primary means to make genetic change in beef cattle.

See Page 25 for photos.

- 2022**
Bob Hough, Colorado
Bobby Rankin, New Mexico
- 2021**
Alison Van Eenennaam, California
Gene Rouse, Iowa
Doyle Wilson, Iowa
Galen Fink, Kansas
- 2020**
Paul Bennett, Virginia
Craig Ludwig, posthumously
Charles McPeake, Georgia
- 2019**
Jim Gibb, Colorado
Jerry Wulf, Minnesota
- 2018**
Tim Holt, Colorado
Craig Huffhines, Texas
Mark Thallman, US Meat Animal Research Center, Nebraska
- 2017**
Harvey Lemmon, posthumously
Dorian Garrick, Iowa State University
- 2016**
Doug Hixon, University of Wyoming
Ronnie Green, University of Nebraska
Bill Rishel, Rishel Angus, Nebraska
- 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 Strohhahn, 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 & 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**
J. 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 Borrer, California
Walter Rowden, Arkansas
- 1991**
Robert A. "Bob" Long, Texas
Bill Turner, Texas
- 1990**
Donn and 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. and 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. and 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. and 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 Recipients

Continuing Service Award winners have made major contributions to the BIF organization. This includes serving on the board of directors, speaking at BIF conventions, working on BIF guidelines and other behind-the-scenes activities. As BIF is a volunteer organization, it is this contribution of time and passion for the beef cattle industry that moves BIF forward.

2022

Jared Decker—University of Missouri
Milt Thomas—Colorado State University
Josh White—Highlands Ranch, Colorado

2021

Lee Leachman—Leachman Cattle Co.
Jane Parish—Mississippi State University

2020

Donnell Brown—RA Brown Ranch, Texas
Frank David Kirkpatrick—University of Tennessee

2019

Craig Bieber—Bieber Red Angus, South Dakota
Scott Greiner—Virginia Tech University
Steve Munger—University of South Dakota

2018

Dan Moser—American Angus Association, Missouri
Lynn Pelton—Pelton Simmental/Red Angus, Kansas
Scott Speidel—Colorado State University

2017

Michelle Elmore—BCIA, Alabama
Shauna Hermel—Angus Journal, Missouri
Matthew Spangler—University of Nebraska-Lincoln
Kevin and Lydia Yon—Yon Family Farms, South Carolina

2016

John Pollakv—US Meat Animal Research Center, Nebraska
Alison Van Eenennaam—University of California, Davis
Alison Sunstrum—GrowSafe, Canada
Steve Kachman—University of Nebraska-Lincoln

2015

Joe Cassidy—South Dakota State University
Andy Boston—Purdue University, Indiana
Lois Schreiner—Kansas State University
Chris Shivers—American Brahman Breeders Association, Texas

2014

Larry Kuehn—US Meat Animal Research Center, Nebraska
Wade Shafer—American Simmental Association, Montana
Warren Snelling—US Meat Animal Research Center, Nebraska
Susan Willmon—American Gelbvieh Association, Colorado

2013

Ben Eggers—Sydenstricker Genetic, Missouri
Brian House—Select Sires, Ohio
Lauren Hyde—American Simmental Association, Montana
Jerry Taylor—University of Missouri
Jack Ward—American Hereford Association, Missouri

2012

Tom Field, Nebraska
Stephen Hammack, Texas
Brian McCulloh, Wisconsin
Larry Olson, South Carolina

2011

Tommy Brown, Alabama
Mark Enns, Colorado
Joe Paschal, Texas
Marty Ropp, Montana
Bob Weaver, Missouri

2010

Bill Bowman, Missouri
Twig Marston, Nebraska
David Patterson, Missouri
Mike Tess, Montana

2009

Darrh Bullock, Kentucky
Dave Daley, California
Renee Lloyd, Iowa
Mark Thallman, Nebraska

2008

Doug Fee, Canada
Dale Kelly, Canada
Duncan Porteous, Canada

2007

Craig Huffhines, Missouri
Sally Northcutt, Missouri

2006

Jimmy Holliman, Alabama
Lisa Kriese-Anderson, Alabama
Dave Notter, Ohio

2005

Jerry Lipsey, Montana
Micheal MacNeil, Montana
Terry O'Neill, Montana
Robert Williams, Missouri

2004

Chris Christensen, South Dakota
Robert "Bob" Hough, Texas
Steven M. Kappes, Nebraska
Richard McClung, Virginia

2003

Sherry Doubet, Colorado
Ronnie Green, Virginia
Connee Quinn, Nebraska
Ronnie Silcox, Georgia

2002

S.R. Evans, Mississippi
Galen Fink, Kansas
Bill Hohenboken, Virginia

2001

William Altenburg, Colorado
Kent Andersen, Colorado
Don Boggs, South Dakota

2000

Ron Bolze, Kansas
Jed Dillard, Florida

1999

Bruce Golden, Colorado
John Hough, Georgia
Gary Johnson, Kansas
Norman Vincil, Virginia

1998

Keith Bertrand, Georgia
Richard Gilbert, Texas
Burke Healey, Oklahoma

1997

Glenn Brinkman, Texas
Russell Danielson, North Dakota
Gene Rouse, Iowa

1996

Doug L. Hixon, Wyoming
Harlan D. Ritchie, Michigan

1995

Paul Bennett, Virginia
Pat Gogginsv, Montana
Brian Pogue, Canada

1994

Bruce E. Cunningham, Montana
Loren Jackson, Texas
Marvin D. Nichols, Iowa
Steve Radakovich, Iowa
Doyle Wilson, Iowa

1993

Robert McGuire, Alabama
Charles McPeake, Georgia
Henry W. Webster, South Carolina

1992

Jack Chase, Wyoming
Leonard Wulf, Minnesota

1991

John Crouch, Missouri

1990

Robert Dickinson, Kansas

1989

Roger McCraw, North Carolina

1984

Bruce Howard, Canada

1987

Bill Borrer, California
Jim Gibb, Missouri
Daryl Strohbehne, Iowa

1986

Larry Benyshek, Georgia
Ken W. Ellis, California
Earl Peterson, Montana

1985

Jim Glenn, IBIA
Dick Spader, Missouri
Roy Wallace, Ohio

1984

James Bennett, Virginia
M.K. Cook, Georgia
Craig Ludwig, Missouri

1983

Art Linton, Montana

1982

J.D. Mankin, Idaho

1981

Mark Keffeler, South Dakota

1980

Glenn Butts, PRI
Jim Gosey, Nebraska

1979

C.K. Allen, Missouri
William Durfey, NAAB

1978

James S. Brinks, Colorado
Martin Jorgensen, South Dakota
Paul D. Miller, Wisconsin

1977

Lloyd Schmitt, Montana
Don Vaniman, Montana

1976

A.L. Eller, Jr., Virginia
Ray Meyer, South Dakota

1975

Larry V. Cundiff, Nebraska
Dixon D. Hubbard, Washington, D.C.
J. David Nichols, Iowa

1974

Frank H. Baker, Oklahoma
D.D. Bennett, Oregon
Richard Willham, Iowa

1973

F. R. Carpenter, Colorado
Robert DeBaca, Iowa
E.J. Warwick, Washington, D.C.

1972

Clarence Burch, Oklahoma



Jared Decker — 2022 BIF Continuing Service Award
 Pictured (l to r) are Matt Perrier, 2021-22 BIF president; and Jared Decker.



Jane Parish — 2021 Continuing Service Award
 Pictured (l to r) are Jane Parish, Mississippi State University, and Marty Ropp, former BIF president.



Milt Thomas — 2022 BIF Continuing Service Award
 Pictured (l to r) are Matt Perrier, 2021-22 BIF president; Milt Thomas,



Lee Leachman — 2021 Continuing Service Award
 Pictured (l to r) are Lisa and Lee Leachman and Donnell Brown, former BIF president.



Josh White — 2022 BIF Continuing Service Award
 Pictured (l to r) are Matt Perrier, 2021-22 BIF president; and Josh White.

BIF Ambassador Award Recipients

The BIF Ambassador Award is given annually by BIF to a member of the media for his or her efforts in spreading the news of BIF and its principles to a larger audience.

- 2022 B. Lynn Gordon, Georgia—Leader Consulting LLC
- 2021 eBEEF
- 2020 Becky Mills, Georgia—Freelance journalist
- 2019 Eric Grant, Missouri—Grant Company
- 2018 Pete Crow, Colorado—Western Livestock Journal
- 2017 Kevin Ochsner, Colorado—NCBA Cattlemen to Cattlemen
- 2016 Bob Hough, Colorado—Freelance writer
- 2015 E. C. Larkin, Texas—Gulf Coast Cattlemen
- 2014 John Maday, Colorado—Drovers CattleNetwork
- 2013 A.J. Smith, Oklahoma—Oklahoma Cowman Magazine
- 2012 Burt Rutherford, Texas—BEEF Magazine
- 2011 Jay Carlson, Kansas—BEEF Magazine
- 2010 Larry Atzenweiler & Andy Atzenweiler, Missouri—Missouri Beef Cattlemen
- 2009 Kelli Toldeo, California—Cornerpost Publications
- 2008 Gren Winslow, Larry Thomas, Canada—Canadian Cattleman Magazine
- 2007 Angie Denton, Missouri—Hereford World
- 2006 Belinda Ary, Alabama—Cattle Today
- 2005 Steve Suther, Kansas—Certified Angus Beef LLC
- 2004 Kindra Gordon, South Dakota—Freelance Writer
- 2003 Troy Marshall, Missouri—Seedstock Digest
- 2002 Joe Roybal, Minnesota—BEEF Magazine
- 2001 Greg Hendersen, Kansas—Drovers
- 2000 Wes Ishmael, Texas—Clear Point Communications
- 1999 Shauna Rose Hermel, Missouri—Angus Journal and BEEF Magazine
- 1998 Keith Evans, Missouri—American Angus Association
- 1997 Bill Miller, Kansas—Beef Today
- 1996 Ed Bible, Missouri—Hereford World
- 1995 Nita Effertz, Idaho—Beef Today
- 1994 Hayes Walker III, Kansas—America's Beef Cattleman
- 1993 J.T. "Johnny" Jenkins, Georgia—Livestock Breeder Journal
- 1991 Dick Crow, Colorado—Western Livestock Journal
- 1990 Robert C. DeBaca, Iowa—The Ideal Beef Memo
- 1989 Forrest Bassford, Colorado—Western Livestock Journal



B. Lynn Gordon — 2022 BIF Ambassador Award
Pictured (l to r) are Matt Perrier, 2021-22 BIF president; and Lynn Gordon.



eBEEF— 2021 BIF Ambassador Award
Pictured (l to r) are Joe Mushrush, 2020-21 BIF president; Dr. Allison Van Eenennaam, University of California-Davis; Dr. Matt Spangler, University of Nebraska-Lincoln; Dr. Darrh Bullock, University of Kentucky; Dr. Jared Decker, University of Missouri; and Dr. Bob Weaber, Kansas State University. Not pictured is Dr. Megan Rolf, Kansas State University.

- 1988 Fred Knop, Kansas—Drovers Journal
- 1987 Chester Peterson, Kansas—Simmental Shield
- 1986 Warren Kester, Minnesota—BEEF Magazine

Baker/Cundiff Essay Contest Award Recipients

The annual Frank Baker/Larry Cundiff Beef Improvement Essay Contest for graduate students provides an opportunity to recognize outstanding student research and competitive writing in honor of Frank Baker and Larry Cundiff. See page 51 for this year's Baker/Cundiff contest winning essay.

2022

Lane Giess, Colorado State University
Haleigh Prosser, West Texas A&M University

2021

Maci Mueller, University of California-Davis

2020

Johnna Baller, University of Nebraska-Lincoln
Kaitlyn Sarlo Davila, University of Florida
Katherine Upshaw, Kansas State University

2019

Madison Butler, Kansas State University

2018

Miranda Culbertson, Colorado State University
Jose Delgadillo Liberona, Texas A&M University

2017

Cashley Ahlberg, Kansas State University
Lindsay Upperman, University of California-Davis

2016

Kathleen Ochsner, University of Nebraska-Lincoln
Kashly Schweer, University of Nebraska-Lincoln

2015 and earlier: award was known as the Frank Baker Scholarship

2015

Justin Buchanan, Oklahoma State University
Jamie Parham, South Dakota State University

2014

Heather Bradford, Kansas State University
Xi Zeng, Colorado State University

2013

Heather Bradford, Kansas State University
Erika Downey, Texas A&M University

2012

Jeremy Howard, University of Nebraska-Lincoln
Kristina Weber, University of California-Davis

2011

Brian Brigham, Colorado State University
Megan Rolf, University of Missouri

2010

Kent A. Gray, North Carolina State University

2009

Lance Leachman, Virginia Polytechnic Institute & State University
Scott Speidel, Colorado State University

2008

Devori W. Beckman, Iowa State University
Kasey L. DeAtley, New Mexico State University

2007

Gabriela C. Márquez Betz, Colorado State University
Yuri Regis Montanholi, University of Guelph

2006

Amy Kelley, Montana State University
Jamie L. Williams, Colorado State University

2005

Matthew A. Cleveland, Colorado State University
David P. Kirschten, Cornell University

2004

Reynold Bergen, University of Guelph
Angel Rios-Utrera, University of Nebraska

2003

Fernando F. Cardoso, Michigan State University
Charles Andrew McPeake, Michigan State University

2002

Katherina A. Donoghue, University of Georgia
Khathutshelo A. Nephawe, University of Nebraska

2001

Khathutshelo A. Nephawe, University of Nebraska
Janice M. Rumph, University of Nebraska

2000

Paul L. Charteris, Colorado State University
Katherine A. Donoghue, University of Georgia

1999

Janice M. Rumph, University of Nebraska
Bruce C. Shanks, Montana State University

1998

Patrick Doyle, Colorado State University
Shannon M. Schafer, Cornell University

1997

Rebecca K. Splan, University of Nebraska
Robert Williams, University of Georgia

1996

D.H. "Denny" Crews, Jr., Louisiana State University
Lowell S. Gould, University of Nebraska

1995

D. H. "Denny" Crews, Jr., Louisiana State University
Dan Moser, University of Georgia

1994

Kelly W. Bruns, Michigan State University
William Herring, University of Georgia



Lane Giess — 2022 BIF Baker/Cundiff Award
Pictured (l to r) are Matt Perrier, 2021-22 BIF president; and Lane Giess.



Haleigh Prosser — 2021 BIF Baker/Cundiff Award
Pictured (l to r) are Matt Perrier, 2022 BIF president; and Haleigh Prosser.

Roy Wallace Memorial Scholarship Recipients

The Roy A. Wallace Memorial Scholarship 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.

Past Scholarship Recipients — GRADUATE

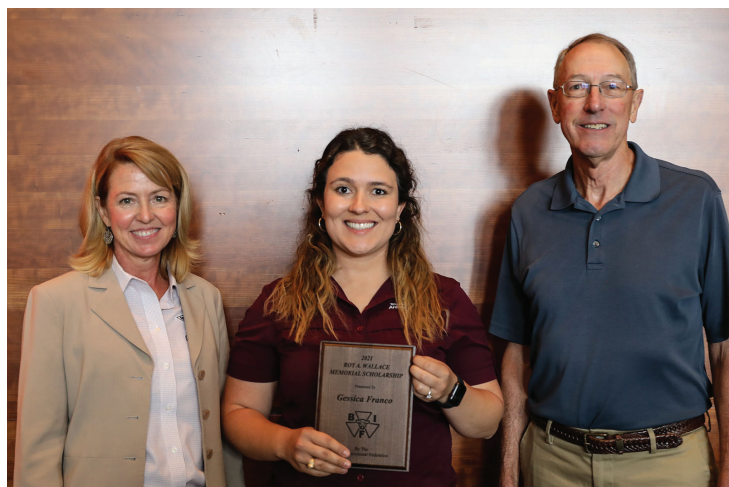
- 2022 Luke Fuerniss, Texas Tech University
- 2021 Gessica Franco, Texas A&M University
- 2020 Lindsay Upperman, University of Nebraska-Lincoln
- 2019 Benjamin Crites, University of Kentucky
- 2018 Johnna Baller, University of Nebraska-Lincoln
- 2017 Dustin Aherin, Kansas State University
- 2016 Will Shaffer, Oklahoma State University
- 2015 Joshua Hasty, Colorado State University
- 2014 Heather Bradford, Kansas State University
- 2013 Loni Woolley, Texas Tech
- 2012 Ky Polher, University of Missouri
- 2011 Jessica Bussard, University of Kentucky
- 2010 Paige Johnson, Texas Tech University



Luke Fuerniss — 2022 BIF Roy Wallace Scholarship Recipient
Pictured (l to r) are Brian House, Select Sires; and Luke Fuerniss

Past Scholarship Recipients — UNDERGRADUATE

- 2022 Macie McCollum, Texas A&M University
- 2021 Eva Hinrichsen, Oklahoma State University
- 2020 Elle Moon, South Dakota State University
- 2019 Taylor Nikkel, Kansas State University
- 2018 Madison Butler, Oklahoma State University
- 2017 Tanner Aherin, Kansas State University
- 2016 Ryan Boldt, Colorado State University
- 2015 Matthew McIntosh, University of Connecticut
- 2014 Maci Lienemann, University of Nebraska- Lincoln
- 2013 Tyler Schultz, Kansas State University
- 2012 Natalie Laubner, Kansas State University
- 2011 Cassandra Kniebel, Kansas State University
- 2010 Sally Ruth Yon, Clemson University



Gessica Franco — 2021 BIF Roy Wallace Scholarship Recipient
Pictured (l to r) are Lorna Marshall, Select Sires; Gessica Franco; and Norm Vincel, Select Sires.

BIF Pioneer Award



Bob Hough — 2022 BIF Pioneer Award
 Pictured (l to r) are Matt Perrier, 2021-22 BIF president; and Bob & Nancy Hough.



Galen Fink — 2021 BIF Pioneer Award
 Pictured (l to r) are Joe Mushrush, 2020-21 BIF president; Galen Fink and Dave Nichols.



Bobby Rankin — 2022 BIF Pioneer Award
 Pictured (l to r) are Matt Perrier, 2021-22 BIF president; and Trina & Bruce Davis (Dr. Rankin's daughter and son-in-law).



Alison Van Eenennaam — 2021 BIF Pioneer Award
 Pictured (l to r) are Matt Spangler and Alison Van Eenennaam.



Gene Rouse and Doyle Wilson — 2021 BIF Pioneer Award
 Pictured (l to r) are Gene Rouse, Doyle Wilson and Scott Greiner.

Sustainability: Rhetoric vs Reality — Ruairaidh Petre, Global Roundtable for Sustainable Beef executive director



Rhetoric

There are numerous opponents of the beef industry, and circumstances have aligned messages from groups that otherwise appear as unlikely allies. Many anti-beef, and anti-livestock positions in general are ideological, and these have been added to over time by those concerned by climate change and misled to believe that ruminants are a leading cause. The rhetoric used includes emissions, animal welfare, human health and biodiversity.

Reality

The reality, both in relation to those negative messages, but also in terms of the global response to them, is much more nuanced. Demand for Beef remains high as do prices. Markets have experienced considerable volatility over the past three years, caused by viruses including African (and classical) Swine Fever, Covid 19 and FMD, with BSE also impacting Brazilian access to the Chinese market. Although the high prices were initially demand led, rising inflation is curbing consumer demand now to some extent while rising input costs push beef prices even higher. The war in Ukraine will undoubtedly have ongoing indirect impacts on livestock markets, particularly in terms of feed, fertilizer and energy costs in Europe and beyond, so we can expect volatility to continue.

Around two thirds of the land we can use for food production consists of grasslands and rangelands, while only around 12% percent is capable of producing a range of human edible crops. It is true that many grazing areas are degraded, and that livestock can be implicated in many cases in that degradation. However, livestock can also be a tool in land restoration.

It is often assumed that intensive systems in more industrialized countries are more polluting than those in lower income countries. This is not actually the case – production systems in industrialised countries have evolved to be efficient

and highly productive per capita, and therefore have a lower emission intensity per kg than those in some other producing regions. Closing that efficiency gap while utilizing the most appropriate production systems in different environments is a key priority for GRSB.

Sustainability

Though we should not boil sustainability concerns down to just one metric, one of the areas we are persistently challenged with is that of climate, which is the reason that GRSB set our target to reduce emissions intensity by 30% by 2030. Many member countries already have targets of their own that will contribute to this including Australia, Europe, New Zealand, The United States and Canada. These are further supported by many corporate commitments through Science Based Targets.

There are many steps that can be taken to reduce enteric emissions. Feed additives are a promising avenue, with products such as 3NOP and Asparagopsis delivering reductions in the order of 80% in trials. A wearable device that can capture and break down methane has also been developed. However, not all solutions need to be so high tech – feed and grazing management, including ration and sward composition can already bring about improvements in the order of 30%, and the benefits of good rotational grazing and rest management extend beyond just reducing emissions, e.g. by increasing soil carbon sequestration. Genetics has a role to play as well, both through conventional breeding and the use of advanced data management, IVF and gene discovery. We can expect to see gene editing offer accelerated improvements in traits in the future. We should not ignore the role of animal health and welfare in delivering efficiency benefits – reductions in morbidity and mortality and increases in reproductive efficiency mean a smaller supporting herd to produce the same amount of meat.

In addition to activities that reduce emissions, we should consider the range of options that can increase sequestration – grazing management has already been mentioned, but further improvements can be gained particularly in tropical regions, through silvopastoral systems where again, there are multiple benefits including feed quality and digestibility, surface temperature / shade and production of biomass. Though expensive to establish, such systems can be orders of magnitude more productive when compared to grass alone.

Manure management also provides some opportunities to increase efficiency; biomethane capture adds value and reduces the amount of methane lost, while good manure and fertilizer management reduces losses from those sources while optimizing use.

Sustainable Beef Network

The global roundtable for sustainable beef, and the network of national roundtables, now spans 24 countries, all committed to delivering on our vision of beefs role in a thriving and sustainable food system. Our membership covers the full chain of the beef industry as well as those organizations with an interest in the

sustainability of the sector including civil society (NGOs and academia).

GRSB released our global goals last year, with the full participation and buy in of our members. They cover:

- Climate impact – a 30% reduction in the intensity of emissions by 2030.
- Animal health and welfare – providing animals with an environment in which they can thrive
- And Nature positive production – the beef industry to be a net positive contributor to nature by 2030.

Activities

GRSB has developed a Carbon Footprint Guideline to support consistency in emissions reporting. This is based on the FAOs LEAP methodology and is aligned with the dairy industry's guideline.

We are working with Emerging Ag to support representation at COP27 in Egypt. We have hired Sure Harvest to work on our MRV system to set baselines and report against the global goals; we will work closely with members and national roundtables to streamline this.

In terms of Nature positive production, clearly there is a priority to end land conversion. Water use is another major concern; planned (AMP) grazing can contribute to soil moisture retention/resilience. Ground cover is very important in reducing runoff. Once again, Silvopastoral systems provide multiple wins, including water services.

Water withdrawals for feed are very significant in the U.S. There will need to be a shift in the coming years. CSU and the National Alliance for Water Innovation as well as several partners in the USRSB are working on this to investigate water savings and non-traditional water sources.

In terms of biodiversity there are many deforestation-free commitments from corporates — increasing interest in transparent supply chains. The proposed legislation from EU

is likely to result in further moves towards transparent and traceable supply chains.

Conversion of native grasslands to cropping — beef industry is on both sides of this equation. Evidence from AMP grazing suggests grassland productivity can be significantly improved and reduce demand for feed inputs (this is context-dependent).

As far as animal health is concerned, we owe the animals in our care a life worth living.

Good health and welfare benefits the animal and the producer and is the minimum consumers expect. Health and welfare contribute to other goals by closing the efficiency gap. Healthy, well-handled cattle do better and are safer to work with. Good animal health contributes to human health through a reduction in zoonoses, as well as reducing the need for pharmaceuticals that are critical to human health, the overuse of which can lead to resistance. Progress is already being measured and reported on by the Australian Beef sustainability framework on adoption of pain mitigation and awareness of animal welfare standards.

Please join us for the Global Conference on Sustainable Beef in Denver on November 7th-10th where you can hear more detail on all of the above.

References

¹Full details and background can be found at: <https://grsbeef.org/sustainability-goals>

²<https://grsbeef.org/grsb-beef-carbon-footprint-guideline/>

³<https://www.sustainableaustralianbeef.com.au/resources/annual-update2/>

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**National
Cattlemen's
Beef Association**

Breeding for Sustainability - Fitting environmental impacts into economic selection indexes — John J. Crowley, AbacusBio Ltd.



Sustainability in agriculture has many facets, with greenhouse gas (GHG) emissions currently being a primary focus. Emissions from farmed livestock have been highlighted as a significant source of total global GHG (Gerber et al., 2013) and so this paper deals with the GHG aspect of “Breeding for Sustainability”. Recently there has been a significant amount of research undertaken endeavouring to reduce the carbon footprint from animal agriculture. For most producers, families, businesses and industries who depend on livestock for their sustenance and livelihoods, and for consumers of numerous and diverse products that they generate, simply reducing livestock numbers and product produced to achieve GHG mitigation is undesirable (Herrero et al., 2013; Amer, 2022). When a reduction in herd size (local or national) is not possible, emissions per unit of product (emissions intensity; EI) becomes a primary focus. Breeding and genetics exists as a solution to GHG mitigation and holds a medium to high level of impact potential (Lanigan et al., 2019; Hristov et al. 2013). Other solutions such as feed additives, diet lipids, land management, fertilizer use and manure storage etc. all hold different levels of mitigation potential in parallel with genetics (a solution which is cumulative and permanent). The objective of this paper is to highlight approaches for including environmental impacts and considerations in a selection objective, and discuss selection criteria pertinent to that objective.

Selection Criteria

Wall et al. (2010) outlined three main classes of traits that can be selected for to influence a reduction in GHG. Generally we can think of a trait as having a direct effect i.e. emissions from and measured on the animal, or indirect i.e. a reduction in system wide emissions due to a change in a trait. Traits that directly target biological functions of the animal that lead to improved outcomes are the first type of trait described by Wall et al. (2010; Type 1) e.g. Methane Yield (MY; g CH₄/kg DMI). Productivity traits that dilute maintenance (Type 2), and survival traits, and traits that reduce the need for replacement animals and the emissions associated with them (Type 3) are additional options for selection criteria. With these types of traits in mind, we can examine different approaches using these criteria to select for an improved beef carbon footprint.

Current selection for profitability encompasses selection pressure on many of the Type 2 and 3 traits (growth, maintenance, calving interval, longevity) and so it is highly probable that EI is also improving. It would be a worthwhile exercise to (regionally or nationally) quantify the contribution of genetics to GHG mitigation, an exercise which would also set up the framework to move the breeding goal toward a more environmental focus. There are also more appropriate selection criteria that can be defined that make it cheaper and easier for breeding programs to make genetic change in traits that improve both farm profit and which also improve environmental outcomes (Amer, 2012) e.g. age at harvest, and these are usually already in the data we have. Novel traits, (all types) can also be developed. Previously mentioned MY is a key trait given that enteric methane is a large proportion of all beef GHG. The trait shows 15-20% phenotypic variation and is moderately heritable (~0.30; personal communication, Irish Cattle Breeding Federation) and has the opportunity to mitigate large amounts of GHG. The trait holds more importance in a total system if the amount of DMI consumed for beef production does not decline. In certain scenarios (e.g. pastoral systems), improvements in feed efficiency may not result in feed saved, but just the same amount of feed fed to more animals. If total DMI used will not change, selection for enteric methane/kg DMI (Richardson et al. 2021a describes some definitions and considerations) can deliver large carbon mitigation (feed additives currently in development also act on the methane/kg DMI process). On the topic of novel traits, development of breeding values for such conditions as pulmonary arterial pressure (PAP) and the ability to select for traits such as slick can have impacts on survivability and longevity, all of which are cost saving traits and contribute positively to overall EI.

Selection Objective

While current multi-trait selection for profitability is a weighted sum of relevant selection criteria, we can further modify trait selection emphases through changes in breeding objectives and index weightings (Cottle et al. 2011) to achieve reductions in emissions intensity and/or reductions in gross emissions per animal. To facilitate this modification of the breeding objective, GHG emission coefficients (EC) can be estimated on a per trait basis (Amer et al. 2017, Quinton et al. 2018, Richardson et al. 2021b) and appropriately scaled and applied to current breeding values. Assuming the current market rate (\$) for carbon as its economic value (EV), current economic weights (EW; EV*discounted genetic expressions (DGE)) per trait can be combined with carbon EV ($[EV_{\text{trait } i} - EC_{\text{trait } i} * EV_{\text{carbon}}] * DGE$) to calculate a new weighting per trait and in turn can sum to a carbon influenced index. Additionally, or alternatively, one can form a carbon sub index that sits outside other profitability indexes by just estimating carbon economic weights (CEW; $EC_{\text{trait } i} * EV_{\text{carbon}} * DGE$) to be applied to relevant traits. The latter subindex approach offers transparency and decouples carbon from profitability in a time where market signals on carbon price related to beef production are weak. Conversely, embedding carbon weights into current indexes allows more direct progress to be made as carbon considerations

are explicitly in the objective and will receive selection emphasis regardless, through selection decisions based on available and published economic selection indexes. It is to be noted that the higher the assumed or actual price of carbon is, the higher the relative emphasis will be on traits that influence direct and/or indirect emissions.

The value of index manipulation to decrease selection emphasis on traits that increase gross emissions must also be treated with caution. Reducing EI and reducing gross emissions of a production system require slightly different approaches and considerations. The traits with the most negative effect on gross emissions per animal in beef are typically growth rate and liveweight (milk yield in dairy). Selection for these traits has driven genetic gain in production efficiency and profitability. To this end, an EI philosophy (as opposed to gross emissions) which tends to favour rather than penalise these traits may in some cases lead to better long-term outcomes (Amer et al. 2017). Conversely, (i.e. for penalising traits with high emissions) appropriate modelling should show that a shift in selection emphasis away from genetic gain in growth rate traits could fit more closely with reductions in beef system intensity, an approach more appropriate to achieve lower gross emissions. With less intensive systems, genetic traits that target cost savings required to offset reduced revenue can increase in relative value to maintain economic viability (Amer, 2022). As previously mentioned, current selection objectives are probably having a favourable impact on beef EI and with more cognizance of carbon costs in the objective, the rate of EI improvement can increase. However, and outside of the control of genetic improvement, if EI is improving, gross system emissions may still increase from the production system if cow numbers increase. If cow numbers remain the same, improved production efficiency resulting in increased output will improve EI and likely gross emissions but to a lesser extent. Larger GHG mitigation can be achieved if increases in production efficiency manifest as product produced remaining stable with a reduced cow herd.

National Focus

North American production systems on average produce beef with a relatively low carbon footprint. This is due to both good genetics and management practices. To focus on reducing gross emissions of the herd (per farm, per county, per state, nationally etc.), production will inevitably have to decrease (barring an extremely steep improvement in EI). This would have detrimental consequences on the global beef carbon footprint as beef produced in other less efficient countries would replace the void in market supply left from reduced North American production. There is potential leakage of emissions to less efficient competing industries when policies targeting emissions result in reduced domestic industry output (Amer, 2022)

Summary

Breeding and genetics can play a significant role in addressing the global challenges facing livestock sustainability. Methodological frameworks exist and continue to evolve for deriving gross emission and EI weighting factors to create carbon influenced selection objectives. Approaches and modifications to current objectives for a gross emission or EI end goal will differ. Generally, current genetic trends in growth and cost saving traits have contributed, and will continue to contribute to substantial improvements in EI. Carbon price has a large impact

on predicted responses to selection and relative emphasis on carbon relevant traits in economic selection indexes. Traits like age at slaughter and methane yield carry a lot of potential when it comes to selecting for a reduced carbon footprint.

Other traits such as liveweight, calving interval, feed efficiency, cow longevity and age at first calving are all examples of criteria that indirectly impact GHG from the system and would tend to feature in a carbon (sub-)index. Focussing on EI would be preferable in zones where the beef carbon footprint is better than average. A focus on gross emissions reduction can reduce overall beef production only with that vacated demand to be met by beef product from less efficient production systems, thus having a negative effect on the global beef carbon footprint. When considering breeding strategies, policy mechanisms and farmer adoption and behaviour will be critical to achieving environmentally conscious genetic progress. Supporting infrastructure enabling performance recording, data collation and genetic improvement can also serve as a good platform to build more elaborate GHG assessment systems.

References

- Amer PR. 2012. Turning science on robust cattle into improved genetic selection decisions. *Animal* 6: 551
- Amer PR, Hely FS, Quinton CD and Cromie AR. 2017. A methodology framework for weighting genetic traits that impact greenhouse gas emission intensities in selection indexes. *Animal* 12:5
- Amer PR. 2022. Genetic progress for environmental outcomes – how do we get it? *Proc. Assoc. Advmt. Anim. Breed. Genet.* 24:34-37
- Cottle D, Nolan J, and Wiedermann S. 2011. Ruminant enteric methane mitigation: a review. *Anim. Prod. Sci.* 51:491
- Gerber PJ, Steinfeld H, Henderson B, Mottet A, Opio C, Dijkman J, Faluccia A and Tempio G. 2013. Tackling climate change through livestock: a global assessment of emissions and mitigation opportunities. Food and Agriculture Organization of the United Nations (FAO), Rome, Italy.
- Herrero M, Grace D, Njuki J, Johnson N, Enahoro D, Silvestri S and Rufino MC. 2013. The role of livestock in developing countries. *Animal* 7 (suppl. 1), 3–18.
- Hristov AN, T Ott, J Tricarico, A Rotz, G Waghorn, A Adesogan, J Dijkstra, F Montes, J Oh, E Kebreab, S J Oosting, P J Gerber, B Henderson, H P S Makkar, J L Firkins. 2013. SPECIAL TOPICS — Mitigation of methane and nitrous oxide emissions from animal operations: III. A review of animal management mitigation options, *J. Anim. Sci.*, 91:11:5095–5113
- Lanigan GJ, Donnellan T et al. 2019. An Analysis of Abatement Potential of Greenhouse Gas Emissions in Irish Agriculture 2021-2030. <https://www.teagasc.ie/media/website/publications/2018>
- Quinton CD, Hely FS, Amer PR, Byrne TJ and Cromie AR. 2018. Prediction of effects of beef selection indexes on greenhouse gas emissions. *Animal* 12:889
- Richardson CM, Nguyen TTT, Abdelsayed M, Moate PJ, Williams SRO, Chud TCS, Schenkel FS, Goddard ME, van den Berg I, Cocks BG, Maret LC, Wales WJ and Pryce JE. 2021a. Genetic parameters for methane emission traits in Australian dairy cows. *J. Dairy Sci.* 104:1:539
- Richardson CM, Amer PR, Hely FS, van den Berg I and Pryce JE. 2021b. Estimating methane coefficients to predict the environmental impact of traits in the Australian dairy breeding program. *J. Dairy Sci.* 104:10:10979
- Wall E, Simm G and Moran D. 2010. Developing breeding schemes to assist mitigation of greenhouse gas emissions. *Animal* 4:366–376.

Where Are They Going and How Are They Doing — Tony Clayton



Introduction

For many years, the United States has been a leader in the export of animal genetics through live animals, semen, and embryos. For being involved in the export industry for over 30 years and exporting beef and dairy cattle, goats, horses, sheep, swine and semen to over 60 countries by truck, air and sea I have seen many markets open to the USA and how countries evolve to be high value customers of the United States while others set trade barriers to limit imports which have an impact on food availability for their consumers.

This presentation will touch on the various factors that will drive the export market and outside factors the US livestock industry will have to address so we will remain competitive in a world market and doing our part to feed a growing world.

The World is Connected!

With the click of a mouse on your computer or a message through social media, the world is a connected more than ever. You can search for any product, any information on management, transportation and finding animal genetics is one of those products a buyer can research or contact any supplier around the world.

Population Growth Will Drive the Market

It is predicted by 2050, the world's population will grow to an estimate 9.5 billion people. The one thing that will connect people all around the world, is we all must have food, shelter and clothing. Some of the countries that will be in the top 10 for population will be third world countries and due to a lack of education, infrastructure, and the inability to look into the future of how they will feed the people of their country. I am a firm believer "That Hungry People are Dangerous People."

More Disposable Income Creates Markets

Regardless of the country, religion, beliefs when consumers have more income and have more information, they buy better products like televisions, homes, cars and especially food. The protein market of meat and milk will become more important to a growing world market which creates opportunity beef and dairy cattle as well as goats, sheep and swine. These export sales of animal genetics have added to the export economy of

the United States and having an impact to breeders, farms and ranches in local economies including all vendors involved in the export chain.

US Genetics are a valued added product because our industry has done more research in the areas of EPD's, genomics and efficiency of producing more food with less animals and the world looks at the USA as the supermarket of the world.

The power of the pedigree is what adds value to years of work breeders, breed associations and universities have done together to identify breeding values for specific traits and genomics international buyers want to acquire. With all the information in pedigrees and many of the countries that will lead the world in population will lack the education to understand the information contained in the pedigree. Much educational work will have to take place to educate buyers on breeding programs and how to identify the traits that are most important to their industry and why they can't always buy only the cattle that are in the top 1-2% of our population.

The Export Process-Cause and Effects

There have always been factors such as economy, currency, oil prices, weather, politics, and disease that have affected various export markets. It just seems now we are affected not by one or two of these factors, but all seem to be in play in 2022 which has made the exports of all products are real challenge. With higher prices due to inflation from transportation, a reduced work force in both the private and government sector, much more planning and closer attention to planning an export shipment is a must to have a successful shipment.

With the situation of COVID and animal diseases such as Foot and Mouth Disease (FMD) and African Swine Fever (ASF), this has changed how our industry allows international visitors to select at farms and ranches because of bio-security concerns. The availability of large animal veterinarians to conduct the export testing and trucks to transport large number of animals to ports of embarkation is a challenge and an industry concern.

International Transportation (Air & Sea)

With the recent impact of COVID there is a tremendous demand for air cargo to transport COVID supplies around the world. The Russia/Ukraine situation has eliminated one of the airlines that provided planes to the US animal export market is not allowed to carry shipments from the US because it is a Russian based company. Because of a lack of knowledge about animals, many airlines have either stopped carrying live animals or greatly reduce the tonnage they carry. Air transportation is an expensive mode of transportation, but still the quickest way to move animals to a new home quickly.

Sea transportation is still the cheapest way to transport large shipments of animals from the USA to international markets. These shipments need to be more than 1,500 head or more, but COVID has impacted the loading efficiency at the ports on both the east and west coast.

Developing Your Market

As breeders identify their plans for marketing internationally, many topics need to be considered such as: Promotional

activities, supply they have available to fill shipments, the export health regulations, risk and how they follow up with customers. The international market is much like the domestic market here in the USA. You must do your missionary work to know your customers; you must be there to sell it and service what you sell.

Disease Will Influence the Market

As much as the USA excels in animal genetics, the one factor around the world that develops much of the market opportunity is animal disease. When a country is affected by FMD, ASF or Avian Influenza, the whole balance of animal protein supply and demand is in play. When countries start a repopulation program backed by the government it may overpay for supply which in turn affects the supply for other markets. Disease has also had a great impact on transportation methods with countries having major restrictions on flight crews coming from some certain countries with COVID.

Animal Identification and Welfare

More and more countries are negotiating with our United States Department of Agriculture-Animal Plant Health Inspection Service-Veterinary Services (USDA/APHIS/VS) for better animal identification. Electronic ear tags (RFID) will be a must for any breeder that is wanting to enter the export industry.

Our industry is being confronted by more and more people concerned about animal welfare. With people watching more loadings taking place at airports and seaports with cell phones our industry will always be under the microscope for not what we do, but how we do it.

Next Opportunities-Feeder Cattle

As China imports more and more cattle from countries like Australia, Brazil, Chile, and others, it will leave a supply void for other countries like Indonesia, Egypt and other Mid-Eastern countries. In the future, there will be a growing demand for feeder cattle to be exported from the USA.

Conclusion

The livestock export industry is a billion-dollar industry. Our industry has a financial impact not only for the breeder, but all involved in the export chain such as veterinarians, truckers, testing labs, quarantine facilities, feed suppliers, insurance companies, banks just to mention a few. The export of animal genetics helps feed a growing population and hopefully helping to keep the peace around the world by feeding hungry people.

References

Slides 6 & 14: Brian Gordon, Senior Vice President & Manager, International Marketing Group, Commerce Bank, Kansas City, MO

Slides 26 & 27: www.Marinetraffic.com

Slides 37 & 38: Valius-Praedium Animal Welfare Services

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DIGITAL CONTENT

**International
Genetic Solutions**

Growth and Genetic Selection of a Vertically Integrated Beef Enterprise in Russia — Phil George



Miratorg Agribusiness Holding is a privately held food company based in Moscow, Russia started in 1995 owned by identical twin brothers. The brothers and their vice president are very involved in day to day management of the company. Their management style and decision making is very quantitative as they are trained as engineers and physicists.

Miratorg began as a trading company in 1995 by importing whey from Poland when food was very scarce in Russia after the breakup of the Soviet Union. Later, they added pork and poultry meat to their imports and set up a distribution network in European Russia. They then began adding value to their imported products thru further processing and repackaging. After 2000, the Russian government offered strong subsidies to encourage meat and dairy products to be produced in Russia. Miratorg began pork production in 2005 with a European model in the Belgorod Region.

The Angus project began in 2011 and the broiler project in 2012. They began establishing retail outlets all cities greater than 1M population in 2015. The prime lamb project was launched in 2017 with the establishment of the first sheep farm in the Kursk Region. It's an accelerated lambing project that will produce 1.5 million lambs per year by 2028.

Today, Miratorg is completely vertically integrated in pork, broiler, beef cattle and lamb production. It has 2 pork plants, a beef plant, a poultry plant, a poultry feed mill, 3 pork feed mills, a soybean processing plant, a tannery, a pet food plant, a rendering plant, a bacon plant, 20 "burger" restaurants in Moscow, a "flag-ship" restaurant (No Fish) restaurant in Moscow and 150 retail stores. It controls nearly 3 million acres and a large agronomy division that produces 95% of the grain and forage for all species. In 2021, it planted and harvested 500,000 acres of corn (as dry corn, high moisture corn or corn silage), 250,000 acres of soybeans and 250,000 acres of wheat or barley. It also has a 7,000 acre, 54 Valley center pivot property that produces fresh carrots, potatoes and beets for its retail outlets.

Most Miratorg products are consumed domestically but the company does export meat and meat products to the other CIS

countries, Saudi Arabia, the UAE (Dubai & Abi Dabi), Hong Kong, China, Japan and Brazil.

Beef Cattle Project

Lynna and I arrived in Russia January 25, 2011. At that time, there were about 15-20 Russian employees and about 25,000 acres of unfenced raw land in the Bryansk Region near Trubchevsk. About 70 Americans and 3 Australians were recruited to train Russians over the next 5 years. The land team began acquiring 2,500 acres per week in 2011 but increased to 5,000-6,000 acres per week by 2016.

One hundred twenty-five thousand (125,000) commercial Angus heifers were imported from the US and Australia (50/50) in 2011, 2012, 2013 and 2014. Most of the US heifers were purchased from ranches in Montana, the Dakotas, Nebraska, Wyoming, Idaho and Oregon. Most Australian heifers were purchased from properties in Victoria, South Australia and New South Wales. All heifers were purchased from their original owners and quarantined before export.

All the US heifers were transported to and quarantined near Garden City, Kansas. Heifers were quarantined from 45 to 120 days, depending on their scheduling for export. All heifer shipments were loaded on the vessel in Galveston. The voyage from Galveston took 18-21 days depending on the Russian port of importation, Ust-Luga (near St. Petersburg and Baltic Sea port) or Novorossiysk (Black Sea port). Shipments from the US were typically 4,000 head per shipment. Heifers were allowed a 1.5-1.7 m² (16-18 ft²) per head on the vessel.

The Australian heifers were quarantined near Portland and Warnabool, Victoria, Deniliquin, New South Wales, Mt. Gambier, South Australia and Freemantle, Western Australia. They were loaded on vessels at Portland, Victoria and Freemantle, Western Australia. Voyages typically took 30 days from Australia, crossing the Indian Ocean, passing through the Suez Canal, the Mediterranean Sea and through the Bosphorus Strait in Turkey into the Black Sea and off loaded at the port of Novorossiysk.

Two thousand registered Angus heifers were imported from the US and Australia to comprise the seed stock herd. About 7,000 registered Angus yearling bulls were purchased from 40 different breeders in the US. About 1,250 registered Angus bulls were purchased from Australian breeders. All bulls had to have CED, BW, YW, CW, Marbling and REA EPDs in the top 50% of the breed. Many ranked in the top 30th percentile of those traits.

About 500 Quarter Horses were also imported from the US to work the cattle along with 500 Western saddles. In the beginning, no Russians had experience saddling and riding or roping. All cattle on the farms are moved, gathered, checked on a horse today.

The company currently maintains 100 cow/calf production farms, 50 replacement heifer development farms and weaned steer backgrounding and grazing farms, 3 feedlots with a one-time capacity of 225,000 head and 1 beef plant with a 100 head/hour chain speed and an annual processing capacity of 500,000 head. Farms are typically 12,500 to 18,000 acres in size and have 25 employees each.

Feeder Cattle Shipments

Fifty thousand feeder cattle (600 to 950 lbs.) were imported from Australia each year over 5 years to augment the company's production until it could domestically fulfill the plant's capacity. Seventy percent plus of the steers were Angus with the balance being black baldies, Hereford or other English crosses.

The steers were purchased in Australia's late spring or summer, quarantined and then arrived in Russia from December thru May. Over half arrived in the heart of the Russian winter when temperatures were 0oF to -25oF. They were completely acclimated to Australian summer conditions with no hair and no time to acclimate on the voyage as temperatures were hot to moderate until they entered the last day of their voyage crossing the Black Sea. They were deeply bedded in straw (2-3 ft deep) and fed a good corn silage ration on arrival. Death loss the first 45 days after arrival averaged 2.1% with the worst shipment reaching 3.5% death loss. Morbidity was a normal 5%. Dry matter intake was very high with 1 shipment reaching a DM intake of 3.45% one month after arrival in -25oF to -30oF weather.

Genetic Improvement Strategy

Specific targets have been set for the most economically important traits in the production herd. Technologies of IVE, sex sorted semen, genomics and the GrowSafe@ System are employed to achieve these targets within 20 years. Once the genetic engine is moving on track, \$6 million USD will be added to the bottom line each year with a projection of \$120 million USD each year after 20 years of genetic improvement.

Four thousand bulls and 60,000 bred heifers are needed as replacement stock in the production herds each year. Two different strategies for bull and replacement heifer production were evaluated: 1) Nucleus herd with a large multiplier herd using natural service and 2) Nucleus herd with no multiplier herd.

The evaluation is based on the following equation (Richard Bourdon, 1999)

$$\Delta = (r \times i \times \sigma) / L$$

Δ = rate of genetic change

r = accuracy

i = intensity

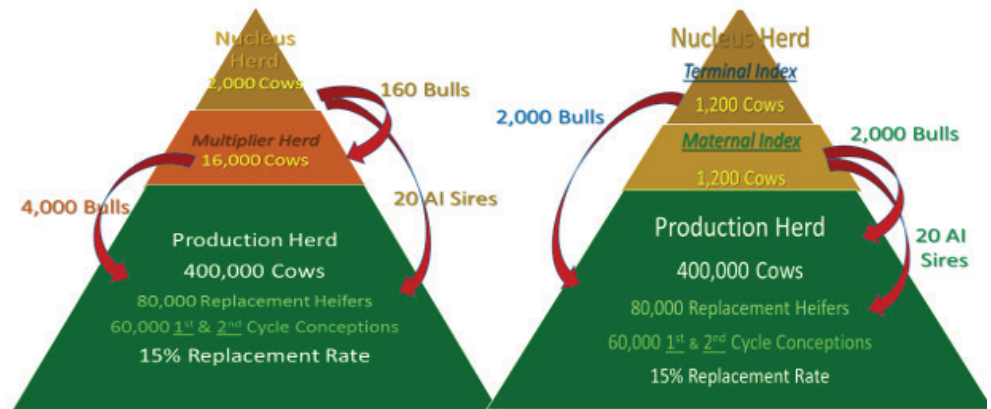
σ = standard deviation of the traits

L = generation interval length

The genetic progress using the multiplier herd strategy was much slower. None of the targets for the economically important traits would be achieved within the 20 year timeline. Many traits would require 50 or more years to achieve their targets. Thus, the multiplier herd strategy was rejected and the strategy was adopted whereby bulls for the production herd are produced directly from the nucleus herd. See Figure 1.

In the multiplier model, most of the 4,000 bulls are produced from the multiplier herd which relies on natural service. In the

Figure 1



non-multiplier model, separate terminal and maternal lines were established within the nucleus herd. Two thousand bulls each are produced from the nucleus terminal and maternal lines, respectively.

Animals within the nucleus herd were then assigned to terminal and maternal herds using genomic EPDs. PCA Analysis of the genotypes and K Cluster Evaluation identified 3 different clusters within the nucleus herd. One of the clusters had 3 different subsets. Subsequently, those within the maternal herd were assigned to 4 different maternal lines based on the K Clustern analysis. Top indexing bulls and heifers within the terminal line and the respective maternal lines are retained within the respective lines. Matings to limit inbreeding within the terminal and maternal lines are base on gemonics rather than pedigree evaluation.

The produciton farms were equally assigned as terminal or maternal farms, i.e., 200,000 cows within terminal farms and 200,000 cows wthin maternal farms. Terminal farms receive bulls from the nucleus terminal line. All calves produced from the terminal farms are destined for the feedlot and the plant. Maternal farms recieve bulls from the respective maternal lines (1, 2, 3, 4). All steers and cull heifers from the maternal farms are destined for the feedlot and plant. Replacment heifers are retained from the maternal farms to provide replacements for the maternal and terminal farms.

Eighty thousand replacment heifers from the production farms are synchronized and AIed each year using the 7-Day CIDR and 14-Day CIDR Fixed-Time AI protocols. The two protocols have different post prostaglandin injection time intervals before fixed time AI so it allows groups to be scheduled for insemination each day at 7 am, 10 am, 1 pm and 4 pm on the same farm.

Genomic data, pedigree information and phenotypic data are all analyzed using single step methodology to provide genomic EPDs and a ranking by the Terminal or Maternal \$Index. The highest ranking heifers from the respective maternal farms are retained as replacments. They must weigh a minimum of 700 lbs and undergo a final phenotypic evaluation to confirm proper development and structure before entering the synchronization protocol.

The primary economically important traits in the Terminal \$Index are carcass value (carcass weight and marbling) and Efficiency. Our strategy for improving efficiency is not to reduce feed intake but instead to simultaneously select for Residual Feed

Intake and Post-Weaning Average Daily Gain. Longevity in bulls, serving capacity and immune competence and resilience are lesser components of the terminal index.

A Breeding Soundness Examination is conducted on all yearling bulls and then on every older bull every year until he is culled. Besides, semen motility and morphology, the bull's weight, foot score and reproductive tract abnormalities are reported at this time. We expect to identify genotypes that are early culls versus those with long productive lives so we can skew our selection favorably.

The primary economically important traits in the Maternal \$index are female fertility, longevity and efficiency. Phenotypic data contributing to the fertility EPD includes heifer, 1st calf heifer and mature cow pregnancy data. The heifer data is reported as AI, bull bred or open. About 20,000 records of the mature cow data is also reported as 1st cycle, pregnant and open.

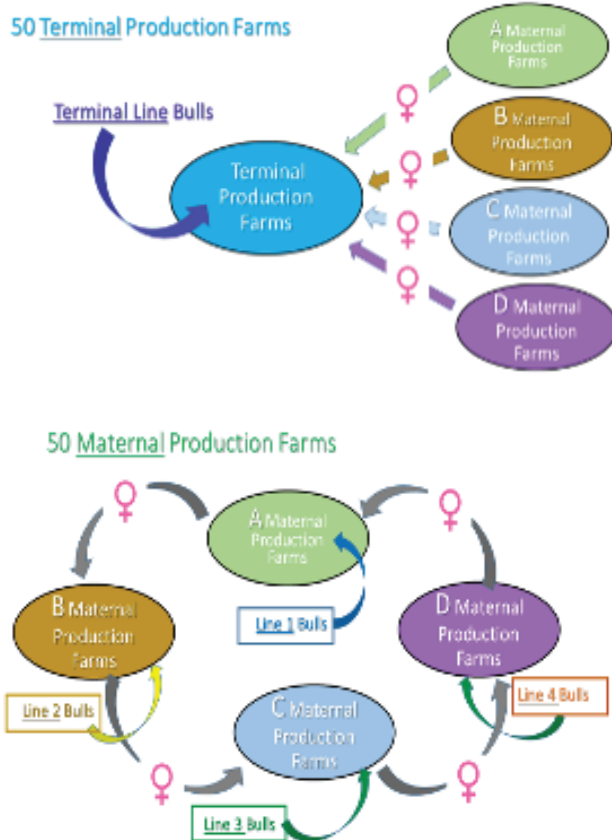
What about crossbreeding? Crossbreeding should improve calf viability and reduce morbidity and mortality in the birth to weaning phase, growing phase and finishing phase. It should also improve fertility in the females and perhaps feedlot feed efficiency. There could also be complimentary trait benefits in larger rib eyes and leaner carcasses.

Bulls of non-Angus breeds from US AI studs that qualified for export to Russia were evaluated as maternal or terminal sires. EPDs of six Hereford bulls and six Simmental or SimAngus bulls were adjusted to an Angus base using USDA=MARC's across breed adjustments. When compared to the maternal Angus sires, the Hereford bulls on average were substantially poorer in all the traits compared. The Simmental or SimAngus sires had better REA, similar WW and Milk EPDs compared to the maternal Angus but substantially bigger BW and poorer YW and Marbling EPDs. Crossbreeding experiments are planned to evaluate its maternal benefits.

EPDs of six Charolais, six Limousin and six terminal Simmental or SimAngus bulls were adjusted to an Angus base using the same across breed EPDs and compared to terminal Angus sires. The non Angus bulls on average had bigger REA EPDs and were leaner but had much bigger BW EPDs and much poorer Carcass Weight and Marbling EPDs. The company concluded that using a Terminal Line Angus was much preferred to crossbreeding.

Summary. What have we learned?

1. Cattle are extremely resilient and adaptable to severe cold weather challenges if they are fed and bedded well. Steers shipped from Australia's summer and arriving in Russia's winter endured temperatures on arrival of 0oF or even -25oF with a 2-3% death loss the first 45 days after arrival.
2. Genomically-enhanced EPDs are extremely reliable in selection. Dystocia was 1% or less on US and Australian heifers using US or Australian bulls ranking in the top 50th EPD percentile for Calving Ease Direct and BW. Steers sired by US or Australian bulls ranking in the top 50th EPD percentile for Marbling graded 30% Prime or better.
3. Reproductive technologies can be successfully implemented on a large scale. Fifty thousand plus replacement heifers have been synchronized and artificially inseminated for the last 8 years consistently achieving AI conceptions rates over 50% and



final conception rates of 90%. Four hundred embryos were produced daily using IVF methods and achieving embryo conception rates of 40%+. Thirty thousand embryos are produced and implanted annually using IVF methods. Sex sorted semen collected and used the same day (fresh) can achieve conception rates equal to frozen conventional semen.

4. Substantial investments were made in a genomics laboratory, semen sorting laboratory, facilities and laboratory to conduct IVF on a large scale and a large scale system to measure individual feed intake and efficiency. All of these technologies will drive the genetic progress in the cattle project and have a payback of 5 years or less once the genetic engine pushes forward.

5. There is great opportunity for genetic progress in beef cattle in identifying embryonic lethals, improving efficiency, fertility, serving capacity, longevity and immune system competence and resilience.

Harnessing Genetic x Environment (G x E) Interactions – are They Important in Production? — Milt Thomas



On Behalf of W1: Beef Cattle Breeding Group of the Agricultural Experiment Stations of the Western States of the U.S.

G x E and (or) fitting animals to the environment

Gene x environment interaction, often referred by the acronym G x E, means that there are animals that perform better in some environments than others; therefore, G x E is important to beef production. The graph below (Figure 1) is an historic example of G x E. These results are from a study conducted by the USDA Agriculture Research Service and experiment stations in Montana and Florida. In brief, Hereford herds were maintained at each location and some cattle at each location were moved to the other location. The results were that the cattle from Montana performed best in Montana and the cattle from Florida performed best in Florida.

A simple explanation of these results is somewhat like home field/court advantage in competitive sports. However, G x E is more than just the E and moving cattle to the other environment. As the ability to do genomic analysis was gained, scientific efforts revealed that there are concentrations of alleles in specific environments (Krehbiel et al, 2019; Rowan et al., 2021). Alleles are alternative forms of genes and recent research revealed that there are frequencies of alleles unique to environment(s), which is a result of breeders selecting cattle that are most suitable to that environment. Because of this knowledge, it encourages the scientific and breed association community to continue to advance research so that environmental adaptability can be determined early in the life of cattle. To most, discussion of G x E is much more about fitting the most appropriate cattle to the resources of a production system; therefore, the definition of G x E can be much more than about environmental adaptability, it can also be about the various types of production systems that can exist within an environment. Examples of such differences could be a cow/calf production system versus a vertically coordinated system that markets beef based through a direct market.

See Figure 1: Gene x environment interaction in Hereford cattle. In brief, cattle bred and residing in Montana had better

weaning weight in Montana than the cattle bred to live in Florida and vice versa (Burns et al., 1979). Figure also published by Hammack (2009).

Environmental challenges and G x E

Even though it is challenging to gather the data needed to conduct statistical analyses to detect G x E, there are substantial environmental differences among beef production systems. Temperature, humidity, annual rainfall and drought, and altitude are obvious within these historic discussions as are conversations of which cattle best fit specific environments. In general, and for the U.S Beef Industry, *Bos indicus*-influenced (Brahman) cattle are most prevalent in hotter climates and *Bos taurus* cattle are most prevalent in cooler and colder climates.

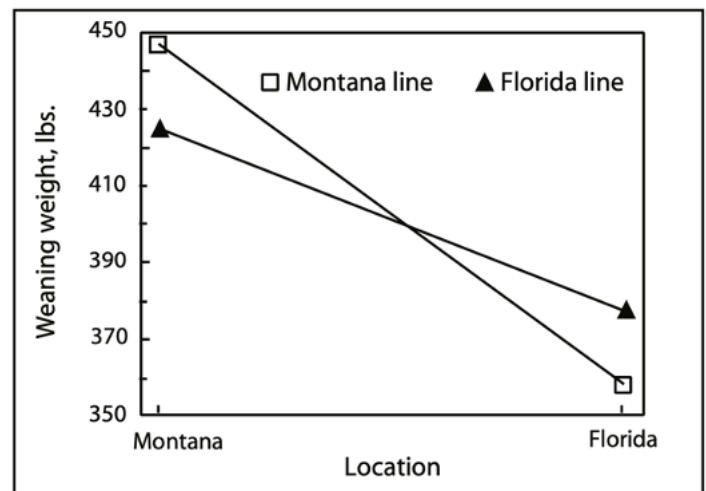
However, and more recently, impacts of climate change and sustainability have become part of the U.S. Beef Industry's strategic planning processes and goals. To be specific, climate neutrality is a goal stated by National Cattlemen's Beef Association and the US Roundtable for Sustainable Beef; therefore, future discussions and efforts to understand and take advantage of G x E as it relates to sustainability factors such as carbon footprint are expected; especially, since beef cattle are ruminants and breathe-out methane (Dillon et al., 2021).

Genetic challenges and G x E

Breeding objectives for beef cattle in the U.S. has changed many times throughout history. For example, belt buckle high (very short) cattle of the 1950s gave way to extremely tall (i.e., high frame score) cattle of the 1980s. More recently, the U.S. Beef Industry has been maintaining a consistent annual supply of beef with a smaller national cow herd because of the increased size (i.e., weight; USDA-NASS, 2022). Traits of size (i.e., yearling weight, mature weight, carcass weight) are of high heritability and the concept of a reduced national cow herd helps with the goal for moving towards a climate neutral industry.

However, in harsh environments and particularly across the Western U.S., traits more indicative of environmental adaptability may be of more importance within breeding objectives than increased size. Examples of environmental adaptability traits

Figure 1: Gene x environment interaction in Hereford cattle



include, milk production, grazing distribution, temperature, and altitude tolerance, etc. Members of the Western U.S. Agricultural Experiment Stations (W1) considered adaptability of the cattle in numerous breeding projects. This consideration was also done with understanding of the importance of hybrid vigor from crossbreeding and (or) composite cattle. The following diagram (Figure 2) illustrates how cow weight and milk production should change with rainfall. Crossbreeding research using Hereford and Brangus cattle helped design this figure and revealed that hybrid vigor was very helpful for productivity in a desert beef production system (Winder et al., 1992).

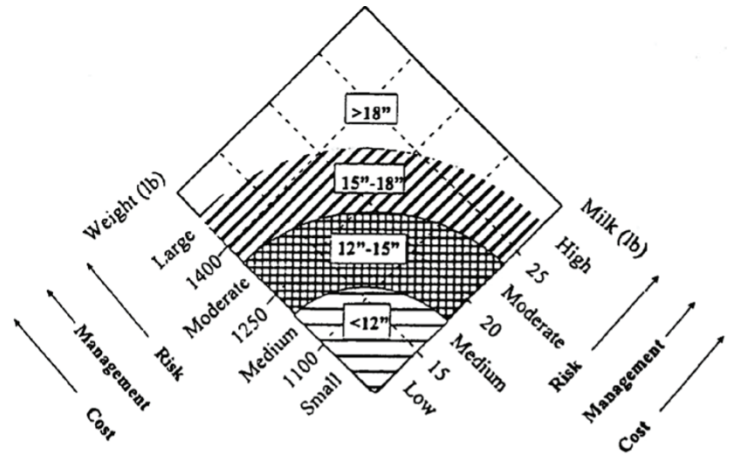
See Figure 2: Matching cow biological type (weight and milk) to range environment, with associated risk, management, and cost. Ranges in inches (12"-15") are annual precipitation and (or) represent availability of winter feed resources (W1, 1999).

Summary and conclusions: G x E exist in beef cattle. It is important to understand this interaction to select cattle that are adapted and fit specific environments and production systems. The ability to detect G x E has increased with genomic approaches and information from spatial databases providing opportunity to study and develop genetic improvement tools for adaptability.

References:

- Burns, W. C., M. Koger, W. T. Butts, O. F. Pahnish, and R. L. Blackwell. 1979. Genotype by environment interaction in Hereford cattle: II. Birth and weaning traits. *J. Animal Sci.* 49:403-409.
- Dillon, J.A., K. R. Stackhouse-Lawson, G. J. Thoma, S. A. Gunter, C. A. Rotz, E. Kebreab, D. G. Riley, L. O. Tedeschi, J. Villalba, F. Mitloehner, A. N. Hristov, S. L. Archibeque, J. P. Ritten, and N. D. Mueller. 2021. Current state of enteric methane and the carbon footprint of beef and dairy cattle in the United States. *Anim. Front.* 11:57-68.
- Hammack, S. P. 2009. Texas adapted genetic strategies for beef cattle II: genetic-environmental interaction. *Tex. A&M AgriLife Extension E-187.*
- Krehbiel, B. C., M. G. Thomas, C. S. Wilson, S. E. Speidel, R. M. Enns, S. R. Paiva, and H. D. Blackburn. 2019. Evaluation of genetic structure across U.S. climate zones using prominent AI sire of Red Angus cattle. *Livst. Sci.* 225:26-31.
- Rowan, T. N., H. J. Durbin, C. M. Seabury, R. D. Schnabel, and J. E. Decker. 2021. Powerful detection of polygenic selection and evidence of environmental adaptation in US beef cattle. *PLoS Genet.* 16:e1009652.
- Winder, J. A., B. J. Rankin, and C. C. Bailey. 1992. Maternal performance of Hereford, Brangus, and reciprocal crossbred cows under semidesert conditions. *J. Anim. Sci.* 70:1032-1038.
- W1. 1999. Crossbred beef cattle for western range environments. 2nd ed. TB-99-1. For e-copy, contact: milt.thomas@colostate.edu or mark.enns@colostate.edu.

Figure 2: Matching biological type (weight and milk) to range environment, with associated risk, management and cost



Toward Climate Positive Beef: An Analysis of Proposed Actions — J.E. Sawyer, PhD, East Foundation and King Ranch® Institute for Ranch Management

Synopsis

Climate positive beef systems are feasible. Current systems may currently be climate neutral to positive in aggregate, depending on system boundaries and emissions metrics utilized. The use of more current metrics of warming equivalence for methane (GWP*) reduces estimated emissions intensity of beef (per unit of carcass weight) by approximately 50% from prior estimates. Accomplishment of small methane emissions reductions, through direct mitigation or improved methods of estimating current emissions, in combination with modest increases in land-based C uptake, can result in a beef warming footprint that is climate positive before 2040. Inclusion of current estimated net carbon uptake by grazing lands inside the system boundary results in a positive climate footprint beginning in the 1980s.

Introduction

Utilization of forages and feedstuffs of no or low value for direct human consumption to produce high-nutrition value protein and numerous co-products is an important function of beef production systems in the US. This feature allows utilization of marginal lands and those unsuited for cultivation as a significant component of US beef production systems, and the management of lands associated with beef production generates significant additional ecosystem services. A consequence of the conversion of low-value (for humans) feedstuffs through ruminal fermentation is the generation of methane as a byproduct. These, and other emissions from production, are often cited as negative to the climate.

Background

Climate neutral production systems are those which do not increase global temperature change, and may serve to offset such effects from other systems (becoming 'climate-positive'). Currently, key drivers of global temperature change are believed to be greenhouse gases and other anthropogenic forcing agents; therefore, climate positive systems are those which internally mitigate such emissions to result in a neutral or negative (cooling) effect. The concentration of these agents in the atmosphere, and their resultant effects on radiative transmission, are considered effectors of global temperature change (Myrhe et al., 2013).

Different GHG exhibit different atmospheric behaviors, both in atmospheric lifetime and in the unit magnitude of radiative forcing effects which drive temperature effects. For very long-lived forcing agents (i.e., those which persist in the atmosphere for long periods of time, centuries to millennia), emissions may be a reasonable indicator of change in atmospheric burden when removal rates are relatively constant. However, for short-lived climate forcing agents (SLCF), the agent degrades in the atmosphere over relatively short time horizons (less than 100 yr). Emission rates are therefore not reliable indicators of atmospheric accumulation; at constant emissions, atmospheric concentration establishes an equilibrium rather than a continuous accumulation. Methane is a key example of a SLCF, and metrics that account for the relative change in emissions (such as GWP*; Allen et al., 2018; Cain et al., 2019; Collins et

al., 2019) more effectively describe its effects on temperature (compared to GWP100, e.g.). The distinction in behavior of forcing agents is important, as it creates a point of departure between the terms 'climate-neutral (positive)' and 'carbon-neutral (positive)'. For a SLCF, it is not necessary for emissions to be zero in order to achieve atmospheric and temperature neutrality (Allen et al., 2018; Pierrehumbert, 2014); therefore, there may be 'carbon emissions' while 'climate neutrality' is achieved. Therefore, the terms 'carbon-neutral' and 'climate neutral' are not synonymous. For this reason that the term 'CO₂ warming equivalent' has been suggested to replace direct emissions-based radiative forcing equivalence metrics for SLCF.

Emissions of GHG result from many activities necessary to sustain beef production, and use of resources that result in emissions often serve to increase the overall output (feeding more people) and reduce the intensity (fewer resources per unit of product) of emissions. In beef production systems (to the farm gate) over 50% of the CO₂-equivalent emissions result from methane generated through enteric fermentation and manure management, with the balance primarily representing direct and indirect CO₂ emissions from energy use in generation of inputs and production activities (53%; Asem-Hiablie et al., 2019). This represents both an outcome of conversion of human-inedible feedstuffs into high-quality protein (Baber et al., 2019) and an energetic loss to feeding systems. Therefore, reducing methane emissions may be a high-leverage objective that improves production efficiency, reduces emissions intensity and (more importantly) warming contributions, and moves beef systems toward climate positivity.

Even as emissions are mitigated, opportunities to remove GHG from the atmosphere within the production system may also exist; when such removals are part of a process within the production system, they serve to move the product toward climate positivity (i.e., reduce its 'climate footprint'; ISO 14067:2018). When such removals occur outside the boundaries of a production system, they are considered as offsets or 'negative emissions' that do not directly reduce the climate impact (footprint) of a discrete product, but may be deployed to counteract those impacts. In US beef production systems, grazing by cattle is a significant land use; grazing or land management practices that are a component of beef production systems can serve as a sink for atmospheric GHG, creating a second leverage point to move toward climate positive beef production.

Objective

The primary objective of this analysis is to evaluate the potential of achieving stated goals to result in climate neutrality or positivity, based on achieving 'net-zero' or better warming potential equivalent emissions. Secondary objectives include: 1) estimation of the historical contribution of US and global beef cattle population expansion to atmospheric methane burden, as an indicator of warming contribution; and 2) estimation of the 'warming intensity' of beef (carcass weight basis) resulting from achievement of stated goals.

Approach

Beef Cattle Inventory

Beef cattle inventory values were taken from annual January 1 inventory estimates reported by the National Agricultural Statistics Service (USDA-NASS). This data series extends from 1867-2020 for all cattle and the subclass of dairy cows. A shorter reference data set (~40 years) was used to estimate the annual inventory of dairy replacement heifers. Dairy cows and dairy replacement heifer inventories were subtracted from the total cattle inventory to estimate the total number of cattle used for beef production. Beef cattle inventory was further refined by class (cows, weaned calves/stockers, feedlot, replacement heifers, bulls) and methane emissions were estimated in alignment with US-EPA greenhouse gas inventory reporting methods defined by the Intergovernmental Panel on Climate Change (IPCC). This value formed the basis of emissions projections in the range of years 1920 through 2020. Future inventory levels were projected to remain, on average, near current levels, with cyclic variation patterned on observed cyclicity over the last 45 years. This allows the direct assessment of the effects of achieving stated goals on target outcomes, without confounding effects of inventory dynamics.

Emissions Estimation

Emissions and warming potential were estimated based on methane (as the object of the mitigation goal) and non-methane CO₂ equivalents. Methane emissions were estimated on an inventory basis, using a Tier 2 approach (IPCC, 2006). Currently the US EPA GHG inventory report uses this Tier 2 method to account for differences among subclasses and provide (in principle) a more granular view of sector level emissions within the livestock population.

Non-methane emissions were predicted from results of Asem-Hiablíe et al. (2019), which provided an LCA-based total GHG emissions value for US beef on a carcass weight basis. Their results were disaggregated to estimate methane- and non-methane contributions to the total emissions footprint, and the proportion derived from non-methane emissions were estimated. In their study, emissions are reported as GWP100 based CO₂ equivalents, using a GWP100 value of 25 (IPCC, 2006) to weight methane emissions. An adjustment for this factor was made, such that non-CH₄ GHG emissions (inclusive) could be estimated as a direct function of total inventory.

Greenhouse Gas Equivalence

Non-GHG emissions were expressed as kg of CO₂ equivalence during estimation and were not adjusted further.

Methane emissions (kg) were adjusted to CO₂ equivalents using 2 methods. First, to maintain correspondence with IPCC reports and other reports using IPCC equivalence calculations, a value of 28 units CO₂ equivalence per unit of methane was utilized to express methane emissions as GWP100 CO₂ equivalents (Myrhe et al., 2013). It is notable that current US EPA reports utilize a GWP100 value of 25 (IPCC, 2006; Forster et al., 2007). Differences in the selected equivalence factor can be a source of discrepancy among reports and LCA analyses; these should be evaluated whenever emissions estimates are compared. In this report, emissions on this basis will be designated as GWP100 and reported as kg of CO₂ equivalents.

Because GWP100 and other forcing-equivalent based

conversion factors do not effectively reflect the effects of SLCF (various reports), methane emission equivalence was also estimated using GWP* methods according to Cain et al. (2019) and Lynch et al. (2020). The GWP* metric uses a GWP100 factor in its calculation to maintain correspondence with (and allow conversion of) missions estimated as GWP100; the GWP100 value of 28 was maintained in the GWP* calculation for this report. GWP* was calculated as:

$$GWP^* = \left(r \times \frac{\Delta E_{slcf}}{\Delta t} \times H + s \times E_{slcf} \right) \times GWP_{100}$$

The time series of population and resultant annual estimates of CH₄ emissions were used to estimate GWP*, fully accounting for inventory (and therefore emissions rate) dynamics. In this report, GWP* values will be reported as kg of GWP* warming equivalents or w.e., to maintain distinction from the GWP100 values.

Land-based Carbon Sequestration

The objective of this analysis was to determine if mitigation pathways based on land-based carbon accumulation were feasible, and their contribution toward climate positive beef. Explicit land-based removals were included beginning in year 2021; uptake of C was converted to CO₂ equivalence by molar mass and treated as a direct removal of CO₂-equivalent emissions, internal to the production system, within each year. This evaluation indicates the efficacy of goal achievement toward the larger objective of climate neutrality (positivity). Carbon mass goals were expressed in terms of C or CO₂ storage per unit of land area, and compared to reported values to provide a feasibility assessment (i.e., is the goal attainable).

This first stage analysis implies only 'additionality' of C sequestration, without consideration of current internal removals. A subsequent analysis was performed (as a pro forma) to estimate current internal removals; these are treated as constant throughout time, based on current estimates of US grazingland area and observed carbon flux from rangeland in the western half of the US (Svejcar et al., 2008). This approach is likely a conservative estimate of historical values, due to decreases in grassland area over time and the relatively lower C uptake of arid and semi-arid rangelands which dominate the flux estimates in the referenced study. Alternate outcomes, considering these current internal removals as direct reductions in net emissions, were estimated as above.

Results

'Bottom-up' GHG inventory methods are all dependent, ultimately, on the number of emitting units. Therefore, the dynamics of the US cattle population are an important component of any evaluation of goals associated with GHG emissions. Figure 1 includes the reported total beef cattle inventory from 1920 through 2020. Following peak cattle inventory in 1975, US beef cattle inventory declined cyclically. Over the last 15 years, population has stabilized although cyclical oscillations in population continue and are likely to do so, while the trend in population is relatively flat over that period.

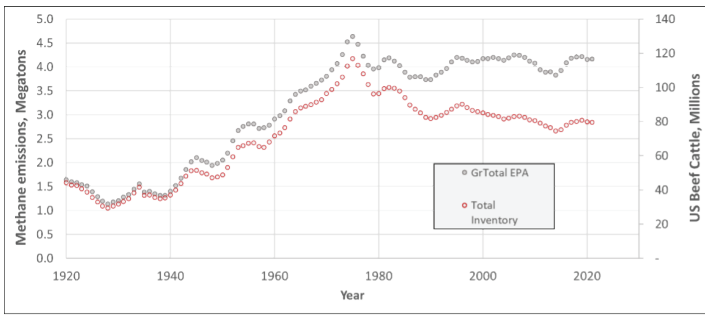


Figure 1. US population, beef cattle inventory, and beef production.

Methane, on a unit basis, generates more radiative forcing than carbon dioxide. Therefore, reductions in methane emissions are viewed as ‘more effective’ at mitigating temperature effects than similar mass reductions in CO₂. In an effort to create comparisons among greenhouse gas emissions effects in common units, emissions values are transformed. The most common transformation is the global warming potential at 100 years (GWP100), which is a direct multiple of emissions and therefore does not account for atmospheric removal of methane, resulting in overstatements of the temperature effects of cumulative methane emissions over time (Allen et al., 2018). An alternate transformation, GWP*, is based on the change in emissions over time rather than direct emissions, and more accurately reflects the behavior of methane in the atmosphere (Cain et al., 2019). Both metrics are expressed as CO₂ equivalents, and both were estimated for this analysis, but GWP* is used for goal assessment (Fig. 2).

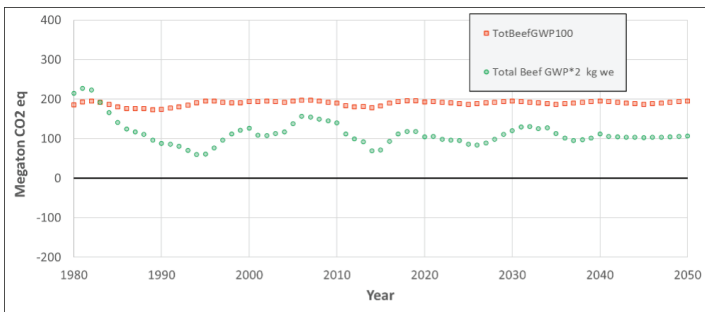


Figure 2. Methane emissions from US beef cattle, 1980-2050 (projected), expressed as GWP100 or GWP* equivalents.

Mitigation strategies that result in annual reductions of methane emissions by 0.4% or 1.5% per year were evaluated (Fig. 3). While a reduction of 0.4% annually is sufficient to result in neutrality of methane emissions alone, this offset is not sufficient to obviate the entirety of non-methane emissions in the production system, most of which are generated in the production of inputs, not directly by beef producers (and as a result are not affected by the beef sector goals in this analysis). Mitigation strategies that combine to achieve 1.5% annual reductions, because GWP* can take on negative values, are sufficient to fully offset the non-methane element, and could achieve warming neutrality by the mid 2030’s.

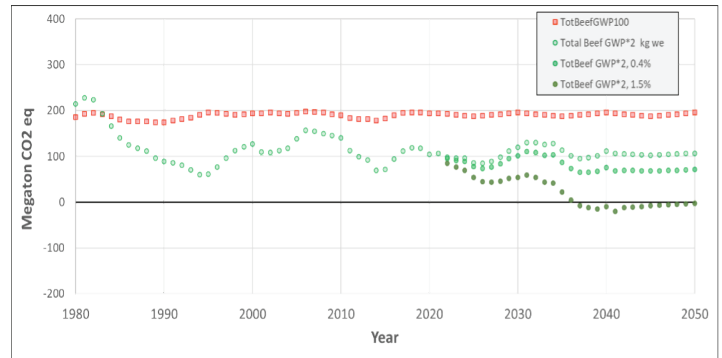


Figure 3. Total emissions from beef production systems, assuming business as usual, a 0.4% or a 1.5% annual reduction in methane emissions, and expressed as GWP* warming equivalents. Unmitigated emissions expressed as GWP100 equivalents are displayed for reference.

Other removals are available in the system. Mitigation resulting from increase carbon uptake in grazinglands used for beef production by 25 kg C/acre or 45 kg C/acre annually result in substantial generation of additional insets (Fig. 4). As observed with methane, the more modest increase in land-based C assimilation is not alone sufficient to result in climate neutrality, but the more ambitious assimilation target offsets all other warming equivalent emissions from beef production and achieves neutrality soon after implementation. These target values are applied across all US grazinglands; while it is unlikely that such uniform change is possible, the amounts are modest enough that they are likely to be achievable. For example, if 75 kg of additional C were assimilated on 1/3 of grazing lands, then the modest goal could be achieved. This is approximately equal to the 0.2 tonnes of CO₂ equivalent uptake suggest by USDA in the COMET planner tool that results from managed grazing, even without consideration of other available practices.

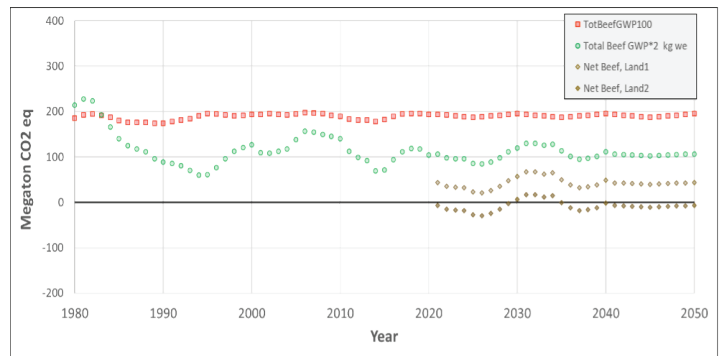


Figure 4. Total emissions from beef production systems, assuming business as usual, a 25 kg C/acre or a 45 kg C/acre annual increase in land-based carbon assimilation, when methane emissions are expressed as GWP* warming equivalents. Unmitigated emissions expressed as GWP100 equivalents are displayed for reference.

The evaluated mitigation pathways are not exclusive; strategies that could achieve the modest target reductions in methane emissions can be deployed simultaneously with those intended to increase land-based carbon assimilation (Fig. 5).

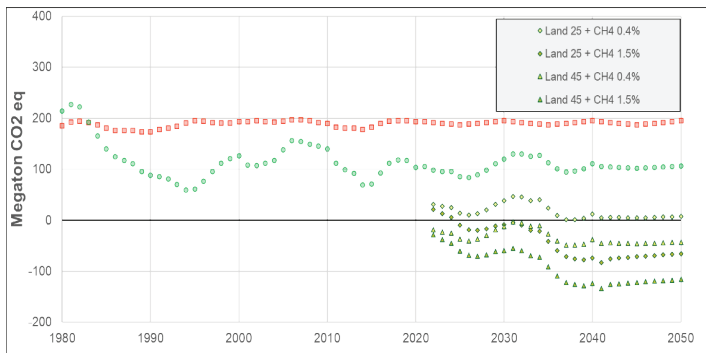


Figure 5. Total emissions from beef production systems, combining methane mitigation and land-based carbon assimilation strategies when methane emissions are expressed as GWP* warming equivalents. Unmitigated emissions expressed as GWP100 equivalents are displayed for reference.

Combining the two most modest strategies (0.4% annual reduction in methane and 25 kg C/acre land-based assimilation) approach neutrality in the near term, and achieve it by 2040. Combinations which include at least one (or both) of the more ambitious strategies result in climate positive beef production over the same time frame. These targets are well within estimates of feasible mitigation using current approaches. For example, commonly applied feed amendments or diet management tools can reduce methane 5 to 30%; genetic selection for methane emissions has been estimated to result in a population level improvement of 0.4% per year; effective range management practices have been demonstrated that can increase soil assimilation 30 to 300 kg/ac per year.

As presented above, the land-based carbon removal goals are treated as pure ‘additionality’. Additionality is a challenging quantitative concept suggesting that only outcomes above ‘what would have happened anyway’ be considered as offsets or removals (external or internal) to systems of production. However, in land-based systems such as beef production, the management of grazing lands is inherent to the system, and uptake of carbon by these lands may be substantial based on the area allocated to this production. Average C flux on western US rangeland sites was estimated at 76 kg C, or 281 kg CO₂, per acre (Svejcar et al., 2008). Note that this accumulation rate is a mean estimated primarily from sites in the western half of the continental US on rangelands, and incorporates significant annual and regional variability. While further refinement of this value is needed, this value is defensible in aggregate, and illustrative. Importantly, when average land-based removal is considered in the beef system, net emissions of GHG from beef has been ‘climate positive’ since 1986 (Fig. 6).

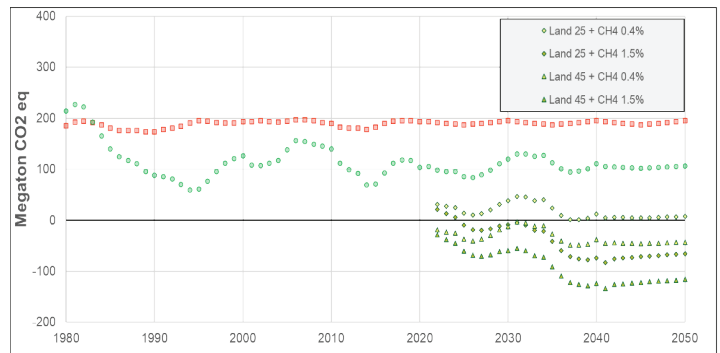


Figure 6. Total emissions from beef production systems, including an estimate of current land-based carbon assimilation (75 kg C/ac; Svejcar et al., 2008) when methane emissions are expressed as GWP* warming equivalents. Unmitigated emissions expressed as GWP100 equivalents are displayed for reference.

These internal removals are not typically accounted for in LCA of beef systems (Asem-Hiablie, 2019), with a few exceptions (Beauchemin et al., 2010; Pelletier et al., 2010; Stanley et al. 2018). Recently, a global evaluation of grassland systems indicates that North American grasslands are a net carbon sink, even after accounting for livestock production and wild ungulate population changes (Chang et al., 2021). Assignment of GHG removals by processes internal to the production system is acceptable within an LCA for greenhouse gas footprinting (ISO, 2018) but may not then be counted as an offset to an emission external to the system (to avoid double counting). It might be a more effective strategy to consider the ‘business as usual’ removals from land management as internal to production, and to consider ‘additionality’ through achievement of land management goals separately, such that they might become assets in an offset marketplace. Accounting for the internal and external nature of removals is technically challenging, and further research and evaluation of this topic is an important component of the overall role of beef production systems and their management in climate mitigation policies.

Conclusions

The total magnitude of US beef system methane contribution to atmospheric methane accumulation (and thus warming) is very small, and statistically is likely insignificant. Efforts to further illustrate the relative impacts of ruminant methane on global climate should be illustrated; the false logic that ‘methane is a greenhouse gas, cattle produce it, therefore cattle cause global warming’ can be misleading and cause creation of policy that is misaligned from effective outcomes.

Expressing methane emissions in units more closely aligned with their impact on warming (GWP* rather than GWP100) results in reduced estimates of the GHG impact of beef production. Importantly, because GWP* is dependent on changes in emissions rates over time, a stable population with constant emissions will result in ongoing constant emissions that are 25% of GWP100 expressed emissions.

Modest reductions in methane emissions estimates, through management or improved measurement of current emissions levels, can result in climate neutrality. Combining these strategies with land management that results in very modest increases in carbon assimilation provide for several pathways that can achieve ‘climate positive beef’ in the US system within decadal time horizons.

Considering current land-based C uptake by grazinglands utilized in beef production at the national aggregate scale as an internal removal should be evaluated. Under preliminary analysis, including land uptake (not the 'additional' uptake implied by the land based assimilation strategies above) suggests that the US beef system has been climate positive since 1986, without other mitigation. Under that scenario, reductions in emissions and achievement of additional carbon sequestration in US grazinglands represent a substantial 'credit' to beef systems.

Climate positive beef systems are not infeasible, and current systems may already be climate neutral to positive in aggregate. Significant departures from previous analyses include the use of more current metrics of warming equivalence for short-lived climate forcing agents (especially methane), and inclusion of grazinglands and their carbon uptake inside the system boundary.

Literature Cited

- Allen, Myles R., Keith P. Shine, Jan S. Fuglestedt, Richard J. Millar, Michelle Cain, David J. Frame and Adrian H. Macey. 2018. A solution to the misrepresentations of CO₂-equivalent emissions of short-lived climate pollutants under ambitious mitigation. *npj Climate and Atmospheric Science* (2018) 1:16. <https://doi.org/10.1038/s41612-018-0026-8>
- Baber, J, JE Sawyer, and TA Wickersham. 2018. Estimation of human-edible protein conversion efficiency, net protein contribution, and enteric methane production from beef production in the United States. *Translational Animal Science* 2:439-450. <https://doi.org/10.1093/tas/txy086>
- Cain, Michelle, John Lynch, Myles R. Allen, Jan S. Fuglestedt, David J. Frame and Adrian H. Macey. 2019. Improved calculation of warming-equivalent emissions for short-lived climate pollutants. *npj Climate and Atmospheric Science* (2019) 2:29. <https://doi.org/10.1038/s41612-019-0086-4>
- Chang, J., Ciais, P., Gasser, T. et al. 2021. Climate warming from managed grasslands cancels the cooling effect of carbon sinks in sparsely grazed and natural grasslands. *Nature Communications* 12:118. <https://doi.org/10.1038/s41467-020-20406-7>
- Collins, William J., David J Frame, Jan S Fuglestedt and Keith P Shine. 2020. Stable climate metrics for emissions of short and long-lived species—combining steps and pulses. *Environ. Res. Lett.* 15:024018. <https://doi.org/10.1088/1748-9326/ab6039>
- FAO. 2018. Food and Agriculture Organization of the United Nations. FAOSTAT Database. Rome, Italy: FAO. Retrieved 20 Oct 2020 from <http://faostat3.fao.org>
- Forster, P., V. Ramaswamy, P. Artaxo, T. Berntsen, R. Betts, D.W. Fahey, J. Haywood, J. Lean, D.C. Lowe, G. Myhre, J. Nganga, R. Prinn, G. Raga, M. Schulz and R. Van Dorland, 2007. Changes in Atmospheric constituents and in Radiative Forcing. In: *Climate Change 2007: The Physical Science Basis. Contribution of Working Group I to the Fourth Assessment Report of the Intergovernmental Panel on Climate Change* [Solomon, S., D. Qin, M. Manning, Z. Chen, M. Marquis, K.B. Averyt, M. Tignor and H.L. Miller (eds.)]. Cambridge University Press, Cambridge, United Kingdom and New York, NY, USA.
- International Standards Organization. 2018. ISO 14067:2018 – Greenhouse gases – carbon footprint of products – Requirements and guidelines for quantification. Accessed 01/05/2021 <https://www.iso.org/obp/ui/#iso:std:iso:14067:ed-1:v1:en>
- IPCC. 2006. 2006 IPCC Guidelines for National Greenhouse Gas Inventories, Vol. 4: Agriculture, Forestry, and Other Land Use. Prepared by the National Greenhouse Gas Inventories Programme, Eggleston H.S., Buendia L., Miwa K., Ngara T. and Tanabe K. (eds). Published: IGES, Japan.
- K.A. Beauchemin, H. Henry Janzen, S.M. Little, T.A. McAllister, S.M. McGinn. 2010. Life cycle assessment of greenhouse gas emissions from beef production in western Canada: a case study. *Agric Syst* 103:371-379
- Myhre, G., D. Shindell, F.-M. Bréon, W. Collins, J. Fuglestedt, J. Huang, D. Koch, J.-F. Lamarque, D. Lee, B. Mendoza, T. Nakajima, A. Robock, G. Stephens, T. Takemura and H. Zhang, 2013: Anthropogenic and Natural Radiative Forcing. In: *Climate Change 2013: The Physical Science Basis. Contribution of Working Group I to the Fifth Assessment Report of the Intergovernmental Panel on Climate Change* [Stocker, T.F., D. Qin, G.-K. Plattner, M. Tignor, S.K. Allen, J. Boschung, A. Nauels, Y. Xia, V. Bex and P.M. Midgley (eds.)]. Cambridge University Press, Cambridge, United Kingdom and New York, NY, USA.
- Naik, V., A. Voulgarakis, A.M. Fiore, et al. 2013. Preindustrial to present-day changes in tropospheric hydroxyl radical and methane lifetime from the Atmospheric Chemistry and Climate Model Intercomparison Project (ACCMIP). *Atmospheric Chemistry and Physics*, 13(10) <https://doi.org/10.5194/acp-13-5277-2013>
- Pelletier, Nathan, Rich Pirog, Rebecca Rasmussen. 2010. Comparative life cycle environmental impacts of three beef production strategies in the Upper Midwestern United States. *Agricultural Systems* 103:380-389. <https://doi.org/10.1016/j.agsy.2010.03.009>
- Pierrehumbert, R.T. Short-lived climate pollution. 2014. *Annu. Rev. Earth Planet. Sci.* 2014. 42:341–79. [10.1146/annurev-earth-060313-054843](https://doi.org/10.1146/annurev-earth-060313-054843)
- Stanley, PL, JE Rowntree, DK Beede, MS DeLonge. 2018. Impacts of soil carbon sequestration on life cycle greenhouse gas emissions in Midwestern USA beef finishing systems. *Agric Systems* 162:249-258. <https://doi.org/10.1016/j.agsy.2018.02.003>
- Stevenson, DS, A Zhao, V Naik, FM O'Connor, S. Tilmes, G Zeng, LT Murray, WJ Collins, PT Griffiths, S Shim, LW Horowitz, LT Sentman, and L Emmons. 2020. Trends in global tropospheric hydroxyl radical and methane lifetime since 1850 from AerChemMIP. *Atmos. Chem. Phys.*, 20:12905–12920 <https://doi.org/10.5194/acp-20-12905-2020>
- Svejcar, T, R. Angell, JA Bradford, W Dugas, et al. 2008. Carbon fluxes on North American Rangelands. *Rangeland Ecol Manage* 61:465-474. <https://doi.org/10.2111/07-108.1>
- Zimmermann, P. H., Brenninkmeijer, C. A. M., Pozzer, A., Jöckel, P., Winterstein, F., Zahn, A., Houweling, S., and Lelieveld, J. 2020. Model simulations of atmospheric methane (1997–2016) and their evaluation using NOAA and AGAGE surface and IAGOS-CARIBIC aircraft observations, *Atmos. Chem. Phys.*, 20, 5787–5809, <https://doi.org/10.5194/acp-20-5787-2020>

BAKER/CUNDIFF ESSAY CONTEST WINNERS

High-impact Data Programs: A framework for expanded opportunities in genetic evaluation — Lane Giess, Colorado State University

INTRODUCTION

Genetic evaluations for beef cattle have evolved significantly in the United States (Golden et al. 2009), where now the information systems for genetic predictions have been bolstered by millions of phenotypes, pedigree, and genomic data points. These data are paramount to the development of robust genetic predictions that allow producers to make more informed selection decisions. Many data points are readily available and relatively easy to collect, inherently lending greater statistical power to their genetic predictions. However, for the performance traits where the data collection is difficult, time consuming or where no existing data collection structure has been clearly defined, these genetic predictions lack informative power and accuracy on young animals.

One of the key goals for genetic evaluations should be to explore the existing data structure of phenotypic records obtained from producers and partner organizations and develop a thorough understanding of possible opportunities for improved genetic prediction and new trait development. These opportunities are not limited to the use of indicator traits to better the genetic prediction of an economically relevant trait (Golden et al. 2000), but rather may include the use of by-product data and leveraging associated opportunities from existing data collection programs. This framework explores the use of high-impact data programs for existing and future genetic evaluations for performance traits in beef cattle.

HIGH-IMPACT DATA

High-impact data may be defined as the value placed on phenotypic information for which a genetic prediction suffers from a lack of quality inputs. An example of this is actual carcass phenotypes, where the genetic predictions for marbling, carcass weight, ribeye area, fat thickness, and tenderness suffer from a critical mass of data. Though ultrasound carcass data provides a satiable alternative to bolster carcass genetic predictions, this may be considered low value data due to sometimes poor genetic correlations of ultrasound carcass to actual carcass traits (AGI, 2013). Angus Genetics Incorporated (2013) reported correlation estimates for actual backfat to ultrasound backfat, actual marbling score to ultrasound marbling, actual ribeye area to ultrasound ribeye area, and carcass to yearling weight of 0.65, 0.71, 0.65, and 0.75 respectively. Few comparisons outside of structured studies have evaluated the correlation of ultrasound to actual carcass data, so evaluating the genetic correlation between ultrasound data and the genetic prediction provide additional insight. International Genetic Solutions (IGS) reports genetic correlation between ultrasound marbling and marbling EPD, ultrasound fat and fat EPD, ultrasound ribeye area and ribeye area EPD and post weaning gain and carcass weight as 0.77, 0.45, 0.52, 0.55 respectively (IGS, 2022).

The evaluation of what constitutes high-impact data may be debated among industry organizations, however for the purposes of this framework, those phenotypes reported on fewer than 20 percent of the animals enrolled in a given year are considered

high-impact data. In addition, traits that are currently being investigated within academic institutions and hold promise for future genetic prediction development may also be considered high-impact data as the need for critical mass is necessary. The process of evaluating new or novel high-impact data is outlined by Garrick et al. (2014a). The following are a sample of notable systems contributing opportunities for high-impact data collection.

Whole Herd Reporting

Inventory-based whole herd reporting (WHR) is a data program recommended by many industry organizations which provides a structure for the collection of whole contemporary group information on mature females and their offspring. Additionally, WHR provides added metrics on a range of economically relevant traits – primarily reproductive efficiencies and longevity (Hough and Ponder, 2001; Cammack et al., 2009), where stayability predictions see added benefit because the inventory system provides the culling and calving performance data needed for effective random regression modelling (Jamrozik et al. 2013).

The implementation of WHR programs amongst industry organizations vary, and the benefits depend upon how WHR is accepted among users. For example, some organizations require mandatory WHR from all users. While this forces every animal record enrolled in a breed registry to originate from whole and complete contemporary groups, this may include the added risk of inaccurate data reporting. The requirements of inventory reporting can be onerous to many cattle producers and rather than collect every data point required on every animal, they may opt to report inaccurate information to satisfy the system inventory reporting requirements.

Adversely, selective WHR systems provide producers the option to register an entire inventory as well as selective enrollments. This method may more appropriately capture quality data points from invested breeders yet continues to allow a portion of users the option to selectively report the animals they deem fit for registration. This disrupts the evaluation of whole contemporary group comparisons and loses the ability to capture a critical mass of fertility and longevity measures.

Regardless of implementation, WHR programs provide vast opportunities for new or improved genetic prediction. Giess et al. (2021) outlined how enrollment, productivity and disposal codes from the American Simmental Association were used in a logic-based system to generate heifer pregnancy (HPG) phenotypes. This implementation of what may usually be considered by-product information, provides added opportunity for the development of new genetic predictions or inherently less onerous data collection programs for producers. Table 1 contains a list of data points collected from WHR programs and existing or future uses for those records.

Table 1 suggests a small sampling of possibilities for the implementation of new or novel genetic predictions, some of which are standalone predictions, whereas others augment an

Table 1: A sampling of proposed and existing uses for data collected from whole herd reporting programs.

Whole Herd Reporting Data	Existing Genetic Prediction Uses	Future Genetic Prediction Uses
Cow Inventory	Whole contemporary group evaluation: Stayability Heifer pregnancy Maternal calving ease Maternal weaning weight Maternal effects for existing predictions Mature weight	Sustained cow fertility Maternal effects for existing predictions Stayability to older ages Gestation Length Maintenance cost
Calf Records	Whole contemporary group evaluation: Growth Maternal calving ease Milk Average daily gain	Pre-weaning survival Post-weaning survival Days to weaning
Enrollment/Productivity/Disposal Codes	Adjustment of cow contemporary group	Heifer pregnancy In-utero survival Respiratory health Udder quality Docility Maintenance Lifetime value Augment existing predictions: Feet and legs Stayability

young bulls from different AI groups and years (Foulley et al. 1982). In recent years the prevalence of these enterprises have dwindled due to difficulty of collecting data, high costs, and the rapid acceptance of genomic capabilities as a substitute. Despite the lack of structured progeny testing sites, these systems provide a vast amount of unbiased data for genetic prediction, and notably, rapidly increase the accuracy of prediction on young sires through sheer amounts of data collection.

The present framework is not meant to justify structured progeny testing, but rather explore its uses when coupled with WHR and when such progeny testing programs demand emphasis for rare and meaningful data collection. It is difficult to justify the cost of paying producers to collect weight data since many producers are well attuned to collecting those measures, yet for genetic evaluations suffering from a lack of phenotypes in a given trait, structured sire progeny testing may be a viable option. Presently, many of the existing sire progeny testing programs implemented among industry organizations put emphasis on the collection of actual carcass data. As described earlier, carcass data is a valuable phenotype to pursue due to its difficulty of collection and lack of substantial indicator metrics.

The inputs necessitated from personnel, costs, and time associated with the management of structured sire progeny tests provide added justification to expand upon data collection emphasis and pursue additional opportunities. While animals with actual carcass data reflects less than approximately 3% of annual enrollments for most industry organizations (ASA Annual Report, 2022), even fewer are animals with actual carcass data and genomic information. Structured sire progeny tests willing to add the additional cost of genotyping the progeny enrolled in the program may provide increased value to the overall genetic evaluation. It's clear the value of obtaining critical mass of phenotypes on animals with genomic markers increases the efficacy of each genomic panel as well as increases the relative accuracy of non-genotyped individuals (Garrick, D. J. 2011).

Carcass performance is closely tied to economic success, and thus emphasis should also be placed on trait complexes influencing the amount of retail product being produced. One area of opportunity is to address the consistent increase of feedlot death over the past 20 years. Figure 1 shows the number of feedlot deaths annually since 2000 (USDA, 2022).

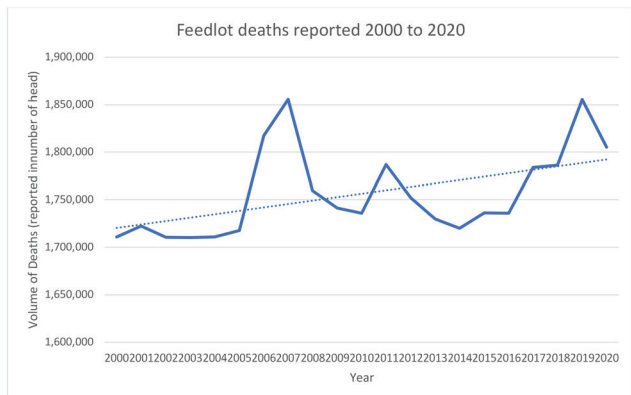
There is developing evidence, suggesting bovine congestive heart failure (BCHF) in late-stage feedlot cattle may be heritable and the risk of late-stage feedlot death might be improved through genetic selection (Kukor et al. 2021). Specific markers have been investigated for association with BCHF where ARRDC3 and NFIA variants showed small yet significant association with the trait (Heaton et al. 2019; Heaton et al. 2022). Implementation of these markers in traditional genetic evaluation systems should be done cautiously, as the selection for genetically superior animals using only genomic indicators may prove ineffective without critical mass of phenotypes and pedigree linkages available.

existing prediction model improvement. In the case of Stayability, where the realized phenotype is measured in multiple years or progeny (Martinez et al. 2005; Brigham et al. 2007; Jamrozik et al. 2013), optimization for the genetic prediction is extremely consequential due to the high economic importance of the trait (Garrick, D. 2006; Garcia et al. 2015).

Structured Sire Progeny Testing

Structured sire progeny testing programs is the practice of placing registered sires in several cooperating herds with the sole responsibility of collecting and reporting data on progeny. This is no novel practice within the beef industry and the benefits of data obtained from progeny clearly outweigh the value of an animal's own phenotype (Robertson and Rendel, 1950). This practice utilizes artificial insemination to distribute genetics quickly and cheaply to participating producers and leverages the use of proven reference sires to facilitate comparisons of

Figure 1: Graph of annual beef cattle feedlot death loss since 2000 – excluding calves



Young sire progeny tests provide an opportunity for data collection on heart and heart fat scores on animals with already important data collection practices in place. Establishing a connection between risk of feedlot death, pulmonary arterial pressure, heart score, carcass performance and the genomic association with all traits provides a valuable opportunity for breed organizations to invest in such programs.

Nondescript Cattle Populations

Traditional genetic evaluation has been predicated upon the use of leveraging sire-identified breeding animals and associated data on themselves and their progeny to build genetic predictions. This practice was improved with the use of genomic markers incorporated into existing predictions and alongside non-genotyped animals (Garrick et al. 2014b).

Whereas genetic predictions are designed to predict merit for economically relevant traits in commercial cattle production, most of the data being submitted to industry organizations are collected on breeding stock, who are rarely exposed to the same level of rigor and selection found in the commercial industry (Garrick and Golden 2009). This is primarily found in feeding cattle, where few seedstock producers retain ownership and slaughter their own calves, and if they do, the resulting effort provides data limited to animals deemed unsuitable for breeding. This point is augmented by the fact nucleus breeders actively accelerate genetic progress by reducing generation interval. While beneficial for increasing the rate of genetic progress, this practice actively eliminates opportunity for data to be collected mature females including; stayability, fertility and mature weight.

These tradeoffs distinguish an inherent weakness in existing genetic evaluations where commercial animals are not represented in the genetic predictions for which commercial producers are selecting their breeding animals.

Historically, the viability of using commercial populations of cattle for genetic prediction was not possible since sire-identification was not widespread. However, determining relatedness of commercial animals is possible through the use of genomic parent verification. In populations where large numbers of parent animals are genotyped this can be accomplished, though perhaps not cost-effectively. Relatedness in the absence of any pedigree information is supported (Tapio et al. 2010) and developing linkages between non-pedigreed and sire-identified populations provide opportunity for rare data collection.

Individually genomically sampling animals may prove to be too costly to be implemented at a large enough scale to truly benefit genetic prediction. The prospect of genomic pooling provides an innovative opportunity to cut costs drastically while facilitating large volumes of data collection on commercial populations (Reverter et al. 2016). Genotyping technology is in its infancy among commercial producers, yet readily available and implemented in a growing population of nucleus breeders. Should genomic pooling provide the necessary catalyst to link commercial data to seedstock populations, the industry will benefit from more powerful and unbiased predictions.

These commercial populations provide the greatest opportunity for the collection of rare and meaningful data already discussed. Developing genomic association with impactful traits from non-descript populations has shown some merit in the absence

of pedigree information. However, for the most effective genetic tools, the use of robust traditional genetic evaluation is more appropriate. Investigation into opportunities for the evaluation of genomically-sampled non-descript cattle alongside traditional registered populations may prove useful, if viable.

Structure for High-Impact Data Programs

As described in Garrick et al. (2011), phenotyping is now the limiting factor in expanding the offering of traits routinely recorded in genetic evaluation systems. Small breed registry's may not have the resources nor technical ability to greatly modify their genetic evaluation and will suffer from the lack of high-impact data programs funneling rare and meaningful phenotypes into their databases. It is with this in mind the necessity of collaboration among industry organizations provides an opportunity for enterprises to share resources and implement shared high-impact data programs.

As the opportunities for high-impact data programs are endless, beef cattle registry services and industry organizations should develop a protocol for evaluating their existing genetic evaluation services and consider unique solutions to build in added statistical power to predictions with rare or novel data points. The development of high-impact data programs may facilitate the mass accumulation of desirable data points. The following structure provides a starting point to evaluate the use of high-impact data programs among industry organizations.

1. Critically evaluate all existing predictions and data influences implemented in the genetic evaluation.
 - a. Take into consideration:
 - i. Average accuracy values
 - ii. Percentage of phenotypes/genotypes reported to animals enrolled annually
 - iii. Percentage of animals genotyped with phenotypes
 - iv. Genomic progeny equivalents
2. Critically evaluate all existing data collection initiatives and programs offered to users of the genetic evaluation.
 - a. Are existing data programs high impact?
 - b. Do the existing data programs further the mission and goal of the organization?
3. Evaluate the merit and cost of implementing a high-impact data program for users of the genetic evaluation.
 - a. Take into consideration:
 - i. Cost of data collection
 1. Phenotype subsidy
 2. Genotype subsidy
 - ii. Volume of participants
 - iii. Staff management and travel
4. Clearly identify goals for which phenotypes, genotypes and research traits you wish to be emphasized.
 - a. Take into consideration:
 - i. Weaknesses in the genetic evaluation
 1. Percentage of phenotypes/genotypes reported to animals enrolled annually
 2. Average accuracy values for traits
5. Survey users to determine the ideal demographic and isolate candidate herds or populations to include in the proposed high-impact data program.
 - a. Identify the number of participants
 - i. Size of cow herd
 - b. Familiarity with data collection
 - c. Education of unfamiliar trait collection
6. Develop protocol and operating policy to set parameters for data collection and facilitate the success of the high-impact data collection program.
7. Implement the high-impact data program with the intent to review and modify as needed.

Conclusion

Genetic evaluations primarily focus on the development of economically relevant traits which allow producers to actively select for improvement in areas of their breeding program directly affecting their bottom-line. While these predictions are paramount to the success of the beef business, a special emphasis on the quality of prediction should also be taken into consideration. The absence of a critical evaluation and validation of existing predictions and lack of well-defined goals in genetic evaluation systems results in lost opportunity to place special emphasis for creative solutions. It is with this outlined framework, that genetic evaluations may start to evaluate their current data programs and how extra information may be captured for relevant traits.

However, as industry genetic evaluations continue to scale in volume with admixed populations, there is a need to fuel specific trait predictions with a higher volume of quality phenotypes, genotypes and associated indicator traits. Research and development efforts into novel traits plays a critical role in improving these evaluations, through understanding emerging trait complexes and correlated inputs. High-impact data programs provide a nexus of data collection opportunities where rare and meaningful data points can be accumulated on whole contemporary groups.

By building a framework for evaluating the merit of existing genetic predictions and developing creative and unique data programs to collect effective indicator traits, genomic information and research inputs it is possible to build a more interconnected and powerful genetic evaluation for beef cattle.

Literature Cited:

AGI. 2013. FAQ – Ultrasound vs genomic data vs actual carcass data. https://www.cuplab.com/Files/content/ultrasound_FAQ_1-4-18.pdf (Accessed April 11, 2022)

ASA Annual Report. 2022. American Simmental Association Annual Report. https://issuu.com/asapublications/docs/annual_report_2021 (Accessed April 12, 2022)

Brigham, B. W., S. E. Speidel, R. M. Enns, and D. J. Garrick. 2007. Stayability to alternate ages. *Western Section Proceedings*. Vol 58:27-30

Foulley, J. L., L. R. Schaeffer, H. Song, and J. W. Wilton. 1982. Progeny group size in an organized progeny test program of AI beef bulls using reference sires. *Can. J. Anim. Sci* 63.1:17-26

Garcia, J., D. Anderson, A. Herring, and D. Riley. 2015. Economic analysis selecting for cow longevity. *Southern Ag. Econ. Assoc.* 2015 Annual Meeting. No. 1375-2016-109490.

Garrick, D. J. 2006. Evaluation, interpretation, and relevance of Stayability in beef cattle genetic improvement. *J. Anim. Sci.* 84(Suppl 2):50

Garrick, D. J. 2011. The nature, scope and impact of genomic prediction in beef cattle in the United States. *Gen. Sel. Evol.* 43:17 <http://www.gsejournal.org/content/43/1/17> (Accessed April 12, 2022)

Garrick, D. J., and B. L. Golden. 2014a. Producing and using genetic evaluations in the United States beef industry of today. *J. Anim. Sci.* 87(E. Suppl.):E11-E18. doi:10.2527/jas.2008-1431

Garrick, D. J., J. C. M. Dekkers, B. L. Golden, and R. L. Fernando. 2014b. Bayesian prediction combining genotyped and non-genotyped individuals. 10th World Congress on Genetics Applied to Livestock Production.

Giess, L. K., M. G. Thomas, S. E. Speidel, M. M. Culbertson, W. R. Shafer, S. C. McGuire, and R. M. Enns. 2021. Whole herd reporting data from the American Simmental Association as a data source for heifer pregnancy phenotypes. *Western Section Proceedings. T. Anim. Sci.* 5:S199-S203 doi.org/10.1093/tas/txab152

Golden, B. L., D. J. Garrick, S. Newman, and R. M. Enns. 2000. Economically relevant traits: A framework for the next generation of EPDs. *Proceedings of the 32nd Research Symposium and Annual Meeting of the Beef Improvement Federation.*

Golden, B. L., D. J. Garrick, and L. L. Benyshek. 2009. Milestones in beef cattle genetic evaluation. *J. Anim. Sci.* 87(E. Suppl.):E3-E10 doi: 10.2527/jas.2008-1430

Heaton M. P., A. S Bassett, K. J. Whitman, G. M. Krasfur, S. I. Lee, J. M Carlson, H. J Clark, H. R. Smith, M. C. Pelster, V. Basnayake, D. M. Grotelueschen, and B. L. Vander Ley. 2019. Evaluation of EPAS1 variants for association with bovine congestive heart failure. *F1000Research*, 8

Heaton, M. P., G. P. Harhay, A. S. Bassett, H. J. Clark, J. M. Carlson, E. E Jobman, H. R. Sadd, M. C. Pelster, A. M. Workman, L. A. Kuehn, T. S. Kalbfleisch, H. Piscatelli, M. Carrie, G. M. Krasfur, D. M. Grotelueschen, and B. L. Vander Ley. 2022. *F1000Research* 11: 385

IGS. M. M. Culbertson. 2022. Personal communication on genetic correlations used for carcass predictions within the IGS multi-breed genetic evaluation powered by BOLT. April 11, 2022.

Jamrozik J., S. McGrath. R. A. Kemp, and S. P. Miller. 2013. Estimates of genetic parameters for Stayability to consecutive calvings of Canadian Simmentals by random regression models. *J. Anim. Sci.* 91:3634-3643 doi:10.2527/jas2012-6126

Kukor, I. M., M. G. Thomas, R. M. Enns, T. Holt, S. E. Speidel, M. A. Cleveland. B. P. Holland, A. B. Word, and G. B. Ellis. 2021. Sire differences within heart and heart fat score in beef cattle. *Western Section Proceedings. T. Anim. Sci.* 5:S149-S153 <https://doi.org/10.1093/tas/txab147>

Martinez, G. E., R. M. Koch, L. V. Cundiff, K. E. Gregory, S. D. Kachman, and L. D. Van Vleck. 2005. Genetic parameters for stayability, stayability at calving, and stayability at weaning to specified ages for Hereford cows. *J. Anim. Sci.* 83:2033-2042.

Reverter, A., L. R. Porto-Neto, M. R. S. Fortes, R. McCulloch, R. E. Lyons, S. Moore, D. Nicol, J. Henshall, and S. A. Lehnert. Genomic analysis of tropical beef cattle fertility based on genotyping pools of Brahman cows with unknown pedigree. *J. Anim. Sci.* 94 doi:10.2527/jas2016-0675

Robertson, A., and J. M. Rendel. 1950. The use of progeny testing with artificial insemination in dairy cattle. *J. Genetics.* 50.1:21-31

Tapio, I., M. Tapio, M. Li. R. Popov. Z. Ivanova, and J. Kantanen. 2010. Estimation of relatedness among non-pedigreed Yakutian cryo-bank bulls using molecular data: implications for conservation and breed management. *Gen. Sel. Evo.* 42:28 <http://www.gsejournal.org/content/42/1/28> (Accessed April 12, 2022)

USDA. 2022. Economic Research Service – National Agricultural Statistics Service quickstats on cattle, (excl calves) - loss, death, measured in head since 2020. <https://quickstats.nass.usda.gov/> (Accessed April 10, 2022)

Effectiveness of a genome-wide association study using DNA pooling to make management decisions in feedlot cattle — Haleigh Prosser, West Texas A&M University

INTRODUCTION

Large-scale genetic testing of beef cattle to predict performance in a feedlot setting and carcass value at harvest would revolutionize cattle production. Advancements in genomic marker research for enhancing feeding, sorting, and buying strategies would improve management decisions for beef cattle producers, meat processors, and consumers alike. In short, DNA testing and the assembly of the bovine whole-genome sequence has permitted this area of research to progress, capable of allowing the allocation of DNA components, such as specified loci or polymorphisms, to production traits. By applying phenotype associations with genomic loci, patterns, and gene-level markers, insights into the biological mechanics and specific genetic components of a desirable or undesirable phenotype can be ascertained. These advancements may further breeding decisions to propagate or eliminate the presentation of production-critical alleles. However, DNA testing on an individual basis, while ideal, cannot be rationalized in a traditional feedlot setting due to cost and logistical setbacks within large-scale beef production systems. Therefore, we propose that combining individual DNA samples into pools based upon predetermined criteria, such as animal source, arrival date, and arrival weight, producers and feedlot managers can perform genetic testing for 10-30 animals at the cost of an individual test. If these pooled DNA tests can accurately predict feedlot performance, the economic advantage achieved by the genetic-based decisions could outweigh the cost of testing.

REVIEW OF LITERATURE

Introduction to DNA Testing and Applications

The development and promotion of deoxyribonucleic acid (DNA) testing continues to revolutionize the ability to predict animal performance, such as weight gain and feed efficiency. Consequently, new technology tends to drive research in applied genetics and DNA evaluation, and the needs exposed by past and current technologies influence the development of further technologies. DNA molecules, composed of a double helix of polynucleotide chains, contain a series of nucleotide bases that correspond to amino acids produced by an organism. This discovery indicated that the sequence of amino acids makes up an organism's genetic code (Alberts et al., 2002). However, prior to the sequencing of DNA, this genetic code remained a mystery to those attempting to pinpoint the markers and material passed from parents to offspring. Two processes were subsequently developed around 1976, the first being a chain terminator procedure introduced by Sanger and Coulson (1977) and the second a chemical cleavage procedure introduced by Maxam and Gilbert (1977), reduced the common one base per month decoding time to hundreds of bases in an afternoon (Shendure et al., 2017). Fluorescence in situ hybridization (FISH), the first technique to bridge cytogenetics and molecular genetics, utilized a fluorescent probe to identify these amino acid sequences to visualize chromosomes and further improved

the base generation speed (Durmaz et al., 2015). By 1982, data repositories contained over half a million bases and in just four years later contained nearly 10 million. In 1987, Applied Biosystems, Smith, and Hood marketed a Sanger sequencing machine, which could generate 1,000 bases per day utilizing fluorescence-based technologies (Shendure et al., 2017). Since completion of the Human Genome Project, in which researchers mapped and sequenced the entire human genome, technologies derived during the project allow even small labs to offer some form of genetic testing. This laboratory feasibility, in combination with the successful applications of genetic information to human science and medicine, sparked interest in the genomic information of livestock. Similar to human biomedical scientists, animal scientists insisted genetic analyses, completed by ever-changing technological breakthroughs, could provide insight into potential performance and health capabilities of animals; thus, the desire to map and sequence the genome of agriculturally important livestock species stimulated extensive animal genome research.

Bovine DNA Testing

Through the 1970s and early 1980s, the laboratory mouse was the only mammal with linkage maps and well-defined genetic markers. Morris Soller, in the late 1970s, began to champion an effort to map the genes responsible for traits in livestock, specifically traits with economic importance. Using these genetic maps, Soller suggested that marker-assisted selection could inform breeding decisions and enhance positive alleles in the population (Womack, 2012). At this time, however, the technologies to compile a whole-genome map of a livestock species did not exist. The discovery and application of short sequences of repeated DNA motifs known as short tandem repeats (STRs), at the time termed sequence tagged microsatellite sites (STMS), led Beckmann and Soller (1990) to propose genetic mapping of livestock; soon after the Beckmann and Soller proposal of STR application began a global search for quantitative trait loci (QTL) in livestock animals (Womack, 2012). The quest for QTL became more straightforward as single nucleotide polymorphisms (SNPs), variations at a single nucleotide position, replaced STRs as more efficient and accurate markers for QTL mapping.

Advancing computational technology attributable to the Human Genome Project, in combination with the introduction of SNPs and a scientific desire to genetically map agriculturally important livestock, inspired an abundance of bovine genome work. By 2012, more than 4,600 mapped cattle QTL represented more than 375 different traits in the Cattle QTL Database (Womack, 2012). The repeated use of FISH technology on the same chromosomes in early experiments ultimately resulted in the sequence of DNA on bovine chromosomes (Womack, 2012), and with the identification of marker genes taken from Fries et al. (1993) and the Texas Standard, whole-genome sequencing of bovines began to occur. A variety of bovine maps exist in the present, each possessing different types of markers of differing resolutions (Womack, 2012). The knowledge and technologies

that have been developed create the opportunities to use marker and linkage maps to pinpoint QTL information for economically important traits in livestock, just as Soller suggested over half a century ago. Application of QTL to traits continues to occur and advance as new maps, increased marker density, and further technology become more accessible and available.

Genome Wide Association Studies (GWAS)

Genome Wide Association Studies (GWAS) test many genetic variants to identify phenotype-genotype associations. GWAS can be used to associate genes with phenotypically-observed traits, diseases, and performance. GWAS applies statistical analysis to genotypic and phenotypic data to pinpoint associations and locate common SNPs between organisms sharing a specific phenotype. In animal research, genotyping takes place on DNA extracted from blood, tissue, or hair samples, most often. SNP data must then undergo a quality control step to eliminate SNPs that will not be utilized in the further analysis; using PLINK software, SNPs with high miss rates, low allele frequencies, and low Hardy-Weinberg equilibrium p-values are removed (Purcell et al., 2007). Many disease-based GWAS studies use PERMORY software (Pahl and Schäfer, 2010) to run random permutations and reveal significantly associated SNPs with a particular trait, eliminating potential false positives with a multiple test correction (Lee et al., 2015). Other GWAS studies, often those with multiple traits or more difficult phenotypes to define, utilize the R package rMVP (Yin et al., 2021) and the fixed and random model Circulating Probability Unification (FarmCPU) (Liu et al., 2016). The FarmCPU software controls for false positives and false negatives using the fixed and random effects in the model. These software programs return results displaying the SNPs that possess significant associations with the phenotypic trait or traits in questions. From those significant SNPs, further analyses to determine the genes closest to these SNPs must occur to select candidate genes. With knowledge of these candidate genes, one can continue to investigate their presence or absence in populations, comparing that information with the presence or absence of a specific phenotype.

Agricultural geneticists in the animal and plant science sectors notice the practicality of GWAS at an increasing rate; GWAS can associate economically essential performance traits of animals and crops, like meat quality in fed hogs (Gao et al., 2021), milk production in dairy cows (Jiang et al., 2019), and frost tolerance in wheat (Soleimani et al., 2022), for example, with significant genetic markers of interest, as well as identify significant risk markers for animal and crop disease. Understanding the genetic controls of these traits allows for more targeted animal selection, more efficient breeding practices, and faster genetic progress. Lee et al. (2015) used a high-density bovine SNP chip to identify Foot-and-Mouth Disease resistant loci in Holstein cattle; this GWAS research located 3 significant SNPs on a single chromosome. Similar to locating disease-resistant loci in dairy cattle, Xue et al. (2020) used GWAS methodologies to identify 14 significant backfat thickness-associated SNPs and 9 significant loin muscle depth-associated SNPs in a crossbred pig population; utilizing these SNPs to select candidate genes to continue research, genetic selection for those two economically important growth traits can occur. In addition to disease and growth traits, genetic markers of meat quality have also been evaluated using GWAS. Gao et al. (2021) completed GWAS analysis to

locate 32 SNPs associated with conductivity, intramuscular fat, marbling score, meat color, moisture, and pH of meat harvested from a crossbred commercial pig population. Using GWAS in agricultural research allows for the application of significant genetic occurrences to commonly observed and economically important phenotypes.

Pooled-Sample DNA Tests

Individual genotyping and individual GWAS studies each possess value in pinpointing the genetic association of a phenotype on an individual level. The practicality, specificity, and accuracy of individual genotype studies have value in many situations within the beef production industry. For example, detecting disease, predicting traits, and making decisions at an individual level can be economically justified in purebred, breed-association settings where DNA samples and genotyping must be completed for registration, breeding, and sale purposes. In crossbred and commercial populations, however, the cost of individually genotyping animals prohibits the process from occurring. Pooling these animals in the commercial sector (commercial ranches, feedlots, stocker operations, or processing plants) allows a relatively large amount of data analysis for the price of a single genomic test. Especially in groups with extreme phenotypes, like the unrelated animals in a commercial setting, pooling can actually provide a more accurate genetic evaluation (Keele et al., 2021). Additionally, allowing commercial operations to perform genetic evaluations using pooling results in the addition of commercial phenotypes to genetic evaluation (Abrams et al., 2021) and further advances the data availability of bovine genomics.

Much of the hesitation to perform genomic evaluations in the commercial sector occurs because of the sheer mass of data necessary to draw conclusions. Subsequently, commercial operations cannot rationalize the price of mass-sequencing hundreds or thousands of individuals. However, pooling DNA reduces this large number of samples to just a few pools of samples (Huang et al., 2010). Pool designs vary by experimental method and objective, but varying pooling techniques can take account of stratification, inter-loci interactions, and allow further haplotype analysis (Sham et al., 2002). Along with GWAS analysis, pool designs can cost- and time-efficiently associate genetic information possessed in a group with the general phenotype of the group. While some studies incorporate a two-pool design, especially those evaluating a basic allelic association, Sham et al. (2002) propose that large-scale studies should utilize a more-complex design with multiple pools. By reducing the number of individuals in each pool to create further pools and subsets or replicate pools, researchers can reduce the chance of error and provide additional opportunity to find marker-marker associations (Sham et al., 2002).

In theory, research using pools of DNA evaluates the genomic makeup of a set of individuals in the cost and time of an individual genomic evaluation. Experiments using pooled DNA can reduce costs by 90% compared to traditional individual genotyping (Keele et al., 2021). However, this break in cost must produce accurate results. In a DNA pooling project evaluating fertility in Holstein cattle, Huang et al. (2010) concluded the significant SNPs in the pooled DNA data also showed significance in individual genotypes, demonstrating the validity of selective

DNA pooling. Similarly, Macgregor et al. (2008) found that DNA pooling, while cost effective, can also capture greater than 80% of the power of individual genotyping in GWAS. If DNA pooling proves significantly accurate as compared to individual genotyping, pools can replace individuals in many studies that do not require individual genotypes.

While a seemingly optimal replacement to individual genome assessment, analyses utilizing pooled DNA must be evaluated and closely observed to assure errors involved in the pooling process do not obscure results. Pool construction error, one of the most common errors in pooling research, includes errors in DNA concentration, sample mixing, pipetting, extraction efficiency, and other often laboratory-based errors (Keele et al., 2021). For this reason, laboratory methodological procedures must be reliable, optimized, and quantitative to prevent technical biases (Sham et al., 2002). Unsurprisingly, reducing experimental error, most commonly in allele frequency estimation, increases the power in selective DNA pooling (Huang et al., 2010). Technical errors, like variation between allele contribution, occur most often because of these pool construction errors; some of this error can be eliminated with use of technical replicates, but replications reduce the cost efficiency of the pooling method (Huang et al., 2010; Keele et al., 2021). Hernandez-Rodriguez et al. (2017) suggest that creating these replicates forms equilibrated pools as well as increases data yield, possibly offsetting the additional cost. Additionally, linear regressions and analysis of variance can allow researchers to evaluate different variables as sources of technical variation (Hernandez-Rodriguez et al., 2017). Sampling error during pool construction arguably creates some of the most difficult decisions for researchers. Estimates must be made to compromise cost and accuracy, to ensure the most accurate data, and to see significant and accurate genetic observations. In theory, and as proved by Keele et al. (2021), based on the Dirichlet distribution, a larger planned animal contribution (thus, a smaller pool) results in larger pool construction error and more variation within pools. Huang et al. (2010), using similar rationality, recommend pooling as many individuals as possible, as allowed by the total mapping population size. While the optimal number for pool size depends largely on both total population and other experimental-specific factors, Barratt et al. (2002) suggest an optimal DNA pool consists of equal concentrations of DNA obtained from 50 individuals. The potential errors associated with pooled DNA samples and research create a need for error prevention and statistical interpretation, but the knowledge of errors common to pooled DNA projects allows researchers to prevent these errors from dismissing the accuracy of the results.

Alternatively, rather than traditional collection of DNA and pooling methodology, Abrams et al. (2021) demonstrated a process to construct pools prior to DNA extraction. One of the most attractive features of this practice is the ability to further reduce the price of genetic testing by requiring only one DNA extraction per pool. Additionally, this process also ensures equal representation of individuals within pools, creating a more uniform sample and more accurate results. The project utilized white blood cell counts to construct pools of samples; then, DNA and genotyping was completed using the one sample. Because white blood cells contain equal concentrations of DNA (Abrams et al., 2021), adding individual samples to the

pool by a certain count of white blood cells ensures an equal individual contribution of DNA. These equal concentrations eliminate the errors addressed above stemming from a variable individual contribution produced by a traditional fluorometric or photometric DNA quantification method. Abrams et al. (2021) found the use of white blood cell count to construct pools predicted the sample representation equally or more accurately than traditional pooling methods. The accuracy of this suggested pooling method only contributes to part of its appeal; the economic benefits of this process are outstanding. In a theoretical scenario containing 100 individuals, the individual genotyping would cost approximately \$2,800 and the genotyping of pooled DNA would cost approximately \$325 for the pool of 100 samples, but the genotyping of pooled DNA based on white blood cell counts would cost approximately \$228 for the pool of 100 samples (Abrams et al., 2021). Utilizing this alternative form of pooled DNA studies, research involving bovine genetics can potentially be both more cost effective and cheaper.

CONCLUSION AND IMPLICATIONS TO GENETIC IMPROVEMENT OF BEEF CATTLE

The introduction of genetics into agricultural sciences, and specifically the bovine sector, have driven large-scale genetic testing research exponentially. Cattle are one of the most agriculturally important livestock species, and the bovine genome has received a great deal of attention after the mapping of other genomes, such as mice and humans. The advances in computing technologies that developed during the Human Genome Project, in combination with the outstanding desire to map the genome of livestock and connect genetic markers to economically important traits, placed bovine genome mapping at a high importance. Once the bovine genome was mapped, further technological advances led to the identification of genes and their corresponding phenotypes; while many of these exist in databases, further research should be completed to continue to locate genes for some of the most economically important traits. By utilizing GWAS methodologies, researchers can detect statistically significant genotype-phenotype relationships by identifying significant SNPs, locating near-distance genes, and further evaluating the presence or absence of the gene of interest in animals showing a certain phenotype. The effectiveness of software like FarmCPU in identifying candidate genes even in complex trait situations, such as meat quality, results in a positive outlook for the identification of genes related to more complex traits; in the beef production industry, disease complexes such as Bovine Respiratory Disease and prediction of carcass merit could reveal a genetic connection through GWAS. Additionally, utilizing DNA pooling processes, research can significantly reduce costs while maintaining much of the statistical power. Research continuously displays the accuracy of pooled SNP associations when compared to individual genotyping, testifying to the effectiveness of pooling. In principle, a 200-fold increase in efficiency is well within reach when using DNA pooling; a situation with 200 cases and 200 controls can be evaluated using two pooled samples rather than 400 individual samples. Further, research suggests that utilizing larger pools would diminish technical error. Additional animals in a pool reduce experimental error, which in turn reduces experimental costs, GWAS with pooling can occur at an even greater level to identify genes

associated with some of the most economically important traits. Utilizing these advances in techniques and technology, pooling research can become even more accurate, cheaper, and efficient. Understanding genes associated with production traits of interest can progress beef cattle production, including breeding, feeding, and harvesting programs, and accurate pooled DNA analyses will streamline the process to this genetic understanding.

LITERATURE CITED

- Abrams, A.N., T.G. McDanel, J.W. Keele, C.G. Chitko-McKown, L.A. Kuehn, and M.G. Gonda. 2021. Evaluating accuracy of DNA pool construction based on white blood cell counts. *Front Genet.* 12:635846. doi:10.3389/fgene.2021.635846
- Alberts, B., J. Lewis, M. Raff, K. Roberts. A. Johnson, P. Walter, D. Bray, and J.D. Watson. 2002. *Molecular biology of the cell.* 4th ed. Garland Science, New York, NY
- Barratt, B.J., F. Payne, H.E. Rance, S. Nutland, J.A. Todd, and D.G. Clayton. 2002. Identification of the sources of error in allele frequency estimations from pooled DNA indicates optimal experimental design. *Ann Hum Genet.* 66(5-6):393-405. doi:10.1046/j.1469-1809.2002.00125.x
- Beckmann, J.S. and M. Soller. 1990. Toward a unified approach to genetic mapping of eukaryotes based on sequence tagged microsatellite sites. *Biotechnology (N Y).* 8(10):930-932. doi:10.1038/nbt1090-930
- Durmaz, A.A., E. Karaca, U. Demkow, G. Toruner, J. Schoumans, and O. Cogulu. 2015. Evolution of genetic techniques: Past, present, and beyond. *Biomed Res Int.* 2015:461524. doi:10.1155/2015/461524
- Fries, R., A. Eggen, and J.E. Womack. 1993. The bovine genome map. *Mamm Genome.* 4:405-428. doi:10.1007/BF00296815
- Gao, G., N. Gao, S. Li, W. Kuang, W. Jiang, W. Yu, J. Guo, Z. Li, C. Yang, and Y. Zhao. 2021. Genome-wide association study of meat quality traits in a three-way crossbred commercial pig population. *Front Genet.* 12:614087. doi:10.3389/fgene.2021.614087
- Hernandez-Rodriguez, J., M. Arandjelovic, J. Lester, C. de Filippo, A. Weihmann, M. Meyer, S. Angedakin, F. Casals, A. Navarro, L. Vigilant, H.S. Kuhl, K. Langergraber, C. Boesch, D. Hughes, and T. Marques-Bonet. 2017. The impact of endogenous content, replicates and pooling on genome capture from faecal samples. *Mol Ecol Resour.* 2018(18):319-333. doi:10.1111/1755-0998.12728
- Huang, W., B.W. Kirkpatrick, G.J.M. Rosa, and H. Khatib. 2010. A genome-wide association study using selective DNA pooling identifies candidate markers for fertility in Holstein cattle. *Anim Genet.* 41:570-578. doi:10.1111/j.1365-2052.2010.02046.x
- Jiang, J., L. Ma, D. Prakapenka, P.M. VanRaden, J.B. Cole, and Y. Da. 2019. A large-scale genome-wide association study in U.S. Holstein cattle. *Front. Genet.* 10:412. doi:10.3389/fgene.2019.00412
- Keele, J., T. McDanel, T. Lawrence, J. Jennings, and L. Kuehn. 2021. Estimation of pool construction and technical error. *Agriculture.* 11:1091. doi:10.3390/agriculture11111091
- Lee, B.-Y., K.-N. Lee, T. Lee, J.-H. Park, S.-M. Kim, H.-S. Lee, D.-S. Chung, H.-S. Shim, H.-K. Lee, and H. Kim. 2015. Bovine genome-wide association study for genetic elements to resist the infection of foot-and-mouth disease in the field. *Asian Australas. J. Anim. Sci.* 28(2):166-170. doi:10.5713/ajas.14.0383
- Liu, X., M. Huang, B. Fan, E.S. Buckler, Z. Zhang. 2016. Iterative usage of fixed and random effect models for powerful and efficient genome-wide association studies. *PLoS Genet.* 12(2):e1005767. doi:10.1371/journal.pgen.1005767
- Macgregor, S., Z.Z. Zhao, A. Henders, M.G. Nicholas, G.W. Montgomery, and P.M. Visscher. 2008. Highly cost-efficient genome-wide association studies using DNA pools and dense SNP arrays. *Nucleic Acids Res.* 36(6):e35. doi:10.1093/nar/gkm1060
- Maxam, A. and W. Gilbert. 1977. A new method for sequencing DNA. *Proc Natl Acad Sci U S A.* 74(2):560-564. doi:10.1073/pnas.74.2.560
- Pahl, R. and H. Schäfer. 2010. PERMORY: an LD-exploiting permutation test algorithm for genome-wide association testing. *Bioinformatics.* 26(17):2093-2100. doi:10.1093/bioinformatics/btq399
- Purcell, S., B. Neale, K. Todd-Brown, L. Thomas, M.A.R. Ferreira, D. Bender, J. Maller, P. Sklar, P.I.W. de Bakker, M.J. Daly, P.C. Sham. 2007. PLINK: a tool set for whole-genome association and population-based linkage analyses. *Am. J. Hum. Genet.* 81:559-575. doi:10.1086/519795
- Sanger, F., S. Nicklen, A.R. Coulson. 1977. DNA sequencing with chain-terminating inhibitors. *Proc Natl Acad Sci U S A.* 74(12):5463-5467. doi:10.1073/pnas.74.12.5463
- Sham, P., J.S. Bader, I. Craig, M. O'Donovan, and M. Owen. 2002. DNA pooling: A tool for large-scale association studies. *Nat Rev Genet.* 3:862-871. doi:10.1038/nrg930
- Shendure, J., S. Balasubramanian, G.M. Church, W. Gilbert, J. Rogers, and J.A. Schloss. 2017. DNA sequencing at 40: past, present and future. *Nature.* 550(7676):345-353. doi:10.1038/nature24286
- Soleimani, B., H. Lehnert, S. Babben, J. Keilwagen, M. Koch, F.A. Arana-Ceballos, Y. Chesnokov, T. Pshenichnikova, J. Schondelmaier, F. Ordon, A. B rner, and D. Perovic. 2022. Genome wide association study of frost tolerance in wheat. *Sci Rep.* 12:5275. doi: 10.1038/s41598-022-08706-y
- Womack, J.E. 2012. First steps: bovine genomics in historical perspective. *Anim Genet.* 43(1):2-8. doi:10.1111/j.1365-2052.2012.02382.x
- Xue, Y., C. Li, D. Duan, M. Wang, X. Han, K. Wang, R. Qiao, X.-J. Li, and X.-L. Li. 2020. Genome-wide association studies for growth-related traits in a crossbreed pig population. *Anim Genet.* 52:217-222. doi:10.1111/age.13032
- Yin, L., H. Zhang, Z. Tang, J. Xu, D. Yin, Z. Zhang, X. Yuan, M. Zhu, S. Zhao, X. Li, X. Liu. 2021. rMVP: a memory-efficient, visualization-enhanced, and parallel-accelerated tool for genome-wide association study. *Genomics Proteomics Bioinformatics.* 19(4):619-628. doi:10.1016/j.gpb.2020.10.007



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