

**Volume 1
Edition 1**

Calendar

June 9-10: NE
Cattlemen Annual
Midyear Meeting

December 6-8: NE
Cattlemen Annual
Convention and Trade
Show

2023 Feb 1-3: Cattle
Industry Convention
and NCBA Trade Show

Cattle Trails

USDA ARS USMARC Cattle Industry Stakeholder Update

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Welcome from the USMARC Director



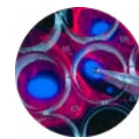
An update from Dr. Boggess regarding our beef programs here on the Center and plans for the future.

Meet the USMARC Manager-Chad Engle



USMARC livestock manager Chad Engle provides an update related to the calving season.

USDA ARS USMARC Research Reports



Research summaries or abstracts regarding the current or recently completed research ARS scientists are performing.

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Hello From the Range!



Hello from the U.S. Meat Animal Research Center (USMARC) and welcome to the first edition of the USMARC and ARS Beef Cow/Calf Stakeholder update! It is our pleasure to bring you this first update and research report! Our goal is to provide our beef industry partners with current research reports and news of interest. And, we have a lot of good news to share! Please let us know what you think!

To start, please see eight outstanding research reports for review in this edition from our USMARC research teams and from our ARS partners. These reports are focused primarily on the cow/calf sector, and we will be providing a fed cattle focused update in the near future. As you might expect, we are excited about our beef programs and excited about our collaborations with

ARS and other research partners! At USMARC, we are aggressively building working teams across ARS and with academia and with industry stakeholders to best utilize our resources and expertise. We greatly value the stakeholder support we receive, and we rely on our critical producer stakeholders to help us develop our research and management programs and to represent our common interests with industry influencers. Your support remains critical to our continued success, and we greatly appreciate it!

At the Center our research is focused on diverse scientific exploration as part of a systems approach to beef production. The systems approach is best illustrated by examining the relationships between genetics (including the cow and related microbiomes), the environment, management approaches, and socio-economic factors. Specific research priorities include heifer fertility and development, germplasm (breed) evaluation, nutritional/growth physiology and feed efficiency, respiratory disease, and precision range management. We work closely with many industry and academic partners, and we have tremendous support from the beef industry and the National Cattlemen's Beef Association.

Of course, our research would not be possible without our great beef production resources and the excellent animal care and management we receive from UNL Livestock manager Chad Engle and his team. See an overview of the unit from Chad in this update. It is important that our research be conducted in an industry relevant production system and the UNL team makes sure that our cattle receive optimal care and that our research programs have maximum impact while representing industry standards to the best of our abilities.

However, even with great management we are always striving to improve. For example, we recently developed a "Blue Ribbon Panel" (BRP) of industry experts to provide us with a comprehensive beef program review. Our BRP includes producers and industry leaders, scientists, animal care staff, and other USMARC stakeholders. The BRP meets periodically on the Center, with an eye on improving overall animal husbandry, animal care and well-being, herd and individual performance, and overall management. The BRP recommends improvements in all programs and facilities, and monitors progress and implementation. We also contrast USMARC program performance with industry benchmarks to identify areas needing focused improvement, and to monitor progress over time. We have not been able to meet as often as we had hoped due to the pandemic but plan to return the beef BRP to a more active role in 2022. Please let us know if you would like to participate in this effort or if you would like more information.

To say that the BRP program has been successful would be a gross understatement. The panel meetings have provided valuable and revealing guidance and we are using them to promote continuous improvements in animal care, management, and research programs. I am certain that this effort will continue to yield benefits into the future. In fact, this effort has led to several improvements across the Center from animal handling facility upgrades to forage management improvements. There is always room to improve.

Our management team and BRP efforts have supported an evolving and proactive relationship with our colleagues at APHIS, who have been charged with providing annual inspections for the Center. These interactions with APHIS are considered opportunities to strengthen our already strong programs for animal care and animal husbandry, and APHIS is a partner in our ongoing success.

Lastly, we are looking to expand our research programs and impact through new and diverse research collaborations. We are working with our leadership in ARS and with our sister locations to describe best ways to develop systems-based research programs and collaborations that focus on real industry needs and on beef industry sustainability. These collaborations will include many land grant university partners as well and we look forward to seeing where these evolving program ideas take us for the beef industry.

So, as I hope you can see, we are very excited and optimistic about the future! Please join us on our journey forward and let us know how we can make our programs even better. We need your support for our research programs, for our partners and stakeholders, and in WDC. Help us to help you!

All the best from the Range!

Mark Boggess

Update from the Livestock Manager



It's spring in cattle country and that means new calves hitting the ground, the end of dormant season and winter feeding, and a brand-new spring full of opportunities and challenges. This is happening all across cattle country, and here, at the U.S. Meat Animal Research Center (USMARC) in south central Nebraska, it is no different.

Many cattlemen will tell you their favorite time of year is calving, but that doesn't mean it's easy. One of my favorite quotes of John Wayne is, "you'll get no rest and damn little sleep." That certainly is the case with the cattle crew here at USMARC. When fully staffed, we have 24 folks on the cow/calf side and 7 feedlot crew members. Together, they feed and care for right at 8,000 cows across 34,000 acres. For those who have not had the opportunity

to tour USMARC, the facility has ten polesheds on Center, which function as their own operation. However, these folks work cohesively as one large unit for USMARC.

Calving started this year with a group of 250 synchronized and artificially inseminated (A.I.) cows from the Germplasm Evaluation (GPE) project on the first of March. This group of cows were part of the fall herd that we have been transitioning to spring over the last two years. They were calved by the polished 12 crew and they did a great job! During the first wave of calves, the crew had over 130 calves born with a survival rate of 98%. It can't be done better than that!

Each year we calve 1200 heifers, and that is the next group to calve, with due dates ranging from March 13th to March 20th, and we started calving the large commercial herds. To date, our heifer calving crews have had right at 70 calves, but that number will be increasing rapidly over the next 2 weeks. The commercial heifers are only exposed to bulls for 28 - 45 days depending on the herd. This creates an intense, but short calving window for the crews. There are many reasons why we choose to breed our commercial heifers using this method, not the least of which is to try to get as many heifers calved as possible before the mature cows start. The GPE heifers will also start calving soon. During the majority of heifer calving, we have folks on Center 24 hours per day. This super dedicated group of "night calvers" work incredibly hard and deserve our appreciation and recognition, as they all take their turns calving at night. We couldn't do it without them!

The mature cow herds start calving in early April and are managed across the entire Center with extra help often coming in from other crews beyond the cow/calf and feedlot. It's a great example of how we work together to best care for the livestock and research data collection each and every day. Calving usually lasts until the first week of June, during which time we gather comprehensive data and information within the first 24 hours of each calf's life. Birthweight, sex, dam, color, horn/polled, birthing difficulty, udder scores, and disposition scores are just a few examples of the information our dedicated stockmen will collect. Each calf is also tagged with a unique identification number that will be used throughout its life on the Center. This information is added to our database weekly, as well as checked for accuracy. This year due to supply shortages, each of these tags was written by hand - over 12,000 tags each written by hand!

In future editions, I look forward to sharing more information on how we care for the land and livestock and collect all the data needed to keep USMARC rolling. Until then, enjoy springtime in cattle country!

Research Reports

The astric () represents the author contact found on page 10.*

Underlined words in the citation represent the original title for the articles.

The effects of maternal nutrition during the first 50 d of gestation on the location and abundance of hexose and cationic amino acid transporters in beef heifer uteroplacental tissues

*Crouse, M.S.*¹, McLean, K.J.², Dwamena, J.³, Neville, T.L.⁴, Menezes, A.C.B.⁵, Ward, A.K.⁶, Reynolds, L.P.⁷, Dahlen, C.R.⁸, Neville, B.W.⁹, Borowicz, P.P.¹⁰, Caton, J.S.¹¹ 2021. The effects of maternal nutrition during the first 50 d of gestation on the location and abundance of hexose and cationic amino acid transporters in beef heifer uteroplacental tissues. *Journal of Animal Science*. 99(1):1-12. <https://doi.org/10.1093/jas/skaa386>.*

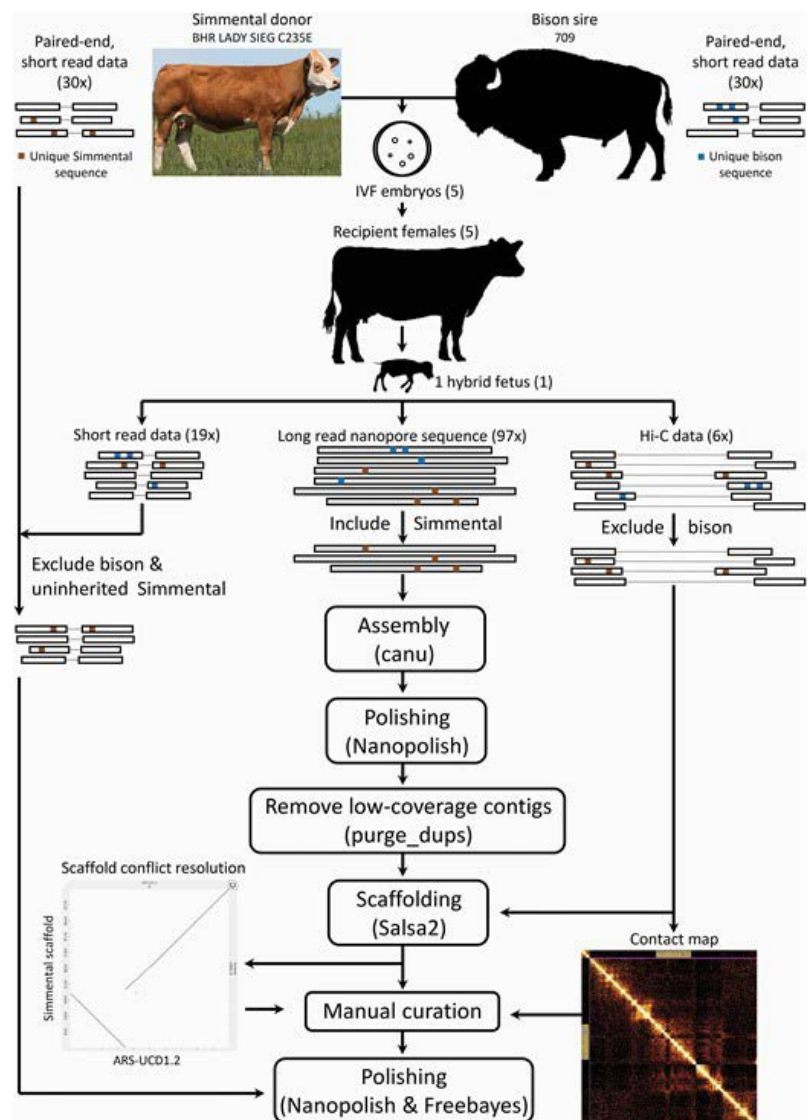
Beef heifers that are bred conceive 90% of the time; however, only 50% of those bred heifers maintain a pregnancy. Therefore, most heifers must be re-bred multiple times to maintain a pregnancy which results in decreased efficiency of livestock production. Although data evaluating how to maintain pregnancies in cattle would have a large impact on beef production, there is little data available to determine how changes in maternal nutrition affect embryonic development and maintenance of pregnancy. In this collaborative manuscript, we found that maternal nutrition does not affect nutrient transporters in the uterus in early pregnancy and that changes in nutrients available to the embryo are possibly due to changes in embryonic metabolism. This work addresses questions from scientists whether maternal nutrition in early gestation changes how embryos receive nutrients, and provides further information on the complex relationship between nutrient supply and demand in heifers and their embryos. Providing increased understanding on the relationship between maternal and fetal nutrition and identification of strategies to increase early embryonic survival will improve the efficiency of beef cattle production.



A reference genome assembly of Simmental cattle, *Bos taurus taurus*

Heaton, M.P.*, Smith, T.P.L., Bickhart, D.M., Vander Ley, B.L., Kuehn, L.A., Oppenheimer, J., Shafer, W.R., Schuetze, F.T., Stroud, B., McClure, J.C., Barfield, J.P., Blackburn, H.D., Kalbfleisch, T.S., Davenport, K.M., Kuhn, K.L., Green, R.E., Shapiro, B., Rosen, B.D. 2021. A reference genome assembly of Simmental cattle, *Bos taurus taurus*. *Journal of Heredity*. 112(2):184-191. <https://doi.org/10.1093/jhered/esab002>.

Bovine genome assemblies represent genetic blueprints for building and maintaining cattle. These blueprints advance our understanding of the genomic elements affecting important traits and aid in identification of genetic differences between animals that contributes to variation in individual performance. A pangenome represents a set of high-quality genome assemblies of multiple individuals and is intended to represent the broadest possible diversity within a species. An international Bovine Pangenome Consortium (BPC) has recently been established to begin assembling genomes from more than 600 recognized breeds of cattle and closely related species. Previously reported genome assemblies for Angus, Brahman, Hereford, and Highland breeds of cattle and yak, gaur, and bison species are part of the initial BPC effort. The present report describes assembly of a fullblood Simmental cow from an F1 bison-cattle hybrid fetus in a process called “trio binning”, that results in an improved product compared to sequencing a purebred Simmental individual. The quality of this genome meets or exceeds that of the best cattle assemblies to date. This approach allows reference assemblies to be readily produced for all breeds of cattle and would pave the way for understanding functional genetic differences between breeds.

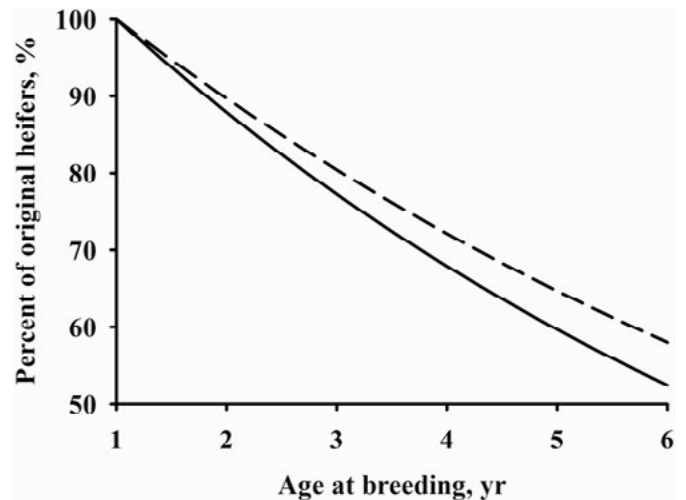


The figure above is a schematic showing the Simmental trio binning and assembly process.

Production performance of cows raised with different postweaning growth patterns

Freetly, H.C.*, Cushman, R.A., Bennett, G.L. 2021. Production performance of cows raised with different postweaning growth patterns. *Translational Animal Science*. 5(3):1-7. <https://doi.org/10.1093/tas/txab031>.

Reducing the number of cows replaced annually decrease the cost of beef production. This study demonstrates that using nutrition to alter the growth pattern of heifers near puberty can increase calf weaning weight, and that these findings are consistent over a wide range of cattle of different genetic types. There is also an indication that altered growth patterns can change the age that a cow is removed from the herd. This study demonstrated the importance of proper nutritional management at young ages on subsequent lifetime cow performance.



Breed and heterotic effects for mature weight in beef cattle

Zimmermann, M.J., Kuehn, L.A.*, Spangler, M.L., Thallman, R.M., Snelling, W.M., Lewis, R.M. 2021. Breed and heterotic effects for mature weight in beef cattle. *Journal of Animal Science*. 99(8).

Article skab209. <https://doi.org/10.1093/jas/skab209>.

Mature cow weight is a driver of cost and efficiency in commercial cattle breeding, primarily due to increased feed requirements. While some production systems can accommodate larger cows, having tools to manage cow weight would be helpful in reducing costs for commercial cattle operations. Our objective was to estimate current breed differences for mature weight from sixteen different breeds using data from the U.S. Meat Animal Research Center Germplasm Evaluation Program, where cows were daughter or granddaughters of influential industry bulls. Mature weight was predicted for all cows at 6 years of age and used to determine breed differences for mature weight. Breed differences were adjusted for industry sampling using bull yearling weight EPDs. Resulting breed differences can be used to inform breeding programs where limiting cow size could increase efficiency and thus overall profitability.



Measuring bull prolificacy across multiple years

Bennett, G.L., Keele, J.W.*, Kuehn, L.A., Snelling, W.M., Dickey, A.M., Light, D.E., Cushman, R.A., Mcdaneld, T.G. 2021. *Using genomics to measure phenomics: Repeatability of bull prolificacy in multiple-bull pastures*. *Agriculture*. 11(7). Article 603. <https://doi.org/10.3390/agriculture11070603>.

Prolificacy of bulls used in multiple-bull pastures for commercial beef production is often unknown because sires of calves are not identified. Sires can be identified by genetic markers but costs are

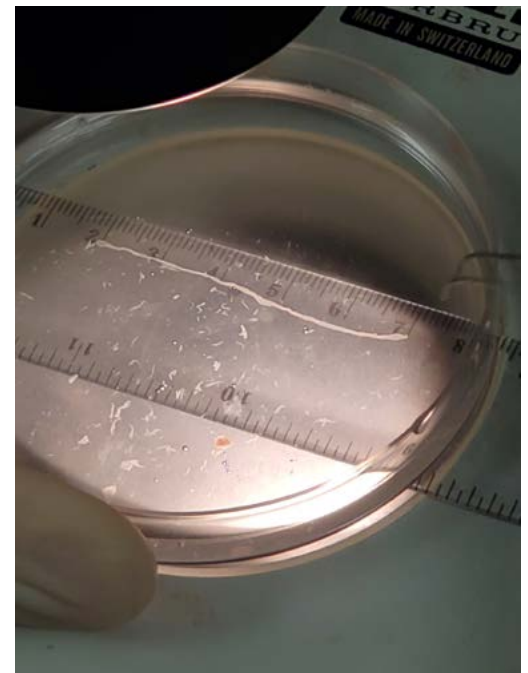


often thought to be too high. Knowing whether a bull sired many or only a few calves could be helpful if prolificacy is repeatable over years. Bulls in multiple-bull pastures and their calves were genotyped to determine their sires. Bulls were used one to four years. Repeatability of bull prolificacy was moderate to high. A less expensive way of estimating prolificacy based on pooling DNA from calves was simulated incorporating pooling errors estimated from previous studies. It resulted in accurate estimates of bull prolificacy. Knowing a bull's prior prolificacy obtained at a lower price could help predict future prolificacy for managing the breeding herd. More available estimates of bull prolificacy could also result in more on-farm and ranch research on breeding herd management as well as improved bull prolificacy through selection.

Influence of estradiol on bovine trophectoderm and uterine gene transcripts around maternal recognition of pregnancy

Northrop-Albrecht, E.J., Rich, J.J., Cushman, R.A.*, Yao, R., Ge, X., Perry, G.A. 2021. *Influence of estradiol on bovine trophectoderm and uterine gene transcripts around maternal recognition of pregnancy*. *Biology of Reproduction*. 105(2):381-392. Article ioab091. <https://doi.org/10.1093/biolre/ioab091>.

Proper uterine function is crucial for pregnancy success in cows. Cows that demonstrate behavioral estrus before artificial insemination have greater circulating estrogen concentrations and greater pregnancy success. The current study examined the influence of estrogen on early embryonic survival and uterine function in beef cows. Estrogen did not improve early embryonic survival, but it did influence uterine proteins that improve pregnancy success after early embryonic development. Cow-calf producers should manage cows to improve the percentage demonstrating behavioral estrus when using artificial insemination.



Association of *ARRDC3* and *NFIA* variants with bovine congestive heart failure in feedlot cattle

Heaton, M.P.*, Harhay, G.P., Bassett, A.S., Clark, H.J., Carlson, J.M., Jobman, E.E., Sadd, H.R., Pelster, M.C., Workman, A.M., Kuehn, L.A., Kalbfleisch, T.S., Piscatelli, H., Carrie, M., Krafur, G.M., Grotelueschen, D.M., Vander Ley, B.L. 2022. Association of *ARRDC3* and *NFIA* variants with bovine congestive heart failure in feedlot cattle. *F1000Research*. 11. Article 385. <https://doi.org/10.12688/f1000research.109488.1>.

Bovine congestive heart failure (BCHF) in feedlot cattle has become increasingly common in the Western Great Plains of North America at moderate elevations (3000 to 4500 ft). This disease is an untreatable, complex condition involving high blood pressure in the lungs, which leads to subsequent heart failure and death. BCHF is fundamentally distinct from the “brisket disease” observed in the high elevations of the Rocky Mountains (>7000 ft), since BCHF occurs at much lower elevations where animals with brisket disease were previously sent to recover. Individual feedlot operations have reported losses from BCHF exceeding \$250,000 annually, which are comparable to losses from bovine respiratory disease at similar locations. Cattle herds affected with BCHF are typically bred and managed with the aim of achieving high-quality carcasses.

Day 1 (bull)



Day 30 (heifer)



Day 238 (steer)



Bovine congestive heart failure (BCHF) clinical cases at different stages of fattening. Heaton *et al.* *F1000Research* 2019, 8:1189

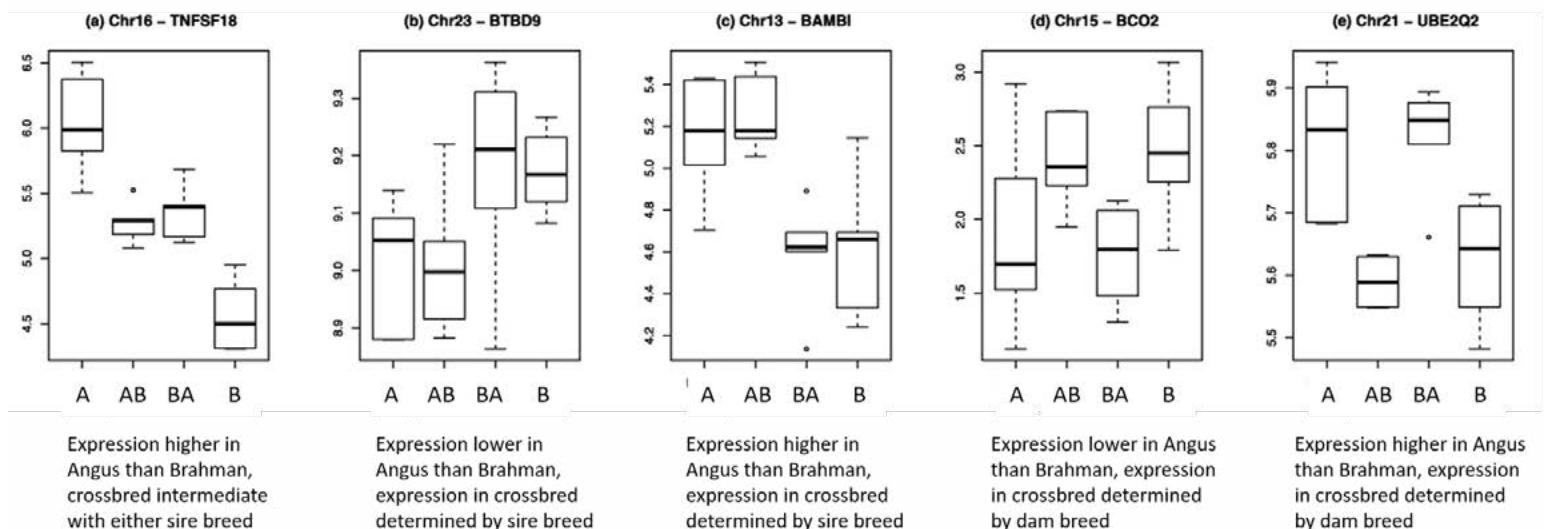
Consequently, reducing the impact of BCHF is a priority for the beef industry. In the present report, animals with end-stage heart failure from 30 different ranch sources were evaluated together with their healthy penmates. DNA sequence variation in two major genes (*ARRDC3* and *NFIA*) was discovered to be associated with BCHF, and thus, these genes may play a role in disease development. Feedlot animals in this study, that were homozygous for the DNA risk markers in both genes, were 28-fold more likely to develop heart failure than those without. A DNA-based test with two markers showed 29% of diseased cattle had homozygous risk alleles in both genes, compared to less than 2.5% in similar unaffected feedlot cattle. This type of testing may be useful for identifying feedlot animals at the highest risk for BCHF in the Western Great Plains of North America. In herds suffering from BCHF, knowledge of which cattle have the highest and lowest genetic risk for disease allows producers to make informed decisions for selective breeding and animal health management.

Distinctive gene expression patterns and imprinting signatures revealed in reciprocal crosses between cattle sub-species

Liu, R., Tearle, R., Low, W., Chen, T., Thomsen, D., Smith, T.P.L.*, Hiendleder, S., Williams, J.L. 2021. Distinctive gene expression patterns and imprinting signatures revealed in reciprocal crosses between cattle sub-species. *Biomed Central (BMC) Genomics*. 22. Article 410. <https://doi.org/10.1186/s12864-021-07667-2>.

There are two subspecies of cattle in the world today, called taurine and indicine cattle types. The taurine types are typified by common breeds in the U.S. like Angus, Holstein, or Hereford and have been intensively selected for production traits of superior milk or meat quality. The indicine types are typified in the U.S. by the Brahman breed, and are known for their tropical adaptations and superior pest and disease resistance qualities, but generally lag in the production traits selected in taurine cattle. Numerous efforts to combine the positive attributes of both types by crossbreeding have been conducted, resulting in some new breeds such as Brangus or Beefmaster. Studies have shown variable effects of crossbreeding depending upon the sex of the animal of each breed used (that is, the results can be different if Angus sires are used on Brahman cows, compared with using Brahman sires on Angus cows). The present work is an effort to understand the differences between the taurine and indicine types using gene expression profiling in Angus and Brahman cattle breeds, and includes crossbreeds of the two types that supports analysis of effects that are sex and breed-specific. The study identified numerous genes that are expressed at different levels in the two breeds, and the crossbred animals were key to identifying the true breed-specific differences and discovering genes that may drive the breed differences observed and provide new insights into contrasting effects that emerge when using a particular sex of each type in crossbreeding.

Gene expression level patterns in Angus (A), Angus x Brahman (AB), Brahman x Angus (BA), and Brahman (B) developing fetuses



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