

Proceedings
Beef Improvement Federation
44th Annual Research Symposium & Meeting



April 18 – 21, 2012

Texas AgriLife Extension Service, Dept. of Animal Science – Texas A&M University,

American Brahman Breeders Association

Houston, Texas

2012 BEEF IMPROVEMENT FEDERATION RESEARCH SYMPOSIUM AND ANNUAL MEETING

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Historical Overview of Animal Breeding and Genetics Research in the South

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INTRODUCTORY REMARKS. This is only an overview of history of this subject, and I hope others will either help me fill in some of the blanks or expand on the subject, independently. After being asked to prepare this material, I realized that much of the information needed to even give an overview has probably already been lost.

THE WORK OF DR. JAY L. LUSH AT TEXAS A&M. Although previous research and observation provided important background information, most people would agree that animal breeding, as an academic field, started with the work of Dr. Jay L. Lush. Since Dr. Lush started his professional career in the South, I will start this historical overview with his early work.

Dr. Lush officially completed his Ph.D. at the University of Wisconsin in early 1922, but he had taken the position of Animal Husbandman at what was then Texas A&M College a few months earlier in 1921. Shortly after coming to Texas A&M, Dr. Lush became involved with the first crossbreeding study involving crossbreeding of *Bos indicus* and *Bos taurus* cattle. This may be a slight overstatement, because, in a report of his research, Dr. Lush cited a report in Germany with a translated title of “Concerning the Zebu and Animal Breeding in Germany.” However, there was apparently no continuation of the work in Germany. I would like to emphasize that I said that Dr. Lush was involved with the first research study involving the crossbreeding of *Bos indicus* and *Bos taurus* cattle. It would also be correct to say that he conducted the first crossbreeding study involving Brahman cattle, but, when his study was initiated, the Brahman breed had not actually been established. It was 1924 before the American Brahman Breeders Association was formed and the name, Brahman, chosen as the official name of the breed.

The crossbreeding study was conducted at the Sonora Ranch Experiment Station (Substation No. 7). Grade Hereford cows were mated to a 3/4 Brahman bull in the earlier years that was replaced by a 61/64 Brahman bull in later years; purebred bulls were almost impossible to find at the time. Steers from the study were fattened and slaughtered and carcass data was collected. F₁ heifers were kept and bred to Hereford bulls. The Brahman / Hereford crossbreeding study was not continued after 1929. Dr. Lush left Texas A&M to accept a job at what was then Iowa State College in 1930.

In addition to the Brahman / Hereford crossbreeding research, Dr. Lush studied fleece characteristics in Rambouillet sheep, reported on a skeletal variation in cattle (the duck legged condition), and conducted various other studies while at Texas A&M.

EARLY BREEDING RESEARCH IN LOUISIANA. About the time Dr. Lush left Texas A&M to go to Iowa State, crossbreeding research involving Brahman cattle was initiated at what was then Louisiana State College (Akerman, 1982). Anthony Doherty of East Baton Rouge Parish gave the college some grade Brahman heifers (apparently either two or four heifers, but both numbers have been reported), and encouraged officials to start a crossbreeding program with them. Shortly after getting the heifers, a 15/16 Brahman bull

was purchased to use in the herd. This bull was eventually used for crossing with Hereford, Shorthorn, and Angus cattle.

In 1934, Angus heifers at the Jeanerette station were bred to Africander bulls (Black, 1935). The King Ranch, in cooperation with the USDA, had imported 16 Africander bulls and 11 Africander females from South Africa in 1931 (Ullman Feature Service, 1944).

Starting in 1932 (Reynolds, 1973), Brahman bulls were mated to Angus cows and Angus bulls were mated to Brahman cows. The crossbred females from these matings were mated Brahman, Angus, or Brahman–Angus bulls to produce crossbreds with various proportions of Brahman and Angus breeding. Crossbred bulls produced in the study were mated to crossbred females from the study for a number of years, and by the early 1970s the cattle were produced were about $3/8$ Brahman and $5/8$ Angus.

Africander–Angus cattle were produced from a system similar to that used to produce the $3/8$ Brahman $5/8$ Angus cattle; according to Reynolds (1973) the program to produce the Africander – Angus crossbred cattle was also started in 1932. The King Ranch, in cooperation with the USDA, had imported 16 Africander bulls and 11 Africander females from South Africa in 1931. In addition to the research results from Louisiana with Africander crosses, cattle from the 1931 importation were the foundation that provided for the research with Africander crosses at Rockhampton, QLD that, among other research results, led to the important work on genotype-environment interactions at Rockhampton.

In the middle 1930s, A.O. Rhoad moved to the Jeanerette station (he had previously worked in Minas Gerais, Brazil) and became the head animal husbandman at the station. Among his other work, he developed the Iberia Heat Tolerance Test for cattle. Rhoad later worked for the King Ranch in South Texas.

EARLY BREEDING RESEARCH IN FLORIDA.

Beef cattle were raised at the Belle Glade Center (formerly the Everglades Experiment Station) beginning in 1931, when a Devon herd was established (Crockett, 1973a). In 1933, a “native” herd was established and graded up to Devon. In 1946, Angus and Brahman herds were established and a crossbreeding study was initiated.

From 1946 to 1951, matings were made to produce $3/8$ Brahman $5/8$ Devon crosses, with plans of *inter se* mating, and a few Angus / Brahman F_1 crosses were produced. In 1952 backcrossing of F_1 females and two breed rotations were added to the study to compare with *inter se* mating of crossbreds and with straightbreeding.

In 1960, the Devon and Devon / Brahman crossbred herds were discontinued because of the poor performance of the *inter se* Devon / Brahman crosses and because of the difficulty of getting satisfactory Devon bulls. At that time, a trial was initiated to evaluate the Angus, Brahman, and Hereford breeds as straightbreds and in all possible

two breed rotations (Crockett, 1973b). Apparently, this was about when Joe Crockett moved to the Belle Glade Center.

Beef cattle breeding research was initiated at the Ona station in 1942 with the purchase of a Shorthorn bull and a few Brahman cows (Peacock et al., 1973). Superiority of the crossbred calves and of the performance of the crossbred cows led to the initiation in 1952 of a crossbreeding study of Brahman and Shorthorns and their crosses under three different forage systems, representing three different nutritional levels. Research on grading up Charolais was started in 1959, and comparisons among the Charolais, Angus and Brahman breeds and their crosses was initiated in 1962.

The Beef Research Unit at Gainesville was stocked with two year old heifers and breeding research was started in 1952 (Koger, 1973). Based on information provided by the seller and the appearance of the heifers they were believed to be about 3/4 Brahman and 1/4 native (Spanish origin) breeding. For the first five years of the project, these purchased females were bred to Angus, Brahman, Hereford, and Shorthorn bulls. Most of the “sound” heifers from these matings were kept.

In 1957, the heifers that had been produced and the remaining cows of the original group were assigned to the following five breeding groups: (1) grading up to Angus, (2) grading up to Hereford, (3) two breed rotation of Angus and Hereford, (4) two breed rotation of Angus and Brahman, and (5) two breed rotation of Hereford and Santa Gertrudis. Eight commercial Santa Gertrudis heifers were purchased to add to the Hereford-Santa Gertrudis group, because Santa Gertrudis bulls had not been used previously in the program.

What is now called the Subtropical Agricultural Research Station, at Brooksville, was established as the West Central Florida Experiment Station in 1933. A total of 86 head of purebred Red Poll cows and bulls, native cows and grade calves “were under test” at the end of the year in 1934. The Red Poll was evaluated as a dual purpose breed, and both milk production and carcass traits were evaluated. By 1938 Red Danish-Red Poll crosses had been produced, and by 1939 Devon-Red Poll crosses had been produced. In 1941 a Santa Gertrudis bull was received on loan from the King Ranch, and Santa Gertrudis crosses were produced in future years. In 1947 some Brahman-Hereford females were purchased and the grade Red Poll cows were bred to a Brahman bull and to a Hereford bull (Florida Agricultural Experiment Station Annual Reports, 1934-1947).

In 1949 a purebred Brahman herd was started with 20 heifers and two bulls purchased from the J.D. Hudgins Ranch in Texas (History of Cattle at the Brooksville Beef Cattle Research Station, 1982). The Angus herd was started in 1953 with cows purchased from the Everglades Experiment Station. Additional females were purchased from 1954 to 1964 and 90 heifers were purchased from Tetley Farms in Virginia in 1967. Starting in 1955, with one exception, only Wye Plantation bulls or sons of Wye bulls born at the station were used (at least until the 1980s). The Hereford herd (horned) was started with cattle purchased in Texas in 1953. Other purchases of horned cattle were made over the years, and in 1958 20 polled females and a bull were purchased from the R.W. Jones herd

in Georgia. Two bulls from Rock Hollow Farm and two from Anhinga Farms were used in the early 1980s.

In 1962 half of the Brooksville Hereford herd was sent to the USDA station at Miles City Montana and a group of females from the Line 1 herd at Miles City was taken to Brooksville for a genotype environment interaction study (e.g., Koger et al., 1979).

A grade Brahman herd was started in 1969 with the purchase, from a Florida commercial herd, of high percentage Brahman crossbred females that were sired by Brahman bulls. These grade females were found to have higher reproductive rates than the purebred Brahman females on the station. Fertility rates were compared for these two groups, a group (BG) produced from the grade cows and purebred bulls, and females produced from the *inter se* mating of the BG cattle (Koger and Burns (1981) and Olson et al. (1990)).

EARLY BREEDING RESEARCH IN VIRGINIA. Shorthorn and Angus herds were established at the Front Royal Station in the late 1940s (Krehbiel et al., 1969). Apparently, the Hereford herd was established at about the same time (Taylor et al., 1960). The Front Royal Station was operated cooperatively by the USDA and the Virginia Station. The Shorthorn herd was established by the transfer of the beef Shorthorn herd from the Beltsville, MD, Research Center of the USDA in the winter of 1948-49. This herd of about 125 head had been maintained as a closed and partially inbred herd for almost twenty years before the transfer to Virginia. The primary objective of the research at the Front Royal Station was the comparison of (1) inbreeding with subsequent line crossing and (2) single trait mass selection.

Starting in 1955, Angus, Hereford, and Shorthorn bulls were tested at the Front Royal Station, and Angus and Hereford (horned and polled) were tested at Culpepper, VA for average daily gain yearling weight, and type score (Schalles and Marlowe, 1967).

Burris and Priode (1956) presented information about the occurrence of Angus, Hereford, and Angus-Hereford crossbred snorter dwarfs at the Front Royal Station. Bovard and Priode (1965) reported the occurrence of a snorter dwarf in an inbred line of Angus cattle (apparently at the Front Royal Station) that had no history of dwarfism. Marlowe (1964) presented evidence of selection of un-intentional selection for the gene for snorter dwarfism.

EARLY BREEDING RESEARCH IN GEORGIA. Starting in 1949, grade Hereford heifers were bred to Angus and Brahman bulls (one of both breeds per year for three years) at the Tifton station.. Performance of the F₁ calves and of the F₁ cows was evaluated (McCormick and Southwell, 1957).

Using primarily females produced in the Reidsville herd for a four year period, starting in 1954, as a foundation, grade Angus, Polled Hereford, and Santa Gertrudis females were used in a cooperative study between the Tifton station and the Georgia State Prison, Reidsville (Chapman et al., 1973a). The objectives were to (1) compare grade purebreds

with crossbreds, (2) estimate breed effects in grading up programs and sire breed effects in crossbreeding systems, and (3) compare two and three breed rotational crossbreeding. The sires of all calves were purebred Angus, Polled Hereford, or Santa Gertrudis. The Angus and Polled Hereford bulls were produced in research herds at Tifton, and most of the Santa Gertrudis bulls were produced at the Brooksville Beef Cattle Research Station at Brooksville. All steers from the study were grown from weaning to slaughter entirely on forage, mostly on pasture.

Brown Swiss crosses were produced from the grade Angus, Polled Hereford, and Santa Gertrudis cows at Reidsville (Chapman et al., 1973b). The half Brown Swiss females were backcrossed to produce calves that were 1/4 Brown Swiss and 3/4 of the respective beef breed. They were compared with the calves produced in the above study, also with the steers grown from weaning to slaughter on forage.

EARLY BREEDING RESEARCH IN OKLAHOMA. Starting in the 1960s, various comparisons were made between British, British-Holstein, and Holstein cows to evaluate the effects of milk production and size on cow productivity and efficiency (e.g., Deutscher and Whiteman (1971) and Holloway et al., 1975). Later, Angus-Hereford F₁ cows (both reciprocals) were compared to crosses of Brown Swiss, Jersey, and Simmental with Angus and Hereford for nutrient intake and efficiency of crossbred cows (Marshall et al., 1984).

Starting in 1960 a selection was started at the El Reno station where selection for weaning weight and for yearling weight were being evaluated in two separate line of Hereford cattle (e.g., Frahm et al., 1985).

EARLY BREEDING RESEARCH IN ARKANSAS. Angus and Hereford cows born from 1950 to 1960 were evaluated for inheritance of and the effects of various environmental factors (including lactational status) on cow weight, height, and other body measurements in daughter-dam pairs of three year old first calf heifers (Brown and Franks, 1964). In earlier reports, proportions of weight, height, and other body dimensions that had been achieved by three years of age were reported. I assume that C.J. Brown went to the University shortly before the data collection for this study started in 1950.

Performance test data from Angus, Hereford, and Shorthorn bulls that were raised, performance tested, and used in Agricultural Experiment Station herds and performance test data for their male progeny, from 1951 to 1962, were used to estimate heritability for growth, weight, feed intake, and feed conversion rates (Brown and Gacula, 1964).

M.A. (Mike) Brown, who was then at the USDA station at Boonville and A.H. (Hayden) Brown at the University of Arkansas, evaluated genotype-environment interactions in Angus and Brahman cows and the reciprocal F₁ crosses, born from 1988 to 1991, when grazed on common bermudagrass compared to endophyte-infected fescue tall pastures (e.g., Brown et al., 1997).

EARLY BREEDING RESEARCH IN SOUTH CAROLINA. From 1954 to 1958, calves were produced at the Coast Experiment Station at Summerville by the same Shorthorn bull and out of Angus, Brahman-Angus, Hereford-Angus, and Brahman-Hereford crossbred cows (Godley et al., 1960). The crossbred cows had all been produced in an earlier breeding study.

EARLY BREEDING RESEARCH IN NORTH CAROLINA. A crossbreeding study was initiated in 1963 at the Umstead and Broughton farm units of the North Carolina Department of Agriculture (Dillard et al., 1980). Purebred Angus and Hereford and various crosses involving Angus, Charolais, and/or Hereford were produced at both locations.

A selection study was started in 1967 to evaluate single trait selection in Herefords (Irgang et al., 1985). The study was conducted at the Tidewater Research Station at Plymouth and at the Agricultural Experiment Station at Raleigh. The same sires or related sires had been used in the two foundation herds since 1947. At the two locations there were separate lines selected for weaning weight and for post weaning gain as well as a randomly selected control line. Approximately equal numbers of calves were produced at the two locations each year. Correlated response in milk yield, bull fertility traits, as well as some other traits, was evaluated.

EARLY BREEDING RESEARCH IN TEXAS (AFTER LUSH'S WORK IN THE 1920'S) Performance testing of Hereford bulls was started at the Balmorhea substation in 1942 (Patterson et al., 1955). Gain testing of bulls from cooperating breeders was continued at the McGregor Station. Angus, Brahman, Charolais, Hereford, Santa Gertrudis, and Shorthorn bulls were tested.

Data was collected on grade Hereford and Brahman-Hereford crossbreds at the Lufkin station starting in 1935. Monthly weights were collected on all cattle at the station from birth to sale or death. The McGregor station was established after World War II on land that had been part of a military installation. Data were collected on Brahman, Hereford, and Brahman-Hereford crosses, beginning in 1950 (Cartwright et al., 1964). That publication was apparently the first to report heterosis estimates in Brahman crosses. It was also apparently the first report of the reciprocal differences in birth weight in *Bos indicus/Bos taurus* crosses.

When Charolais bulls were entered (and had the highest weights and weight gains) in the performance tests at McGregor, it became clear to Tom Cartwright that it was necessary to consider beef cattle breeding from a system standpoint. This led to analyses of cow size (e.g., Fitzhugh, 1967) and a series of systems analysis studies (e.g., Long et al., 1975).

EARLY BREEDING RESEARCH IN ALABAMA. Crossbreeding research was conducted at the Black Belt Substation at Marion Junction, initially by mating high grade Hereford cows to Brahman, Shorthorn, and Angus bulls. Starting in 1950 (Collins et al.,

1972), Angus and Hereford bulls were bred to Hereford, Angus-Hereford, Shorthorn-Hereford, and Brahman-Hereford F₁ cows.

At the main station at Auburn, starting in 1957 all possible crosses were made among the Angus, Hereford and Shorthorn breeds, followed, starting in 1961, with the continued production of all types of reciprocal F₁ crosses, and the production of all types of three breed cross calves from purebred bulls and F₁ cows. All of the foundation cows were from the purebred herds of Angus, Hereford, and Shorthorn cattle at Auburn University (Collins et al., 1972).

Later Charolais-, Holstein-, and Brown Swiss-Hereford cross cows were evaluated at the Upper Coastal Plain Substation at Winfield (Patterson et al., 1974).

SOUTHERN REGIONAL BEEF CATTLE BREEDING RESEARCH PROJECT. The Southern Regional Beef Cattle Breeding Research Project (the S-10 project) was apparently started in 1950, with E.J. Warwick as the first director of the project. The various regional projects, including S-10, were cooperative efforts between the USDA and the state experiment stations. C.M. (Charlie) Kincaid, who had previously been at what was then Virginia Polytechnic Institute, became the director later. He, in turn, was replaced as S-10 Director by W.S. (Bob) Temple, who was later replaced by W.T. (Will) Butts. At some point the title of “director” was replaced by the title of “Investigations Leader.” Butts was designated by this latter title in a publication in 1978.

It was apparently in the 1980s that directors (or investigation leaders) were no longer provided by the USDA for the regional projects. At that time (and possibly earlier), administrative advisors were designated for these projects. These were administrators at state experiment stations that were members of the regional projects. In at least most years, there was also a USDA (CSREES) advisor and a department head advisor, who was a department head at one of the participating universities. Two CSREES advisors that did take active roles in the project were R.R. (Dick) Frahm (who had previously been the S-10 representative from Oklahoma) and Pete Burfening.

In the later years of S-10, Doyle Chambers, who was director of the Louisiana State University Experiment Station was the administrative advisor. Starting in 1958 and continuing until 1966, Dr. Lowell T. Frobish, the Director of the Experiment Station at Auburn was the administrative advisor. He was replaced by Dr. D.O. (Don) Richardson, from the University of Tennessee, who was the administrative advisor until his retirement. From 1966 until his retirement this last December, Dr. David Morrison, Associate Director of the Louisiana State University Experiment Station was the administrative advisor for the project.

For many years, the project continued with the S-10 designation, with periodic renewals of the project. Starting in the late 1980s or early 1990s, the USDA gave new numbers to regional projects each time they were renewed. Hence the S10 project was renewed as the S-243 Project. Upon the renewal of the project in 1995, the new designation was S-

277. After renewal in 2003, the project received the designation of S-1013. Last year (2011), the regional project was re-designated as Project S-1045.

SUMMARY AND CONCLUSIONS. An historical overview of some of the early beef cattle animal breeding genetics research in the southern U.S. is presented. A large amount of additional research has been conducted and more is in progress.

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Size, Efficiency, and Complementarity

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The following is from an invited presentation at the 2012 Beef Improvement Federation Annual Meeting. It is based on the findings and ideas of many notable investigators and thinkers, and the reflections and opinions of the author.

Size. Size can be assessed by visual estimates, measurements, or weight. Measurement of volume or capacity appraises body size more accurately than a measure of skeletal size such as height. But weight (or some function of weight) is most useful since that is what is relevant in nutritional requirements and also in marketing beef. Size has varied over the years, depending largely on what cattle are asked to do.

Cattle became smallest in the 1950s in response to demand beginning in the 1930s for smaller, early maturing, quickly fattening types. Beginning in the 1960s, interest developed in changing direction. Selection began for larger breeding stock in our traditional breeds and several large Continental breeds were introduced in the late 1960s-70s. Today, not only have all breeds become larger in the last 40 years, and are still increasing in size, but also differences among breeds have largely disappeared.

Efficiency. The most common measure of biological efficiency of growing animals has been feed:gain (feed conversion). Time-constant periods have been and continue to be the norm for evaluation of potential breeding stock. Over the same period of time, larger animals tend to gain faster and convert feed more efficiently. But when cattle of varying size are fed to the same level of fatness, smaller animals often convert feed more efficiently. A relatively new measure, residual feed intake, appears to reduce misleading conclusions that can occur when comparing different types of animals for the same length of time. In short, research has not shown any simple biological relationship in growing animals between size and efficiency. The same is true of the cow.

Biological efficiency of the cow has most often been measured as pounds of calf weaned per cow exposed to breeding, a trait of an individual cow. This value can mislead. Larger cows can potentially wean heavier calves. But fewer large cows can be maintained on the fixed forage resource of a cow herd. Consequently, cow-calf producers should think of efficiency in terms not of the individual but of the total herd.

Just as with growing animals, size and efficiency interact. Larger (and higher-milking) cows tend to be more biologically efficient when forage supply, quality, and consistency are high and environmental stress is low. Smaller (and lower-milking) cows are favored where those conditions are reversed. Optimum size also is affected by acceptable range of carcass weight. For both the cow-calf and growing-finishing segments, economic efficiency often differs from biological efficiency.

Complementarity. Breeds can be combined to create new genetic packages more useful for some applications. Some combinations may eventually be considered to be new breeds. Merely combining results in progeny with both the strengths and weaknesses of the base breeds. However, breed strengths can be exploited and weaknesses minimized through *complementarity*, which derives not just from combining but from how combinations are made.

An example of complementarity is the use of large sires on small dams. In this way, more calf weight can be produced from the cow weight maintained, so efficiency is improved. This benefit declines if heifers are retained since they are larger than their dams. So, maximum complementarity requires a terminal breeding system. Some terminal systems can be complex and difficult to carry out. For these reasons and since breeds are now more similar, there will probably not be much complementarity obtained due to size. In subtropical climates of the U. S., complementarity will continue to be realized from crossing British and Continental sires (to improve market advantage) on well-adapted Brahman-base cows.

Final Thoughts. It has been estimated that the cow-calf segment requires about two-thirds of the total nutrients consumed from conception to product. Economics dictates these nutrients must come primarily from relatively low-cost forages. The U. S. beef industry will not be sustainable if this is ignored. Market preferences are important, but size of cattle will ultimately rest on what is feasible in the nation's cow herds.

Among other resources, the author relied extensively for this presentation on the following symposia:

- “Crossbreeding for Beef” – 1969 ASAS Annual Meeting, in May, 1970 JAS
- “Beef Cattle Type for Maximum Efficiency” 1971 ASAS Annual Meeting, in May, 1972 JAS
- “Size as a Component of Efficiency” – 1977 ASAS Annual Meeting, in April, 1979 JAS
- “Beef Cow Efficiency Forum” – Proceedings, May, 1984 Michigan St. Univ. and Colorado St. Univ.
- “The Optimum Beef Cow” - 1995 BIF Annual Meeting
- “Measuring Beef Cattle Efficiency” - 2002 BIF Annual Meeting

Brahman Crossbred Performance in Distinct Segments of the United States Beef Industry

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Introduction

Brahman crossbred cows comprise a large portion of the cow-calf industry segment throughout the South, producing calves of generally $\frac{1}{4}$ or less Brahman inheritance. Brahman cattle are very well-adapted to conditions across the Southern United States. Although some calves are managed as stockers in the South and some are fed in South Texas or Southern Arizona, the majority of Southern cattle enter the stocker and feeder segments on the Great Plains. The very obvious environmental differences between that region and the South are climatic and nutritional. Climatic differences are seasonal, as temperatures greatly differ in fall, winter, and spring of most years; humidity is generally lower for most of the year in the Southern Great Plains region than for the Southeastern United States but similar to South-central or Southwestern regions. The nutritional/social world of these Southern calves changes completely in conjunction with long-distance transportation. This results in enormous stress associated with the demand to shift from living and growing in an environment they are well-suited to (especially in the case of calves with $\frac{1}{2}$ or more Brahman background), to an environment to which they are not well-adapted. This unusual combination of requirements surely has no equal in the natural world. After completing this feeding process and conversion to product, there is equal market competition with beef from animals not subjected to this routine. It is not surprising that there are difficulties encountered by the calves in this very un-natural process. The purpose of this paper is to examine experimental results associated with performance of Brahman crossbreds in both environments, that is, in the Southern cow-calf environment and in the stocker and feeder segments. In any evaluation of the performance of Brahman crosses, the way crossbred animals were produced may dramatically influence experimental results. The presence of maternal heterosis (dependent upon the cross) will greatly affect performance of $\frac{3}{4}$ Brahman calves. Probably of greater importance is the fact that calves produced from matings of Brahman bulls to *Bos taurus* cows are much heavier at birth than calves produced by reciprocal matings; research evidence of this difference for other traits is being accumulated.

Brahman Crossbred Cows in the Southern United States

The *Bos indicus* ancestors of the Brahman breed were originally imported and used in the Southern United States (and in similar or harsher areas around the world) because of their adaptation to the extreme conditions characteristic of the region. The ability to survive and reproduce in harsh tropical and subtropical conditions was almost certainly the initial reason that the Brahman breed became an important part of the U.S. beef production system. There is ample research that documents the ability of Brahman purebred and crossbred cattle to live and perform in such subtropical conditions. Brahman cattle have the ability to maintain lower body temperatures and respiration rates under heat duress; they produce less heat than *Bos taurus* cattle, and may be better able to dissipate that heat. They cope better with parasites such as ticks and horn flies than most cattle of European origin. Brahman and Brahman crosses have been documented with better performance in a variety of traits including a superior ability to minimize the toxic effects of grazing certain fescue varieties in the upper South. Adaptation will continue to be of great importance in beef production.

Almost as important as adaptation today is Brahman contribution to heterosis. Heterosis is the difference between averages of crossbreds and straightbreds for a trait. Substantial levels of heterosis have been experimentally documented for almost all traits of relevance for beef production for Brahman crosses in multiple research settings. Brahman-*Bos taurus* levels of heterosis are generally much larger than heterosis in crosses of *Bos taurus* breeds. This heterosis is especially effective for improving traits that are not easily influenced by selection. These include reproductive traits of cows, which are critical for cattlemen. Every crossbreeding study in the Southern United States that has involved Brahman has reported tremendous superiority of Brahman crossbred cows. These have included estimates of heterosis for traits like calving rate or weaning rate from 10 to 45% of the weighted straightbred average. Brahman crossbreds have also been highly productive on the U.S. Great Plains, where they have ranked at or near the best for calving rates, weaning rates, weaning weights of their calves and weaning weight per cow exposed to breeding in the GermPlasm Evaluation (**GPE**) multi-year multi-cycle project in Nebraska (Cundiff, 2005). Excellent performance of F₁ Brahman-British cows has been documented in Alberta (Peters and Slen, 1967).

In Florida, an experimental cow herd was built using straightbreds and crossbreds of Brahman, Angus, and Romosinuano (criollo *Bos taurus* breed). These cows were born from 2002 through 2005 and were then evaluated through 2010. F₁ cows (reciprocal crosses included) were bred to bulls that were of the third breed; straightbred cows of each breed were divided into 2 groups and bred to bulls of the other 2 breeds. Table 1 documents the superior calving rates and weaning rates of the F₁ Brahman-Angus and Brahman-Romosinuano (this is a popular South American cross because of the reputation for high fertility) cows in this project. Estimates of heterosis were 22% and 16% for Brahman-Angus and Brahman-Romosinuano, respectively, for weaning rate (Table 1). This work extended the confirmation of this hybrid advantage to Brahman crossed with criollo cattle—Brahman had previously been documented as having high levels of heterosis with every other evaluated *Bos taurus* breedtype.

Crossbred Brahman cows excelled in performance on the harsh conditions presented by endophyte-infected tall fescue. In the work of Brown et al. (2005) Brahman-Angus cows (reciprocal crosses included) grazing bermudagrass had calving rate 13% greater than the purebred average; the corresponding estimate for cows grazing endophyte-infected tall fescue was 49% greater than the purebred average. It seems (particularly in this case) that the severity of the environment appears to augment the effects of heterosis.

The advantages in heterosis and adaptation offered by the Brahman crossbred cows are too big to ignore in the Southern United States. These advantages support the widespread use of Brahman crossbred cows throughout the South. Approximately 35 to 40% of the calves that enter the U.S. beef production chain have some Brahman background. This large fraction is notable considering market pressure against calves with visible Brahman background (Barham and Troxel, 2007); however, as crosses with Angus (F₁ Brahman Angus and ¼ Brahman ¾ Angus) sale price per hundred lb was very high relative to other crossbred groups (Troxel and Barham, 2012).

Transportation/Receiving

There are at least 3 major stressors for cattle moved from the Southeastern United States to the Great Plains for stocker and feedlot phases. Those include weaning, long-haul transportation, and the potential for large change (decrease) in ambient temperatures. Many of the cattle moved from the South or Southeast to the Great Plains are freshly weaned in the fall of the year and are consequently very susceptible to health problems, which are exacerbated by the long transport and the colder

weather encountered after arrival. Tropical adaptation that is an advantage in the South becomes a detriment on the Great Plains through the winter. Cattle of any breed or type would find these a challenging set of scenarios.

Brahman F₁ steers were heavier than all other steers in Florida at weaning at 7 months of age; they also gained more in the 21 to 35 day period immediately after weaning compared to purebred Brahman and Angus (Table 2; Coleman et al., 2012). Heterosis for ADG in this period was enormous (64%, Table 3). These steers were shipped each year to a research location in Central Oklahoma. F₁ Brahman steers had greater shrink on that 24-hour ride than the other breed groups and unfavorable heterosis for shrink (Table 2), but they had greater daily gain in the 28 days after arrival in Oklahoma (relative to receiving weight), with heterosis of 43% (Table 3). This large estimate may in part represent recovery of water lost in transit. There was no death loss during transportation and the receiving period. These steers were not commingled with steers from other locations, which may have helped minimize potential problems.

Brahman on Winter Pasture

Among those steers (Coleman et al., 2012), ADG of F₁ Brahman-Angus steers grazing winter wheat did not differ from that of Angus steers (Table 2). Brahman-Angus heterosis was 11% (0.2 lb) for ADG during this phase (Table 3). These steers grazed wheat from November through May; the lower ADG of straightbred Brahman and Romosinuano and F₁ Brahman-Romosinuano probably is due in part to their inability to cope well with cold weather, since each of these breed groups would be expected to have minimal adaptation to winter conditions of temperate areas. Straightbred Brahman steers had lower ADG than F₁ Brahman-Angus, F₁ Brahman-Tuli (African *Bos taurus* breed), and ¼ Brahman ¼ Hereford ½ Simmental steers on winter pastures in Oklahoma and Texas (Rouquette et al., 2005); ADG of F₁ Brahman-Angus steers and ¼ Brahman ¼ Hereford ½ Simmental steers did not differ (Table 4). Ferrell et al. (2006) evaluated steers with fractions of 0, ¼, ½, and ¾ Brahman inheritance in Nebraska; the complementary fraction within each group of steers was MARC III composite (¾ British ¼ Continental). These steers were produced by artificial insemination of MARC III cows and F₁ Brahman-MARC III cows to Brahman bulls (½ and ¾ Brahman steers) and F₁ Brahman-MARC III cows bred to MARC III bulls (¼ Brahman steers). Steers were fed either bromegrass hay (as a low-gain, forage-based diet) or corn silage (as a high-gain, forage-based diet) in a 119-day growing period in dry lot in order to measure intake. Dry matter intake, crude protein intake, metabolizable energy intake (metabolizable energy is that energy available for maintenance or growth above that required to digest the source from which it was obtained), and ADG of ½ Brahman steers were highest but did not differ from MARC III steers (Table 5). There were no breed group differences in these intakes per pound of gain; that is steers with different fractions of Brahman background responded to these different growing diets similarly. These steers were evaluated in winter, which may have influenced results.

Brahman in Feedlot

Gain

In the evaluation of Florida steers, the feedlot phase occurred from May through September in Oklahoma; summers on the Great Plains often have high temperatures. Straightbred Brahman had lower ADG in the feedlot phase than all other breed groups (Table 2), which were similar to each other (Coleman et al., 2012). Brahman-Angus heterosis for ADG was 14% (0.26 lb, Table 3). Feedlot ADG of F₁ Brahman-Angus steers did not differ from ¼ Brahman ¼ Hereford ½ Simmental steers (Table 4); these

steers were fed during Texas Panhandle summer conditions (Rouquette et al., 2005). Huffman et al. (1990) reported the highest ADG for Angus steers, followed by $\frac{3}{4}$ Brahman, $\frac{1}{2}$ Brahman, and $\frac{1}{4}$ Brahman steers (Table 6). Pringle et al. (1997) evaluated steers with fractions 0, $\frac{1}{4}$, $\frac{3}{8}$, $\frac{1}{2}$, $\frac{3}{4}$, and 1 Brahman (with Angus as the complementary fraction). Days of feeding to reach target backfat end points were lowest for straight Angus, $\frac{1}{4}$, and $\frac{3}{8}$ Brahman steers (Table 7). Steers in both those studies (Huffman et al., 1990; Pringle et al., 1997) were fed in Florida. Sherbeck et al. (1995) reported the highest ADG for Hereford steers as compared to $\frac{1}{4}$ Brahman $\frac{3}{4}$ Hereford and $\frac{1}{2}$ Brahman $\frac{1}{2}$ Hereford that were fed in Eastern Colorado (Table 8).

Steers from Cycle V of GPE were evaluated to assess the different aspects of gain while being fed a high concentrate diet (Ferrell and Jenkins, 1998). F_1 steers sired by Brahman, Angus, Hereford, Boran, and Tuli sires and out of MARC III cows were assigned to one of 3 groups: 1) an initial (prior to test) slaughter group, in order to facilitate regression estimates of various types of gain; 2) a limit-fed group; and 3) a group fed ad libitum. Table 9 shows means for intake and gain by breed group for these steers. Among the steers in the limit-fed group, Angus and Hereford F_1 steers had greater energy gain than the Brahman F_1 steers. In the ad libitum group, however, there were no differences in energy gain among these 3 breed groups; all were greater than Boran and Tuli F_1 steers. There were no differences for carcass traits within breed and feeding group combinations. Angus F_1 steers had greater carcass weight, backfat, and yield grades than Brahman and Hereford (Table 10). Quality grades were lower for Brahman F_1 steers, but ribeye area was similar for these 3 breed groups. At low intakes, Brahman F_1 steers organ weights were lower than Angus F_1 steers, but were similar at high intakes, indicating greater adaptability or responsiveness to increased feed intake than Angus F_1 steers. Brahman F_1 steers had greater fasting heat production (that is, independent of the heat production associated with digestion) than Angus, and consequently they required a higher metabolizable energy intake for maintenance. Brahman F_1 steers had the highest efficiency of use of metabolizable energy for gain; Angus had the lowest. This work did not support the notion that Brahman cattle have lower energy requirements for maintenance than *Bos taurus* cattle under those conditions. The influence of the winter feeding conditions of this project was not assessed. Brahman F_1 steers seemed to adapt (respond and gain) to a greater extent than the *Bos taurus* steers when permitted the higher intake associated with ad libitum feeding.

Intake

Intake of straightbred Brahman cattle has been reported to be low relative to other breeds or crosses (e.g., Elzo et al., 2009; Table 11); intake of F_1 Brahman cattle has often been reported to be high relative to other groups. Dry matter intake means of F_1 Brahman-Angus and Angus were essentially the same (Table 2, Coleman et al., 2012). F_1 Brahman-Angus and $\frac{3}{4}$ Brahman $\frac{1}{4}$ Angus steers had greater dry matter intake than Angus (Table 6; Huffman et al., 1990); these steers were fed in Florida under conditions which may have depressed the appetites of straightbred Angus steers. Among steers and heifers fed in North Florida, Elzo et al. (2009) reported intake means of animals grouped by residual feed intake (RFI) values. Residual feed intake is daily dry matter intake of an animal adjusted to the average size (metabolic weight) and growth rate (ADG) of cattle evaluated together; low (that is, negative values, since by definition the mean RFI = 0) RFI values are considered to be favorable. Among those calves (from the work of Elzo et al., 2009) that were in the high RFI group (that is, inefficient) and the medium RFI group, F_1 Brahman-Angus, $\frac{3}{8}$ Brahman $\frac{5}{8}$ Angus and $\frac{1}{4}$ Brahman $\frac{3}{4}$ Angus all had higher daily intake than Angus (Table 11). However, the breed group daily intake differences were much lower among the low RFI (efficient) group of calves. In their comparison of F_1 steers, Ferrell and Jenkins (1998) reported greater F_1 Angus-MARC III intake (dry matter and metabolizable energy) than that of F_1 Brahman-MARC

III steers when fed ad libitum; Brahman F₁ steer intake did not differ from F₁ Hereford-MARC III intake (Table 9). They reported no breed differences when steers were limit-fed. Ferrell et al. (2006) reported that dry matter intake, crude protein intake, and metabolizable energy intake of F₁ Brahman-MARC III steers and MARC III steers did not differ in a growing phase when fed a high roughage diet or when fed a high concentrate feed diet; these were higher than ¼ Brahman and Brahman steers (Table 5). Estimates of heritability for intake or RFI are as large as those for weight traits, which are easily altered with selection. Selective improvement of efficiency by lowering RFI of steers would almost certainly result in decreased intake in their half siblings that will become the cows on pasture in the South (C. L. Ferrell, J. O. Sanders, personal communication). This seems counter to the best interests of a producing cow in order to conceive, maintain pregnancy, and perform maternally. Forbes et al. (1998) reported superior intakes of F₁ Brahman cows on pasture relative to other breed types. There may be heterosis for intake on pasture or for the efficient utilization of nutrients from such a forage diet. There may be heterosis for intake in steers fed a high concentrate diet; but it was not detected in Brahman-Angus, Brahman-Romosinuano, or Angus-Romosinuano (Coleman et al., 2012).

Brahman Carcass Traits

In U.S. research trials (Tables 2, 4-8, 10, 12, 13), Brahman F₁ steers have generally had better than average carcass traits related to quantity (carcass weight, dressing percentage, backfat thickness, ribeye area, and yield grade; of course under the assumption that less fat is desirable), but generally lower values for traits related to quality (marbling score, Warner-Bratzler shear force, trained sensory evaluation of tenderness). Results of Brahman (and other *Bos indicus* breeds) across the duration of the GPE cycles in Nebraska were similar (Wheeler et al., 2005). Experimental results have indicated that ¼ Brahman steers did not differ from straightbred *Bos taurus* for marbling score/quality grade or Warner-Bratzler shear force/sensory panel tenderness (Tables 5, 6). Exceptions to this included the results (Tables 7 and 8) of Sherbeck et al. (1995) and Pringle et al. (1997). However, Pringle et al. (1997) reported no difference between quality grades of ¼ Brahman and Angus groups, as well as no marbling score differences of F₁ Brahman-Angus and straightbred Angus steers. No interaction of sire breed and dam breed (representative of breed type) was detected in analyses of marbling score, Warner-Bratzler shear force, and sensory panel tenderness (Riley et al., 2012), but Brahman sire breed means were lower than Angus and Romosinuano for these traits (Table 12). Results from one of the largest comparisons of steers with differing backgrounds of Brahman (Elzo et al., 2012) indicated no difference in tenderness of steaks from ¼ Brahman, F₁ Brahman-Angus, and Angus steers, but Warner-Bratzler shear forces of Angus were slightly better than either. All breed groups with any proportion Brahman had lower marbling scores than Angus steers (Table 13). The differences between straightbred Brahman and *Bos taurus* shear force are real and confirmed by most research to date. Much of the research results involving F₁ Brahman, and really almost all of the ¼ Brahman results (especially when carcasses were electrically-stimulated) reported Warner-Bratzler shear force averages of 10 lb or less, which fits into at least a category of 'slightly tender' (see Platter et al., 2005; Boleman et al. [1997] and Miller et al. [2001] also presented different assessments of consumer acceptability and Warner-Bratzler shear force values in which this threshold of 10 lb appears consistent). Within GPE, F₁ Brahman steers had higher Warner-Bratzler shear force and lower sensory panel tenderness means than F₁ Hereford-Angus, F₁ Hereford-MARC III, and F₁ Angus-MARC III, and were more variable (Wheeler et al., 2005). Marbling score of crossbred Brahman steers has been consistently reported to be lower than Angus or British crossbreds. There appears to be substantial additive genetic variation to permit selective improvement of marbling score in the Brahman breed (Smith et al., 2009).

Summary

1. Brahman crossbred cows continue to be widely used across the Southern United States because of superior adaptability to rough conditions and the extremely high levels of heterosis for most traits (but especially reproductive traits) as crosses with really any *Bos taurus* breed.
2. The movement of Brahman crossbred calves from the South to the Great Plains represents an enormous stress on these animals. However, calves with as much as ½ Brahman background appear to grow and perform very well in the stocker and feeder phases on the Great Plains, especially during the summer. Stocker programs in the South may be advantageous for cattle to recover from the stress of weaning and gain weight, but also to avoid spending winter on the Great Plains. Crossbreds with more than ½ Brahman would likely perform better in feedlots in areas with milder winters, e.g., South Texas or Southern Arizona.
3. After feeding, Brahman crossbred carcasses generally have very good values for traits related to quantity of beef. Most research has documented lower marbling scores (as well as all fat content) and therefore quality grades of carcasses from Brahman crossbreds. There appear to be selective opportunities to improve marbling score in the Brahman breed, should that become an appropriate goal.
4. Steers of ¼ Brahman inheritance and to a lesser extent, F₁ Brahman steers, are the most likely Brahman crossbreds to enter the conventional beef production process, especially the feedlot segment on the Great Plains. Cattle that are ¼ Brahman will qualify for many premium carcass programs. There is substantial research that indicates that both types will perform acceptably for most traits of economic importance.
5. Selection for reduced RFI as a method of improving efficiency during the feedlot stage is discouraged within the breed, as anything that would suppress intake of Brahman crossbred cows on pasture conditions would be undesirable.

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Table 1. Brahman, Angus, and Romosinuano straightbred and crossbred cow reproductive traits

	N	Pregnancy rate	Calving rate	Weaning rate
<u>Straightbred</u>				
Brahman	175	0.76	0.76	0.70
Angus	161	0.84	0.84	0.82
Romosinuano	194	0.82	0.82	0.78
<u>F₁</u>				
Brahman-Angus	420	0.95	0.95	0.93
Brahman-Romosinuano	462	0.89	0.89	0.86
Romosinuano-Angus	397	0.87	0.86	0.81
<u>Heterosis</u>				
Brahman-Angus		0.15 (18%)	0.15 (19%)	0.17 (22%)
Brahman-Romosinuano		0.10 (13%)	0.10 (13%)	0.12 (16%)

¹Cows were born from 2002 to 2005 and were first exposed to bulls as yearlings. First calves as 2-year olds not included in these results. Records through 2010 were included in these results.

²Cows were exposed to bulls annually: F₁ cows were exposed to bulls of the 3rd breed. Straightbred cows of each breed were exposed in approximately equal numbers to bulls of the other 2 breeds.

³Reciprocal F₁ cows combined into single groups.

⁴Heterosis was not detected for Romosinuano-Angus cows for these traits.

⁵Numbers represent numbers of cows in each breed group for palpation. Cows in excess of 40 for each breed group were sold as bred 3-year olds.

⁶Cows were culled after 2 failures to wean a calf.

Table 2. Growth of straightbred and F₁ steers weaned in Florida and transported to Oklahoma

	Brahman	Angus	Romosinuano	F₁ BA	F₁ BR	F₁ RA
N	48	38	74	77	113	118
Prewean ADG, lb/day	1.9	1.7	1.7	2.0	2.0	1.8
Weaning BW, lb	518	441	465	537	524	487
Postwean recovery						
ADG, lb/d (21 to 35 d)	0.8	0.7	0.6	1.2	0.9	0.9
Transition						
Shipping BW, lb	545	465	483	579	555	518
Ship loss, %	8.5	9.5	8.7	9.1	8.7	9.4
Receiving ADG, lb/day (28 d)	0.4	1.0	0.4	1.0	0.5	0.5
Wheat pasture						
Final BW, lb	811	853	784	951	864	872
ADG, lb/d	1.5	2.1	1.7	2.0	1.7	2.0
Feedlot						
Final BW, lb	1045	1100	1062	1217	1121	1159
ADG, lb/d	1.8	2.1	2.1	2.2	2.1	2.2
Overall ADG, lb/day (wean to final)	1.4	1.9	1.6	1.9	1.7	1.8
Intake/efficiency						
N	27	30	29	57	61	57
DMI, lb/d	17.5	18.9	18.7	19.2	18.0	19.5
Feed:Gain	7.75	8.2	7.58	7.91	7.84	7.97
Residual feed intake	-0.37	0.6	-0.01	-0.20	-0.44	0.60
Carcass						
N	48	38	72	79	109	118
Carcass wt, lb	657	695	671	778	721	738
Dressing percentage	61.5	61.5	61.5	63.1	62.1	62.5
Fat thickness, in	0.42	0.6	0.41	0.63	0.48	0.52
Ribeye area, in ²	11.1	12.1	12.0	12.4	12	12.6
Ribeye area, in ² /100 lb carcass	1.70	1.7	1.81	1.61	1.68	1.72
Yield grade	2.9	3.3	2.7	3.5	3.2	3.1

¹Means of F₁ steers include reciprocal crosses.

²Postwean recovery period was from 21 to 35 d. Steers were weaned at average of 7 months of age.

³Steers were weighed immediately prior to loading in Florida and immediately after unloading in Oklahoma. Steers were kept in a grass paddock with access to feed for the 28-day receiving period.

⁴Steers grazed wheat pasture for an average of 120 days.

⁵A subset of steers (n = 90) from all breed groups was evaluated for intake and efficiency each year (2003, 2004, 2005) using Calan feeding system.

⁶Steers were randomly assigned to feeding periods which averaged 101, 129, and 157 days (summer feeding), and were slaughtered commercially in the Texas Panhandle.

⁷Adapted from Coleman et al. (2012) and Riley et al. (2012).

Table 3. Estimates of heterosis, direct and maternal breed effects for steer traits

	Heterosis					
	Brahman-Angus		Brahman-Romosinuano		Romosinuano-Angus	
	Amount	%	Amount	%	Amount	%
Prewean ADG, lb/day	0.20	11	0.13	7.2	0.13	7.8
Wean BW, lb	57	12	33	6.7	35	7.8
Postwean recovery ADG, lb/day	0.46	63.6			0.29	46
Shipping BW, lb	75	14.8	39.7	7.7	44	9.3
Ship loss, lb	8.4	18.5	5.5	12.5	6.2	14.4
Arrival BW, lb	66.1	14.4	35.3	7.5	37.5	8.7
Receive ADG, lb/day	0.29	42.6	0.15	42.4	-0.20	-30
Winter wheat						
Initial BW, lb	81.6	15.5	44.1	8.4	35.3	7.1
Final BW, lb	119.1	14.3	66.1	8.3	52.9	6.5
ADG, lb/day	0.20	11	0.13	8.3	0.07	3.4
Feedlot						
Final BW, lb	29.5	13.4	66.1	6.3	77.2	7.1
ADG, lb/d	0.26	13.6				
Overall ADG, lb/day	0.26	16.1	0.13	8.6	0.11	6.3
Feed:Gain	8.17	14.1				
Carcass wt, lb	102	15.1	57	8.6	56	8.1
Dressing percentage	1.7	2.7			1.1	1.7
Fat thickness, in	0.10	19.9	0.06	15.6		
Ribeye area, in ²	0.82	7.1	0.39	3.3	0.56	5
Ribeye area, in ² / 100 lb	-0.11	-6.6	-0.08	-4.3	-0.06	-3
Yield grade	0.4	13.6	0.3	9.5		

¹Adapted from Coleman et al. (2012). Trait details correspond to those described in Table 1.

²Empty cells indicate that effects were not statistically different from 0.

³Traits from Table 2 are omitted here if no heterosis was detected.

⁴Adapted from Coleman et al. (2012) and Riley et al. (2012).

Table 4. Growth and carcass traits of Brahman straightbred and crossbred steers

	¼ Brahman ¼ Hereford ¼ Simmental	½ Brahman ½ Angus	½ Brahman ½ Tuli	Brahman
N	47	35	37	30
ADG winter, lb/day	2.5	2.4	2.0	1.7
ADG feedlot, lb/day	3.2	3.4	2.6	2.9
Carcass wt, lb	889	848	685	672
Backfat, in	0.37	0.48	0.33	0.25
Ribeye area, in ²	14	13.5	12.3	11.4
Yield grade	2.78	3.06	2.44	2.47
Marbling score	366	392	367	342
Shear force, lb	7.9	8.1	8.1	10.3
Tenderness score	6.0	5.8	6.0	5.3

¹Weaned steers grazed cool-season annuals in East Texas or Central Oklahoma from December to mid-May.

²Steers were commercially-fed in the Texas Panhandle in the summers of 1993 and 1994 to a target of 0.4 inches of backfat.

³Marbling score 300 to 399 = Select.

⁴Tenderness scores evaluated by a trained panel using values from 1 (extremely tough) to 8 (extremely tender).

⁵Adapted from Rouquette et al. (2005).

Table 5. Comparison of intake, growth, and carcass traits of steers with different fractions of Brahman inheritance in Nebraska

Fraction of Brahman inheritance	0	¼	½	¾
N	15	20	7	9
Growing period				
Initial weight, lb	602	562	708	604
Final weight, lb	796	717	906	747
ADG, lb/day	1.6	1.3	1.7	1.2
Dry matter intake lb/day	16.1	13.7	17.6	14.6
Crude protein intake, lb/day	1.7	1.5	1.9	1.6
Metabolizable energy intake, Mcal/day	18.1	15.2	19.7	16.2
DMI/gain lb/lb	13.2	13.9	13.2	19.2
Crude protein intake/gain, lb/lb	1.3	1.4	1.4	1.9
Metabolizable energy intake/gain lb/lb	30.8	32.5	31	44.3
Residual ADG	-0.02	0.03	0.02	-0.03
Residual metabolizable energy intake	0.46	-0.44	-0.03	-0.13
Finishing period				
Initial weight, lb	796	717	906	747
Final weight, lb	1241	1213	1268	1246
Days to finish	155	196	134	199
ADG, lb/day	2.9	2.6	2.6	2.6
Dry matter intake lb/day	18.5	17.0	18.5	15.0
Crude protein intake, lb/day	2.2	2.0	2.2	1.8
Metabolizable energy intake, Mcal/day	26	23.8	25.9	21
Dry matter intake/gain lb/lb	6.5	6.6	7.1	5.9
Crude protein intake/gain lb/lb	0.75	0.74	0.82	0.68
Metabolizable energy intake/gain lb/lb	20.1	20.5	21.9	18.3
Residual ADG	0.04	-0.05	-0.01	0.05
Residual metabolizable energy intake	0.46	-0.44	-0.03	-0.13
Final wt, lb	1243	1213	1268	1248
Carcass				
Carcass wt, lb	750	745	792	769
Dressing percentage	60.4	61.6	62.3	61.6
Marbling score	470	490	390	364
Quality grade	16.2	16.2	15	14.3
Fat thickness, in	0.40	0.59	0.51	0.57
Adjusted fat thickness, in	0.35	0.51	0.43	0.53
Ribeye area, in ²	12.4	11.5	12.2	11.8
Yield grade	2.86	3.45	3.38	3.29

¹The complementary fraction of steers in each breed group was MARC III (¾ British ¼ Continental).

²Steers were fed through the winter either diets of bromegrass hay or corn silage during the growing period of 119 days.

³Steers were fed to a target body weight of 1,235 lb.

⁴Marbling score: Slight = 300; Small = 400; Modest = 500.

⁵Quality grade: Select⁰ = 14, Select⁺ = 15, Choice⁻ = 16.

⁶Adapted from Ferrell et al. (2006).

Table 6. Growth, efficiency, and carcass means for steers of different fractions of Brahman inheritance

Fraction of Brahman inheritance	0	¼	½	¾
Feedlot				
N	41	42	41	41
Days on feed	121	103	102	107
Slaughter wt, lb	1012	990	1087	1100
ADG, lb/day	3.5	3.6	3.9	3.9
Dry matter intake, lb/day	19.4	19.4	21.6	21.8
Feed:Gain	5.6	5.4	5.6	5.6
Carcass				
N	31	32	31	31
Carcass wt, lb	637	624	683	701
Dressing percentage	63	62	62.6	63.4
Ribeye area, in ²	11.6	10.9	11.3	11.6
Ribeye area, in ² /100 lb	1.83	1.76	1.69	1.69
Yield grade	2.8	3	3.1	3.1
Marbling score	Sm ¹³	Sm ¹¹	Sl ⁷⁰	Sl ³⁰
% Choice	55	66	29	7
% Select	45	34	65	74
% Standard	0	0	6	19

¹The complementary fraction of breed inheritance was Angus.

²Steers were either fed as calves or grazed winter pastures until June and were then fed in Florida in 1985 and 1986. They were fed to 2 backfat end point targets: 0.4 or 0.6 in. Intake was assessed using the Calan system. No breed by age-season interactions detected.

³Adapted from Huffman et al. (1990).

Table 7. Growth and carcass traits for steers with different fractions of Brahman inheritance

Fraction of Brahman inheritance	0	¼	⅓	½	¾	1
N	11	13	10	12	12	11
Days on feed	156	156	157	172	168	202
Carcass						
Carcass wt, lb	692	728	679	739	697	712
Dressing percentage	60.7	61.8	60.5	63.1	61.9	62.7
Fat thickness, in	0.47	0.51	0.39	0.43	0.47	0.39
Ribeye area, in ²	12.4	11.6	11.3	12.4	11.3	73
Ribeye area, in ² /100 lb	1.83	1.62	1.69	1.69	1.62	1.62
Yield grade	2.8	3.2	2.8	2.8	3.1	3
Marbling score	436	418	416	366	354	315
Quality grade	607	594	595	556	547	521
% Choice	82	54	60	25	17	9
% Select	18	46	40	58	58	64
% Standard	0	0	0	17	25	27
Shear force (14 days aging), lb	9.5	11.0	9.3	10.4	10.6	13.4
Tenderness	5.9	5.3	6.1	5.6	5.5	4.4
Connective tissue amount	6.1	5.9	6.3	6	6	5

¹The complementary fraction of inheritance in these steers was Angus.

²Steers grazed winter pastures until approximately 1 year of age. They were contract fed in Florida through the winter to backfat end points of either 0.4 or 0.6 inch and slaughtered at University of Florida facilities.

³Marbling score: Slight = 300 to 399; Small = 400 to 499.

⁴Quality grade: Select⁻ = 500 to 549; Select⁺ = 550 to 599; Choice⁻ = 600 to 633.

⁵Detectable amount of connective tissue and tenderness scores evaluated by a trained panel using values from 1 (extremely tough; abundant amount) to 8 (none detected, extremely tender).

⁶Adapted from Pringle et al. (1997).

Table 8. Growth and carcass traits of steers with different fractions of Brahman inheritance

Fraction of Brahman inheritance	0	¼	½
N	77	80	79
ADG, lb/day	4.0	3.5	3.3
Carcass wt, lb	699	703	719
Fat thickness, in	0.45	0.44	0.41
Ribeye area, in ²	11.8	12.4	12.4
Yield grade	3.11	2.91	2.92
Marbling score	SI ⁹¹	SI ⁴⁷	SI ⁴⁵
Shear force, (6 days aging), lb	7.9	9.0	10.1
Tenderness, (6 days aging)	4.9	4.7	4.1
Shear force, (18 days aging), lb	6.4	7.3	8.4
Tenderness, (18 days aging)	5.5	5.3	4.8

¹The complementary fraction of breed inheritance was Hereford.

²Steers had grazed native Great Plains pasture or had been fed a backgrounding diet in a dry lot; time of year not reported. Steers (11 or 12 months of age) were fed to 1 of 4 days-on-feed (84, 98, 112, or 126 days) in Eastern Colorado in 1994. Purebred Hereford were from temperate areas of the United States. Crossbred Brahman steers were from Texas and Mississippi.

³Adapted from Sherbeck et al. (1995).

Table 9. Intake and growth on feed of F₁ steers

	<u>Dry matter intake</u>			<u>Metabolizable energy intake</u>		Days on feed	Initial wt, lb	ADG, lb/d
	N	lb/d	lb/(wt ^{0.75} /d)	Mcal/d	kcal/(wt ^{0.75} /d)			
<u>Limit-fed</u>								
Angus	4	7.5	0.097	10.7	137	137	780	0.93
Boran	8	6.7	0.095	9.5	134	139	657	0.73
Brahman	8	7.0	0.097	9.9	137	140	690	0.66
Hereford	4	6.9	0.097	9.9	138	143	685	0.71
Tuli	8	6.8	0.099	9.7	141	138	666	0.44
<u>Ad libitum</u>								
Angus	4	18.1	0.204	25.8	290	137	796	2.87
Boran	8	12.7	0.164	18.1	233	139	637	2.25
Brahman	8	16.2	0.190	23.0	270	140	708	2.80
Hereford	4	16.7	0.197	23.7	280	143	717	2.78
Tuli	8	14.4	0.177	20.0	251	138	677	2.14

¹Steers were out of MARC III (¾ British ¼ Continental) dams.

²Fed as calves through the winter in Nebraska.

³Adapted from Ferrell and Jenkins (1998).

Table 10. Carcass traits of F₁ steers

Initial slaughter group	N	Carcass wt, lb	Ribeye area, in	Fat thickness, in	Yield grade	Quality grade
Angus	4	434	9.0	0.16	2.0	12.5
Boran	8	348	7.8	0.11	1.8	11.9
Brahman	8	401	8.6	0.11	1.8	11.5
Hereford	4	366	8.2	0.07	1.6	12.3
Tuli	8	357	8.5	0.09	1.6	12.0
Limit-fed						
Angus	4	520	8.9	0.09	2.1	14.0
Boran	8	443	8.7	0.11	1.9	12.4
Brahman	8	463	8.5	0.09	1.9	12.1
Hereford	4	459	9.3	0.11	1.8	13.0
Tuli	8	430	8.5	0.09	1.9	12.5
Ad libitum						
Angus	4	710	11.3	0.56	3.6	16.0
Boran	8	564	10.4	0.27	2.6	13.4
Brahman	8	679	10.5	0.46	3.4	13.9
Hereford	4	661	11.1	0.49	3.2	16.0
Tuli	8	589	11.3	0.34	2.6	14.5

¹Steers were out of MARC III (¾ British ¼ Continental) dams.

²Fed as calves through the winter in Nebraska. Limit-fed steers were fed approximately 77 kcal ME/lb^{0.75}

³Quality grade: Standard⁰ = 11, Standard⁺ = 12, Select⁻ = 13, Select⁰ = 14, Select⁺ = 15, Choice⁻ = 16.

⁴Steers in the initial slaughter group were slaughtered after an adaptation period of 3 months. Steers in the other groups were slaughtered after 140 days on feed.

⁵Adapted from Ferrell and Jenkins (1998).

Table 11. Postweaning efficiency traits in steers and heifers with varying fractions of Brahman inheritance

RFI group/fraction Brahman	N	Gain, lb	Feed:Gain	Intake, lb/day	RFI
High RFI					
1	21	154	11.24	24.1	2.24
¾	14	170	10.96	25.4	2.51
½	37	183	11.05	27.0	2.42
⅜	20	197	10.08	27.7	2.95
¼	22	208	9.69	27.3	2.33
0	30	180	10.43	25.8	2.34
Medium RFI					
1	23	154	9.53	18.9	-0.04
¾	27	207	7.41	21.0	-0.16
½	44	208	7.77	21.4	-0.13
⅜	63	228	6.93	21.6	-0.11
¼	33	224	7.16	21.9	-0.02
0	72	210	7.36	20.8	-0.10
Low RFI					
1	47	156	6.94	14.0	-2.21
¾	8	191	6.86	18.1	-1.35
½	34	186	6.70	16.8	-1.92
⅜	24	211	6.14	18.1	-1.58
¼	11	198	6.49	17.2	-2.34
0	51	186	6.81	16.8	-1.70

¹Calves were evaluated in a 70-day trial after 2 weeks of acclimation to procedures in a GrowSafe feeding system. Calves were an average of 8 months of age and had been weaned for approximately 1 month.

²After adjustment of intake for body weight and ADG (RFI = residual feed intake) during the test period (which was from November through early January), calves were ranked by intake from lowest to highest and divided into

low (RFI < overall mean – 1 standard deviation),

medium (overall mean – 1 standard deviation < RFI < overall mean + 1 standard deviation), and

high (RFI > overall mean + 1 standard deviation) groups.

³Adapted from Elzo et al. (2009).

Table 12. Sire breed averages for carcass traits of steers produced by crosses of Brahman, Angus, and Romosinuano

Breed	Brahman	Angus	Romosinuano
Marbling score	360	475	393
% Choice	31	75	46
% Standard	23	5	10
Shear force, lb	9.7	8.6	9.3
Tenderness	5.4	5.8	5.8
Connective tissue amount	6.1	6.5	6.5

¹Steers were commercially slaughtered after averages of 101, 129, or 157 days on feed. All steers previously grazed wheat pasture for an average of 120 days through the winter in Oklahoma.

²Dam breed was also significant as a main effect for these traits and means were similar to these.

³Marbling score: Slight = 300 to 399; Small = 400 to 499.

⁴Tenderness scores and detectable amount of connective tissue evaluated by a trained panel using values from 1 (extremely tough; abundant amount) to 8 (extremely tender; none detected).

⁵Dam breed means were similar to the sire breed means.

⁶Adapted from Riley et al. (2012).

Table 13. Carcass traits of steers with different fractions of Brahman inheritance

Fraction of Brahman inheritance	0	¼	⅓	½	¾	1
N	216	182	224	341	206	198
Carcass wt, lb	713	753	751	793	756	719
Dressing percentage	61.7	62.4	62.6	63.2	63.2	63.3
WBSF, lb	7.6	7.9	8.1	8.3	8.7	9.2
Tenderness	5.8	5.6	5.5	5.5	5.1	4.6
Connective tissue amount	6.1	6	5.9	5.9	5.5	5.1
Marbling score	446	420	407	394	367	341
Ribeye area, in ²	12.6	12.9	12.8	13.2	12.6	12.0
Fat thickness, in	0.51	0.51	0.51	0.51	0.43	0.35

¹Fractions of Brahman inheritance reported here are categories—actual fractions were ranges. The complementary fraction was Angus.

²From 1989 to 1995 steers were fed in a South Texas feedyard. From 2006 to 2009 they were contract fed in North Florida. Steers were fed as calves through the winter to a target of 0.5 inch backfat and slaughtered commercially in South Texas.

³Detectable amount of connective tissue and tenderness scores evaluated by a trained panel using values from 1 (extremely tough; abundant amount) to 6 (none detected) or 8 (extremely tender).

⁴Marbling score: Slight = 300 to 399; Small = 400 to 499.

⁵Adapted from Elzo et al. (2012).

Productive Longevity in Beef Cows

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Introduction. Cow longevity is one of the most economically important traits in the beef cow. Longevity is inter-related to other important traits, and, therefore, it is difficult to separate the importance of longevity, itself, from the importance of traits that are related to longevity. For example, reproductive performance is usually part of the culling criteria. It is often stated that reproductive performance is the single most economically important trait in beef cattle. It can be argued that, if reproductive performance is included as a criterion for culling, productive longevity can be the most economically important trait to the cow-calf producer. Since the only reason that the seedstock industry exists as a business is to meet the demands of the commercial cattle industry, I will discuss longevity as a factor in commercial herds. However, since most of the genetic improvement for longevity must come from seedstock producers, it is also important to consider longevity in purebred (or other seedstock) herds.

Experimental results have shown that both breed differences and hybrid vigor can have major effects on cow longevity. There are also individual genetic differences within breeds for factors that affect longevity.

Reasons that cows leave herds. I will discuss productive longevity as the length of time that a cow can stay in a herd without dying or being culled. Of course, cows can leave a herd for other reasons besides death and culling. Some other reasons are sales of cows due to drought, reductions in herd size due to selling land or losing a lease on pasture land, the sale of young productive cows as breeding cows, or converting to a different breeding program.

Culling criteria can differ greatly between different producers. Generally, in a commercial herd, a cow should be culled when she can no longer be expected to be profitable in the herd. In a sense, this could be considered to be the case in seedstock herds, but profit may be realized in a different manner, through the future sale of breeding stock. That is, the culling criteria in a purebred or other seedstock herd may be part of the genetic improvement program. In our research herds, we have attempted to use a culling criterion that provides the most information about how long a cow of a given type can remain productive.

For example, in a commercial herd of a particular breed or cross in a particular location, it may be feasible to cull all remaining cows at a given age, because, on the average, cows of this age have too high of a probability of losing their next calf, weaning too light of a calf, dying, or being too thin to have adequate value as a cull cow, if kept for another year.

By contrast, if a seedstock producer is trying to improve genetic merit for longevity, cows of this same age may be given the opportunity to produce additional calves to determine which cows can stay productive to advanced ages so bulls can be kept out of them

In our research herds, we use a criterion that we think provides the most information about cows of a given type, with regard to them staying productive to advanced ages.

Culling Criteria. Some of the culling criteria that are used are reproductive performance, tooth wear (and/or lost teeth), udder problems, eye problems, poor body condition of the cow, lameness or skeletal unsoundness of the cow, death of her calf, light or unthrifty calf at or before weaning, and age of the cow (independent of other factors),

Of course, these reasons for culling are (or can be) related to each other. Some of the reasons for culling for factors other than reproduction would cause reproductive problems if the cow remained in the herd.

Since cows can leave a breeding herd for a variety of reasons, longevity is actually a combination of a number of different traits. Since different producers place different amounts of emphasis on different traits in their culling criteria, the effects of different traits on longevity can differ between operations. Also, different environmental and management differences can affect the ability of a cow to remain productive.

Longevity is mostly a lack of problems. Therefore, it is easier to consider the reasons that cows leave the breeding herd (through either death or culling) than it is to consider why other cows stay in the herd longer.

I have heard someone say (and it may or not have been original from the person from whom I heard it): “The best cow is the one that goes the longest before you notice her.” Of course this implies that you didn’t notice her because she didn’t cause (or have) any problems.

Age of the Cow. In some commercial herds all cows are culled when they reach a certain age. As I said earlier, this may be feasible, if, on the average, cows of this age have too high of a probability of losing their next calf, weaning too light of a calf, dying, or being too thin to have adequate value as a cull cow, if kept for another year. However, there are genetic differences that affect all of these factors. For example, experience may have shown that it is not profitable to keep cows of a given breed after they are ten years of age at a given location; however, cows of another breed or cross may last longer under those same conditions. Even for the same breed of cow, current prices can determine whether it makes sense to sell cows of a given age in a particular year.

Tooth Wear and/or Lost Teeth. In some cases, cows are culled based on the condition of the mouth (i.e., based on the size and/or condition of the incisors (front teeth)). Most people (myself included) have considered the problem with lost or badly worn teeth to be that cows with bad mouths were not able to graze as effectively as those whose mouths were in better condition. However, we have probably all seen cows that have stayed productive after their mouths were smooth. We have usually thought that the kind of pasture that cows were on determined whether cows could stay productive after their mouths had deteriorated.

This is probably true, but, as we have learned more about gum disease (in both people and animals), it seems likely that bad mouths may lead to problems even if the bad mouth does not impair the cow's ability to graze.

There are major genetic differences in the age at which cows' teeth are lost or worn down. In a crossbreeding study at Ft. Robinson, Nebraska, involving straightbred Angus, Hereford, and Shorthorn cows and all of the first crosses of these breeds, cow's mouths were scored for cows from 10 to 15 years of age (Núñez –Dominguez et al., 1991). There were differences among the three different breeds, and the crossbreds had significantly better mouth scores than the straightbred cows.

In a study that we started at the Riesel station and completed at the McGregor station, we found that first crosses of five *Bos indicus* breeds with the Hereford all had significantly better mouth scores than Angus-Hereford first cross cows (Riley et al., (2001).

In what was then Rhodesia, Steenkamp (1969, 1970) found that Hereford cattle had more wear and earlier loss of their temporary incisor teeth than local indigenous Sanga cattle. They measured the hardness of the enamel and studied the type of occlusion (bite) in the two different breeds. They found that the tooth enamel was significantly harder in the indigenous cattle than in the Herefords at 31 to 35 months of age. They also found that, in the Hereford cattle, the incisors bit into the maxillary pad, whereas, in the indigenous cattle the incisors closed on the front edge of the pad. They concluded that this difference in occlusion (bite) caused the teeth of the indigenous cattle to get sharper with age and the teeth of the Hereford cattle to wear prematurely.

In a study at the McGregor station we artificially inseminated both Angus and Hereford cows to Brahman, Boran (an East African *Bos indicus* breed), and Tuli (a Sanga breed from Zimbabwe) in 1992 and 1993. We took mouth scores on the resulting crossbred cows starting in 2004 (when the cows were either 11 or 12 years of age). Both the Brahman and Boran crosses had better mouth scores (more solid mouths and fewer broken or smooth mouths) than the Tuli crosses (Sanders et. al., 2005, and Muntean, 2011).

In these studies where mouths have been scored in old cows, it is possible that some of the cows that were culled at earlier ages for reproductive (or other) reasons could have had bad mouths (badly worn or lost teeth).

Udder Problems. In some cases, cows are culled for udder problems. In other cases, cows lose their calves because of udder problems and the cows are culled because they fail to wean a calf. There are two very different types of udder problems. One is the lack of milk, and the other is the inability of the calf to nurse without assistance because of pendulous udders and/or large teats (length and/or diameter).

In our research herds, we have culled cows if their calves are unable to nurse without assistance and it appears that the udder is bad enough that future calves would not be able to nurse without assistance. That is, we do not cull cows due to the appearance of the udder unless it is rather clear that future calf will be unable to nurse without assistance.

Of course, there are large breed differences in udder characteristics. The main problems are pendulous udders and/or large teats (length and/or diameter). Udder problems can be confounded by the amount of milk that a cow has. Of course, this can lead to more udder problems in cows that produce more milk. However, feed conditions can also lead to udder problems. In many case, a cow whose calves can nurse with no difficulty in the fall or winter will have problems if she calves under lush forage conditions in the spring.

In our study that I referred to earlier, where we compared five crosses of five *Bos indicus* breeds with the Hereford, we made detailed evaluations of the udders each time that a cow calved. There were major differences in udder characteristics and major differences in the proportions of cows that were culled for udder problems. None of the Angus-Hereford crosses or Nellore-Hereford crosses were culled for udder problems, but 19% or more of the other four crossbred types had left the herd for udder problems by the time they were 14 years of age. As stated earlier, cows were culled for udder problems only if their calves could not nurse without assistance. These cows all calved in the spring, often with very lush forage conditions. Therefore, the amount of udder problems was probably higher than it would have been under some other conditions.

In our current genomics project at the McGregor station (using second generation *Bos indicus*-British crosses), we make detailed udder measurements, somewhat like we did in the earlier breed evaluation. We recently have reported apparent chromosomal locations for genes affecting teat length, teat diameter, and udder support score (Williams et al., 2012).

Eye Problems. Most of the eye problems that cause cows to leave the breeding herd are associated with cancer eye. Cancer eye is known to be more prevalent in cows with white pigment around their eyes, and there are probably genetic differences in the susceptibility to cancer eye that are independent of pigmentation.

Reproductive Performance. There are many different ways that reproductive performance can be evaluated and used as culling criteria. As with longevity, high fertility is largely a lack of problems. There are certainly genetic differences in inherent fertility, but many reproductive problems result from the failure to meet nutritional requirements, either due to high nutritional requirements and/or due to inadequate adaptation to the environment.

I believe that the most severe culling for reproductive performance that I know about is that used by Casey Beefmasters at Albany, TX. They require that a yearling heifer conceive in a 45 day breeding season, calve as a two year old, raise a calf every year, and continue to conceive in a 45 day breeding season each year.

It is difficult to genetically improve reproductive performance by selection, but, for the environment in which the cattle are raised, this program combined with selection of bulls out of old cows that have survived the program, probably places about as much emphasis on reproductive longevity as is possible with our current state of knowledge.

As I wrote earlier, some of the other reasons for culling can cause reproductive problems. Depending on the amount and kind of available forage, mouth problems (mainly worn or missing front teeth) can limit the amount that a cow can eat, and, in turn, cause her to fail to come into heat and get bred. There are major genetic differences in the age at which teeth deteriorate.

Selection for longevity. If longevity is measured by a single number (such as the age at which a given cow leaves the breeding herd), then, almost by definition, longevity is low in heritability. This does not mean, however, that genetic effects on longevity are not important. Since productive longevity is closely related to fertility, I think it is useful to simultaneously consider genetic effects on fertility.

It is well recognized that fertility traits are low in heritability. As with longevity, this does not mean that genetic effects on fertility are not important. Many years ago, Tom Cartwright wrote a short article titled “Heredity Must be Important in Cow Fertility.” He used it for class notes, and it may have been printed in a magazine, but I’m not sure about that. In the article, he discussed that, although we know that fertility traits are low in heritability, there are obvious (and major) genetic effects on fertility. Some of the genetic differences in fertility include breed differences, the higher fertility in crossbreds compared to purebreds (hybrid vigor or heterosis), and the lower average fertility in highly inbred cattle (inbreeding depression).

It is tempting to assume that everyone that reads this will understand how there can be large genetic effects on a trait that is low in heritability, but, since the term heritability is so widely mis-used, I think it is necessary to give some explanation. If a trait is high in heritability, a particular animal’s performance for the trait will give a good indication of its genetic merit (breeding value or transmitting ability) in relation to other animals in the same breeding population.

There can be (and are) large average genetic differences between different breeds or crosses for traits that are low in heritability. There can also be large genetic differences between individual animals within a breed for traits that are low in heritability, but it is difficult to make genetic improvement based on individual animal performance.

It has been stated that most of the “fallout” has already happened by the time a cow is four years old. That is, if a heifer gets bred as a yearling, breeds back as a two year old and again as a three year old, most of them will stay productive up until about ten years of age. If all cows are culled that fail to wean a calf, genetic prediction based on the proportion should be effective in increasing the proportion that stay productive to nine or ten years of age. The differences among breeds and crosses in their ability to stay productive to more advanced ages, indicate, to me, that even more can be done if we place enough emphasis on longevity.

Remember that selection response is negatively related to selection response. However, both accuracy and intensity of selection for longevity requires that cows be given the

opportunity to express their inherent ability for the trait. As discussed under the section on reproductive performance, selection of old bulls out of cows that stay productive to advanced ages provides the opportunity to place emphasis on longevity. Selection and use of young bulls out of old cows, as a continuous process, seems to be a logical approach.

Summary and conclusions. There are definitely genetic differences associated with the components of productive longevity. The commercial producer can take advantage of crossbreeding and breed differences. Hopefully the seedstock industry will provide improvements in individual breeds and herds as well.

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SELECTION TOOLS FOR TEMPERAMENT

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WHAT IS TEMPERAMENT?

THE REACTIVITY OR FEAR RESPONSE TO HUMANS

(Fordyce et al., 1988)

TEMPERAMENTAL CATTLE ARE MORE EASILY STRESSED THAN THEIR CALMER HERD MATES

(Curley et al., 2006, 2008)

Why Is Temperament Important To Cattle Producers?

1. Risk of injury to handlers and cattle.
2. Reduced growth rates, carcass traits and immune function.

Temperamental Cattle Have Reduced:

1. Feed Intake
2. Average Daily Gain
3. Intramuscular Fat
4. Carcass Quality
5. Response to Vaccination

Temperamental Cattle Have Increased:

1. Shear Force (tougher meat)
2. Bruised Trim
3. Dark Cutters

How Can Cattle Be Evaluated For Temperament?

Table 1. BIF Guidelines – Docility Score (Chute Score)

Score 1	Docile. Mild disposition. Gentle and easily handled. Stands and moves slowly during processing. Undisturbed, settled, somewhat dull. Does not pull on headgate when in chute. Exits chute calmly.
Score 2	Restless. Quieter than average, but may be stubborn during processing. May try to back out of chute or pull back on headgate. Some flicking of tail. Exits chute promptly.
Score 3	Nervous. Typical temperament is manageable, but nervous and impatient. A moderate amount of struggling, movement and tail flicking. Repeated pushing and pulling headgate. Exits chute briskly.
Score 4	Flighty (Wild). Jumpy and out of control, quivers and struggles violently. May bellow and froth at the mouth. Frantically runs fence line and may jump when penned individually. Exhibits long flight distance and exits chute wildly.
Score 5	Aggressive. May be similar to Score 4, but with added aggressive behavior, fearfulness, extreme agitation, and continuous movement which may include jumping and bellowing while in chute. Exits chute frantically and may exhibit attack behavior when handled alone.
Score 6	Very Aggressive. Extremely aggressive temperament. Thrashes about or attacks wildly when confined in small, tight places. Pronounced attack behavior.

The docility score (chute score) is recommended to be used at or near weaning. The head should be caught but without the squeeze applied.

Advantages of the Docility Score (Chute Score):

1. Easy to use during routine handling.
2. Positively correlated with other measures of temperament ($r \geq 0.35$, $P < 0.005$).

Disadvantages of the Docility Score (Chute Score):

1. Not correlated ($r = 0.09$, $P = 0.46$) with cortisol concentrations in the blood.

BIF Guidelines – Pen Score

1 = Non-aggressive (docile)	Walks slowly, can be approached closely by humans, not excited by humans or facilities
2 = Slightly Aggressive	Runs along fences, will stand in corner if humans stay away, may pace fence
3 = Moderately Aggressive	Runs along fences, head up and will run if humans move closer, stops before hitting gates and fences, avoids humans
4 = Aggressive	Runs, stays in back group, head high and very aware of humans, may run into fences and gates even with some distance, will likely run into fences if alone in pen
5 = Very Aggressive	Excited, runs into fences, runs over humans and anything else in path, “crazy”

The pen score should be evaluated at or near weaning. A small group of calves (n = 5) are penned in a small lot (approximately 24 x 24 feet) and approached by two observers for scoring.

Advantages of Pen Scoring:

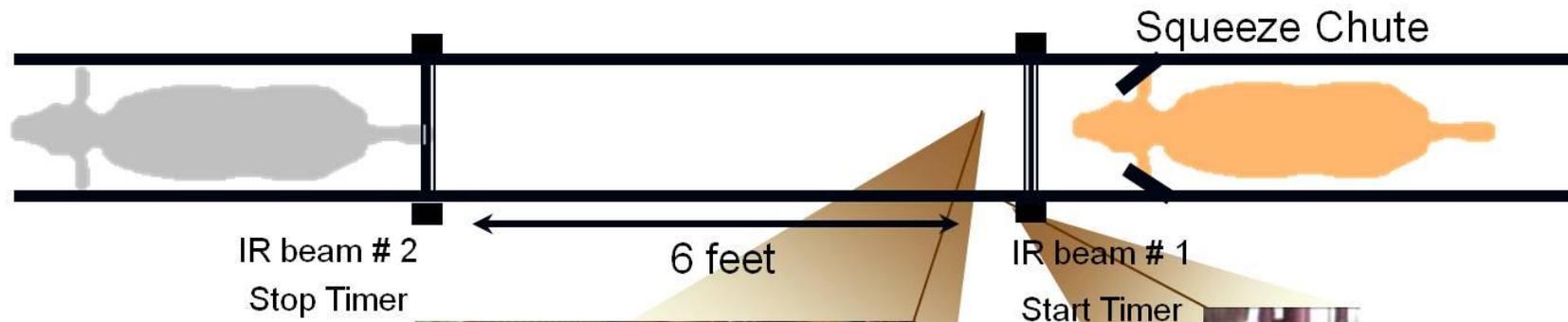
1. Correlated with cortisol concentrations in the blood ($r = 0.29$, $P < 0.05$).
2. Correlated ($r = 0.35$, $P < 0.005$) with other measurements of temperament.
3. Repeated measurements are correlated ($r = 0.25$; $P < 0.05$) with each other and cortisol concentrations in the blood.

Disadvantages of Pen Scoring:

1. Requires another handling of the calves.

Exit Velocity (Flight Speed)

Exit Velocity is the time in feet/second that it takes the calf to travel 6 feet (Burrow et al., 1988).



This method also is recommended to be used at or near weaning.

Advantages of Exit Velocity:

1. It is an objective measurement with no observer bias.
2. Exit velocity is correlated ($r = 0.35$; $P < 0.005$) with other measurements of temperament.
3. Exit velocity is correlated ($r = 0.26$; $P < 0.005$) with concentrations of cortisol in the blood.

Disadvantages of Exit Velocity:

1. Requires equipment for measurements.
2. Does not measure all aspects of temperament such as aggression.
3. The principal behavior measured is likely fear and dislike of being restrained alone.

Other Factors of Exit Velocity

1. Exit velocity can be measured earlier in life (3 weeks of age).
2. Temperamental calves exit velocity increases with age of the calves at a faster rate (0.011 ± 0.0009 feet/second daily; $P < 0.001$) compared with calmer calves.
3. With exit velocity temperamental calves can be identified before weaning.

McGregor Genomics Project

Temperament Scoring

Aggressiveness willingness to hit evaluators	1 = nonaggressive	9 = extremely aggressive
Nervousness animals pacing, running, shaking, vocalizing	1 = completely calm	9 = extremely nervous
Flightiness attempt to escape from handlers	1 = totally quiet	9 = extreme flight
Gregariousness desire to return to the herd	1 = totally willing to be separate	9 = extreme desire to return to the herd
Overall Disposition (scored as a separate trait and not an average of component traits)	1 = completely docile	9 = crazy

The McGregor Genomics Project temperament scoring system requires 4 evaluators to assign scores postweaning. Two evaluators are located at each end of an alley approximately 12 x 75 feet long. Two calves are evaluated at a time in the alley.

Advantages of the McGregor Genomics Project System:

1. Evaluates multiple aspects of behavior.
2. Increased precision of measurement with the 1 to 9 scale.

Disadvantages of the McGregor Genomics Project System:

1. Requires 4 qualified observers.
2. Requires another handling of the calves.

WHAT IS BEING USED BY BREED ASSOCIATIONS?

Docility or Temperament Scores

Breed	System	Range	Age
Angus	BIF Docility	1 – 6	yearling
Brangus	BIF Docility	1 – 6	weaning and yearling
Simmental	BIF Docility	1 – 6	weaning and yearling
Limousin	BIF Docility	1 – 6	weaning and yearling
Brahman	Pen Score	1 – 5	weaning
Saler	Docility Score	1 – 5	weaning and yearling

COMMERCIAL COMPANIES ARE
PROVIDING GENETIC MARKES FOR
TEMPERAMENT IN CONJUNCTION
WITH OTHER MARKERS

TEMPERAMENT IS A HERITABLE TRAIT

HERITABILITY ESTIMATES RANGE FROM 0.25 TO 0.48 FOR BEEF CATTLE

BIF GUIDELINES STATE THAT
TEMPERAMENT IS A
MODERATELY HERITABLE TRAIT

ELIMINATION OF THE MOST
TEMPERAMENTAL CATTLE FROM
A BREEDING HERD WILL IMPROVE
PERFORMANCE OF A HERD

ELIMINATION OF THE MOST
TEMPERAMENTAL CATTLE FROM
A BREED WILL IMPROVE
PERFORMANCE OF A BREED

Selection Tools for Temperament

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Introduction

Temperament in cattle has been defined as the reactivity, or fear response, to humans (Fordyce et al., 1988). Many production practices such as weaning, ear tagging, branding, castration and vaccination have been reported to be stressful to cattle (Burdick et al., 2010; 2011a). Other factors such as social mixing and transportation were also reported to be capable of being stressful. Temperamental cattle have been reported to be more easily stressed than are their calmer herd mates (Curley et al. 2006a-b, 2008). Temperament, the behavioral response to handling, can negatively affect management and beef production as more temperamental cattle can increase the risk of injury to both the handler and the animal (Burrow, 1997). Furthermore, temperamental cattle have reduced growth rates, carcass traits and immune function (Voisinet et al., 1997; Fell et al., 1999; Mondal et al., 2006; Oliphint et al., 2006). Reduction of stress in a herd of cattle should result in improved productivity and therefore profit. Selection of cattle with more easily managed temperaments will result in less stress as well as reduced risk in handling the cattle for routine management. Methods for scoring temperament were developed as early as the 1960s (Strickin and Kautz-Scanavy, 1984). There are several tools available for beef cattle producers to evaluate their cattle for temperament. As temperament is a complex mixture of behaviors each method has some limitations as they are designed.

Docility Score (Chute Score)

The Beef Improvement Federation guidelines include a method termed docility score which is designed to evaluate temperament when cattle are processed in a squeeze chute. Many refer to this method as “chute score”. This system is recommended to be used at or near weaning as the animal’s behavior can be altered by past experiences. The animal should be evaluated with its head caught but without the squeeze applied. The scoring system is presented in Table 1.

Table 1. BIF Guidelines – Docility Score (Chute Score)

Score 1	Docile. Mild disposition. Gentle and easily handled. Stands and moves slowly during processing. Undisturbed, settled, somewhat dull. Does not pull on headgate when in chute. Exits chute calmly.
Score 2	Restless. Quieter than average, but may be stubborn during processing. May try to back out of chute or pull back on headgate. Some flicking of tail. Exits chute promptly.
Score 3	Nervous. Typical temperament is manageable, but nervous and impatient. A moderate amount of struggling, movement and tail flicking. Repeated pushing and pulling headgate. Exits chute briskly.
Score 4	Flighty (Wild). Jumpy and out of control, quivers and struggles violently. May bellow and froth at the mouth. Frantically runs fence line and may jump when penned individually. Exhibits long flight distance and exits chute wildly.
Score 5	Aggressive. May be similar to Score 4, but with added aggressive behavior, fearfulness, extreme agitation, and continuous movement which may include jumping and bellowing while in chute. Exits chute frantically and may exhibit attack behavior when handled alone.
Score 6	Very Aggressive. Extremely aggressive temperament. Thrashes about or attacks wildly when confined in small, tight places. Pronounced attack behavior.

What are the positive or negative factors for using the docility or chute score? One positive factor is that it is easy to use as calves are routinely handled for management at weaning. This score is positively correlated ($r \geq 0.35$, $P < 0.005$) with other measures of temperament to be discussed later in this paper. However chute score was not correlated ($r = 0.09$, $P = 0.46$) with cortisol concentrations in the blood (Curley et al., 2006a). The lack of a correlation with the stress hormones reduces the utility of this measurement of temperament. More excitable cattle which are temperamental have greater amounts of the hormone, cortisol, in their blood (Stahringer et al., 1990; Burdick et al., 2010; 2011a).

Pen Score

The Beef Improvement Federation guidelines include another measurement of temperament termed pen score. As with docility or chute score the recommendation is to evaluate pen score at or near weaning. This is to avoid the adaptation of the animals to repeated handling (Curley et al., 2006a). For this measurement a small group ($n = 5$) of calves are penned in a small lot (approximately 24 feet x 24 feet) and approached by two observers. The individual calf is scored for its response to two observers approaching it on a 1 to 5 scale (Table 2).

Table 2. BIF Guidelines – Pen Score

1 = Non-aggressive (docile)	Walks slowly, can be approached closely by humans, not excited by humans or facilities
2 = Slightly Aggressive	Runs along fences, will stand in corner if humans stay away, may pace fence
3 = Moderately Aggressive	Runs along fences, head up and will run if humans move closer, stops before hitting gates and fences, avoids humans
4 = Aggressive	Runs, stays in back group, head high and very aware of humans, may run into fences and gates even with some distance, will likely run into fences if alone in pen
5 = Very Aggressive	Excited, runs into fences, runs over humans and anything else in path, “crazy”

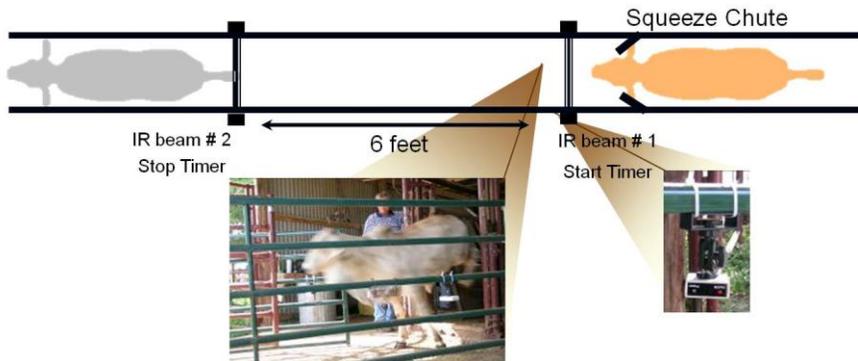
Pen score measures different behaviors than are measured by the docility or chute score. These behaviors are more highly correlated with cortisol concentrations in the blood ($r = 0.29$, $P < 0.05$) than was found for the docility or chute score. It is correlated ($r = 0.35$, $P < 0.005$) with other measurements of temperament (Curley et al., 2006a). Repeated measurements of pen score over several months were correlated ($r = 0.25$; $P < 0.05$) with each other and with cortisol concentrations in the blood. The first pen score rank was predictive of later pen score rank even after the animals were more adapted to handling by humans.

Exit Velocity (Flight Speed)

An objective method to evaluate temperament in cattle is to determine exit velocity or flight speed (Burrow et al., 1988; Curley et al., 2006a). This method determines the velocity at which an animal leaves a squeeze chute. The standard distance to measure velocity is over 6 feet. The first electronic trigger is placed in front of the squeeze chute within 6 feet and the second trigger 6 feet from the first. The elapsed time is converted to velocity by dividing the distance by the elapsed time. The method uses infrared light beams in a timing system developed for competition horse events (Figure 1).

Figure 1. Exit velocity (Flight speed)

Exit Velocity is the time in feet/second that it takes the calf to travel 6 feet (Burrow et al., 1988).



One positive attribute for exit velocity is that it is an objective measurement of temperament. There is no observer bias as it is a measure of time elapsed for the animal to travel 6 feet after being restrained in a chute. Exit velocity is correlated ($r = 0.35$; $P < 0.005$) with chute score or pen score. Exit velocity is correlated ($r = 0.26$; $P < 0.005$) with concentrations of cortisol in the blood (Curley et al., 2006a). Exit velocity can be measured as early as 3 weeks of age in calves. Exit velocity increases as day of age increases from 3 weeks of age through weaning (Burdick et al., 2011b). Temperamental calves exit velocity increased at a faster rate with age ($P < 0.001$; estimated to be 0.011 ± 0.0009 feet/second daily) compared with intermediate (0.0067 ± 0.0011 feet/second daily) and calm calves (0.0016 ± 0.0011 feet/second daily). Temperamental calves increase their rate of speed more rapidly than their calmer herd mates and can be identified before weaning. There are some aspects of temperament such as aggression which are not measured by exit velocity. The principal behavior measured by exit velocity is likely fear and dislike of being restrained and apart from other cattle.

McGregor Genomics Project Temperament Scoring System

An in depth temperament scoring system has been developed for use by the McGregor Genomics Project (Herring et al., 2005). In this system 4 evaluators assign disposition scores post-weaning. Two evaluators are located at each end of an alley that is approximately 12 feet wide and 75 feet long. The evaluators are approximately 50 feet apart. Calves are kept in a pen near the evaluation alley and 2 calves at a time are evaluated in the alley. After 2 minutes an animal is returned to the holding pen and the remaining animal is scored and released into another holding pen. Each animal is scored on a 1 to 9 scale for aggression, nervousness, flightiness, gregariousness and overall temperament (Table 3).

Table 3. McGregor Genomics Project Temperament Scoring

Aggressiveness willingness to hit evaluators	1 = nonaggressive	9 = extremely aggressive
Nervousness animals pacing, running, shaking, vocalizing	1 = completely calm	9 = extremely nervous
Flightiness attempt to escape from handlers	1 = totally quiet	9 = extreme flight
Gregariousness desire to return to the herd	1 = totally willing to be separate	9 = extreme desire to return to the herd
Overall Disposition (scored as a separate trait and not an average of component traits)	1 = completely docile	9 = crazy

The advantages of the McGregor Genomics Project System reside in the evaluation of multiple aspects of behavior which make up the complex behavior we know as temperament or disposition. The overall disposition score is very similar to the pen score but it has a wider scale from 1 to 9. The precision of this system is appropriate for research purposes.

Systems in Use (Breed Associations)

Some breed associations are using the 1 to 6 scoring system of BIF. Some are recording docility scores at weaning, some at yearling and some at both ages. Other associations are using docility or pen scoring systems recorded from 1 to 5 (Table 4).

Table 4. Docility or Temperament Scores

Breed	System	Range	Age
Angus	BIF Docility	1 – 6	yearling
Brangus	BIF Docility	1 – 6	weaning and yearling
Simmental	BIF Docility	1 – 6	weaning and yearling
Limousin	BIF Docility	1 – 6	weaning and yearling
Brahman	Pen Score	1 – 5	weaning
Saler	Docility Score	1 – 5	weaning and yearling

Markers for Temperament

Genetic markers for temperament or docility are available from commercial DNA laboratories. These markers are usually marketed in conjunction with markers for carcass or efficiency traits. Data regarding the correlation between these markers and behavior is not available in the literature as it is regarded as a commercial secret and may be covered by patents. Therefore it is difficult to determine the predictive value of these markers. They may be extremely valuable if a producer's cattle match the types of cattle the markers were developed for. If animals are not similar to the population used to develop the markers the predictive value may be lower.

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Flight speed has been estimated to have a heritability of 0.37 for weaned Australian cattle (Prayaga and Henshall, 2005). Weaning heritability estimates for Brahman and Brahman influenced cattle in the United States for pen score and exit velocity were 0.48 and 0.29, respectively (Loyd et al., 2011). When a combination of pen score and exit velocity was calculated (pen score + exit velocity / 2) to develop a temperament score the estimated heritability of the combined temperament score was 0.43. Heritability estimates for Angus cattle are 0.37 and similar estimates have been made for Limousin cattle. These estimates of heritability fit well with the statement in the BIF guidelines that temperament is a moderately heritable trait.

Summary

Temperament is a heritable trait which will respond to selection similar to selection for growth traits. Several methods are available for use by breeders which measure different aspects of behavior related to temperament. All of these measurements change as cattle are exposed to human handling. One principal factor is that these measurements must be done as early in the production process as possible. The evaluation of temperament should be done at or near weaning from a practical viewpoint. The docility or chute score is less robust than the other systems as is, is not correlated with the stress hormones. Both pen score and exit velocity are correlated with concentrations of cortisol in the blood making them more robust than the docility or chute score. From a research standpoint measurement of as many behaviors as possible is appropriate. However, from a practical production view point some selection of a system for evaluating temperament must be selected. The pen scoring system has the

highest heritability and does not require purchase of equipment. It is correlated with the stress hormones and stress responsiveness. If only one system is to be employed the pen score system should be used.

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Selection Tools for Temperament

R.D. Randel¹, R.C. Vann² and T.H. Welsh, Jr.³

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Introduction

Temperament in cattle has been defined as the reactivity, or fear response, to humans (Fordyce et al., 1988). Many production practices such as weaning, ear tagging, branding, castration and vaccination have been reported to be stressful to cattle (Burdick et al., 2010; 2011a). Other factors such as social mixing and transportation were also reported to be capable of being stressful. Temperamental cattle have been reported to be more easily stressed than are their calmer herd mates (Curley et al. 2006a-b, 2008). Temperament, the behavioral response to handling, can negatively affect management and beef production as more temperamental cattle can increase the risk of injury to both the handler and the animal (Burrow, 1997). Furthermore, temperamental cattle have reduced growth rates, carcass traits and immune function (Voisinet et al., 1997; Fell et al., 1999; Mondal et al., 2006; Oliphint et al., 2006). Reduction of stress in a herd of cattle should result in improved productivity and therefore profit. Selection of cattle with more easily managed temperaments will result in less stress as well as reduced risk in handling the cattle for routine management. Methods for scoring temperament were developed as early as the 1960s (Strickin and Kautz-Scanavy, 1984). There are several tools available for beef cattle producers to evaluate their cattle for temperament. As temperament is a complex mixture of behaviors each method has some limitations as they are designed.

Docility Score (Chute Score)

The Beef Improvement Federation guidelines include a method termed docility score which is designed to evaluate temperament when cattle are processed in a squeeze chute. Many refer to this method as “chute score”. This system is recommended to be used at or near weaning as the animal’s behavior can be altered by past experiences. The animal should be evaluated with its head caught but without the squeeze applied. The scoring system is presented in Table 1.

Table 1. BIF Guidelines – Docility Score (Chute Score)

Score 1	Docile. Mild disposition. Gentle and easily handled. Stands and moves slowly during processing. Undisturbed, settled, somewhat dull. Does not pull on headgate when in chute. Exits chute calmly.
Score 2	Restless. Quieter than average, but may be stubborn during processing. May try to back out of chute or pull back on headgate. Some flicking of tail. Exits chute promptly.
Score 3	Nervous. Typical temperament is manageable, but nervous and impatient. A moderate amount of struggling, movement and tail flicking. Repeated pushing and pulling headgate. Exits chute briskly.
Score 4	Flighty (Wild). Jumpy and out of control, quivers and struggles violently. May bellow and froth at the mouth. Frantically runs fence line and may jump when penned individually. Exhibits long flight distance and exits chute wildly.
Score 5	Aggressive. May be similar to Score 4, but with added aggressive behavior, fearfulness, extreme agitation, and continuous movement which may include jumping and bellowing while in chute. Exits chute frantically and may exhibit attack behavior when handled alone.
Score 6	Very Aggressive. Extremely aggressive temperament. Thrashes about or attacks wildly when confined in small, tight places. Pronounced attack behavior.

What are the positive or negative factors for using the docility or chute score? One positive factor is that it is easy to use as calves are routinely handled for management at weaning. This score is positively correlated ($r \geq 0.35$, $P < 0.005$) with other measures of temperament to be discussed later in this paper. However chute score was not correlated ($r = 0.09$, $P = 0.46$) with cortisol concentrations in the blood (Curley et al., 2006a). The lack of a correlation with the stress hormones reduces the utility of this measurement of temperament. More excitable cattle which are temperamental have greater amounts of the hormone, cortisol, in their blood (Stahringer et al., 1990; Burdick et al., 2010; 2011a).

Pen Score

The Beef Improvement Federation guidelines include another measurement of temperament termed pen score. As with docility or chute score the recommendation is to evaluate pen score at or near weaning. This is to avoid the adaptation of the animals to repeated handling (Curley et al., 2006a). For this measurement a small group ($n = 5$) of calves are penned in a small lot (approximately 24 feet x 24 feet) and approached by two observers. The individual calf is scored for its response to two observers approaching it on a 1 to 5 scale (Table 2).

Table 2. BIF Guidelines – Pen Score

1 = Non-aggressive (docile)	Walks slowly, can be approached closely by humans, not excited by humans or facilities
2 = Slightly Aggressive	Runs along fences, will stand in corner if humans stay away, may pace fence
3 = Moderately Aggressive	Runs along fences, head up and will run if humans move closer, stops before hitting gates and fences, avoids humans
4 = Aggressive	Runs, stays in back group, head high and very aware of humans, may run into fences and gates even with some distance, will likely run into fences if alone in pen
5 = Very Aggressive	Excited, runs into fences, runs over humans and anything else in path, “crazy”

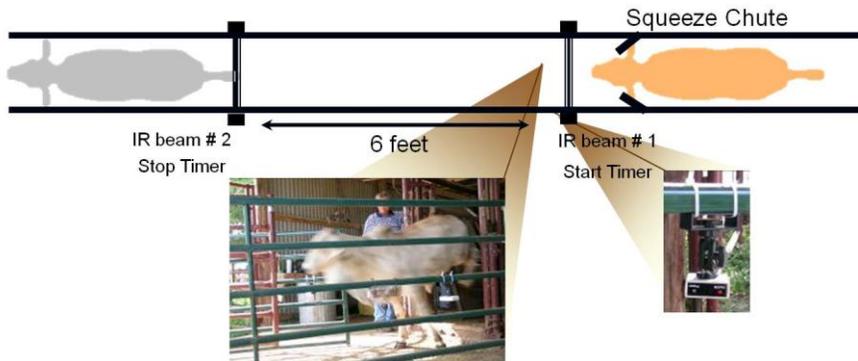
Pen score measures different behaviors than are measured by the docility or chute score. These behaviors are more highly correlated with cortisol concentrations in the blood ($r = 0.29$, $P < 0.05$) than was found for the docility or chute score. It is correlated ($r = 0.35$, $P < 0.005$) with other measurements of temperament (Curley et al., 2006a). Repeated measurements of pen score over several months were correlated ($r = 0.25$; $P < 0.05$) with each other and with cortisol concentrations in the blood. The first pen score rank was predictive of later pen score rank even after the animals were more adapted to handling by humans.

Exit Velocity (Flight Speed)

An objective method to evaluate temperament in cattle is to determine exit velocity or flight speed (Burrow et al., 1988; Curley et al., 2006a). This method determines the velocity at which an animal leaves a squeeze chute. The standard distance to measure velocity is over 6 feet. The first electronic trigger is placed in front of the squeeze chute within 6 feet and the second trigger 6 feet from the first. The elapsed time is converted to velocity by dividing the distance by the elapsed time. The method uses infrared light beams in a timing system developed for competition horse events (Figure 1).

Figure 1. Exit velocity (Flight speed)

Exit Velocity is the time in feet/second that it takes the calf to travel 6 feet (Burrow et al., 1988).



One positive attribute for exit velocity is that it is an objective measurement of temperament. There is no observer bias as it is a measure of time elapsed for the animal to travel 6 feet after being restrained in a chute. Exit velocity is correlated ($r = 0.35$; $P < 0.005$) with chute score or pen score. Exit velocity is correlated ($r = 0.26$; $P < 0.005$) with concentrations of cortisol in the blood (Curley et al., 2006a). Exit velocity can be measured as early as 3 weeks of age in calves. Exit velocity increases as day of age increases from 3 weeks of age through weaning (Burdick et al., 2011b). Temperamental calves exit velocity increased at a faster rate with age ($P < 0.001$; estimated to be 0.011 ± 0.0009 feet/second daily) compared with intermediate (0.0067 ± 0.0011 feet/second daily) and calm calves (0.0016 ± 0.0011 feet/second daily). Temperamental calves increase their rate of speed more rapidly than their calmer herd mates and can be identified before weaning. There are some aspects of temperament such as aggression which are not measured by exit velocity. The principal behavior measured by exit velocity is likely fear and dislike of being restrained and apart from other cattle.

McGregor Genomics Project Temperament Scoring System

An in depth temperament scoring system has been developed for use by the McGregor Genomics Project (Herring et al., 2005). In this system 4 evaluators assign disposition scores post-weaning. Two evaluators are located at each end of an alley that is approximately 12 feet wide and 75 feet long. The evaluators are approximately 50 feet apart. Calves are kept in a pen near the evaluation alley and 2 calves at a time are evaluated in the alley. After 2 minutes an animal is returned to the holding pen and the remaining animal is scored and released into another holding pen. Each animal is scored on a 1 to 9 scale for aggression, nervousness, flightiness, gregariousness and overall temperament (Table 3).

Table 3. McGregor Genomics Project Temperament Scoring

Aggressiveness willingness to hit evaluators	1 = nonaggressive	9 = extremely aggressive
Nervousness animals pacing, running, shaking, vocalizing	1 = completely calm	9 = extremely nervous
Flightiness attempt to escape from handlers	1 = totally quiet	9 = extreme flight
Gregariousness desire to return to the herd	1 = totally willing to be separate	9 = extreme desire to return to the herd
Overall Disposition (scored as a separate trait and not an average of component traits)	1 = completely docile	9 = crazy

The advantages of the McGregor Genomics Project System reside in the evaluation of multiple aspects of behavior which make up the complex behavior we know as temperament or disposition. The overall disposition score is very similar to the pen score but it has a wider scale from 1 to 9. The precision of this system is appropriate for research purposes.

Systems in Use (Breed Associations)

Some breed associations are using the 1 to 6 scoring system of BIF. Some are recording docility scores at weaning, some at yearling and some at both ages. Other associations are using docility or pen scoring systems recorded from 1 to 5 (Table 4).

Table 4. Docility or Temperament Scores

Breed	System	Range	Age
Angus	BIF Docility	1 – 6	yearling
Brangus	BIF Docility	1 – 6	weaning and yearling
Simmental	BIF Docility	1 – 6	weaning and yearling
Limousin	BIF Docility	1 – 6	weaning and yearling
Brahman	Pen Score	1 – 5	weaning
Saler	Docility Score	1 – 5	weaning and yearling

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Genetic markers for temperament or docility are available from commercial DNA laboratories. These markers are usually marketed in conjunction with markers for carcass or efficiency traits. Data regarding the correlation between these markers and behavior is not available in the literature as it is regarded as a commercial secret and may be covered by patents. Therefore it is difficult to determine the predictive value of these markers. They may be extremely valuable if a producer's cattle match the types of cattle the markers were developed for. If animals are not similar to the population used to develop the markers the predictive value may be lower.

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Flight speed has been estimated to have a heritability of 0.37 for weaned Australian cattle (Prayaga and Henshall, 2005). Weaning heritability estimates for Brahman and Brahman influenced cattle in the United States for pen score and exit velocity were 0.48 and 0.29, respectively (Loyd et al., 2011). When a combination of pen score and exit velocity was calculated (pen score + exit velocity / 2) to develop a temperament score the estimated heritability of the combined temperament score was 0.43. Heritability estimates for Angus cattle are 0.37 and similar estimates have been made for Limousin cattle. These estimates of heritability fit well with the statement in the BIF guidelines that temperament is a moderately heritable trait.

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Temperament is a heritable trait which will respond to selection similar to selection for growth traits. Several methods are available for use by breeders which measure different aspects of behavior related to temperament. All of these measurements change as cattle are exposed to human handling. One principal factor is that these measurements must be done as early in the production process as possible. The evaluation of temperament should be done at or near weaning from a practical viewpoint. The docility or chute score is less robust than the other systems as is, is not correlated with the stress hormones. Both pen score and exit velocity are correlated with concentrations of cortisol in the blood making them more robust than the docility or chute score. From a research standpoint measurement of as many behaviors as possible is appropriate. However, from a practical production view point some selection of a system for evaluating temperament must be selected. The pen scoring system has the

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FETAL PROGRAMMING: IMPLICATIONS FOR BEEF CATTLE PRODUCTION

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Introduction

The concept of fetal programming, also known as developmental programming, was first hypothesized using human epidemiological data in which environmental stimulus *in utero* resulted in altered long term development, growth, and disease susceptibility in children from undernourished mothers during the Dutch famine (Barker et al., 1993). Recently, literature regarding the effects of fetal programming in domesticated livestock has been reviewed (Funston et al., 2010a).

Many factors influence livestock nutrient requirements including breed, season, and physiological function (NRC, 2000). Fetal programming responses due to a negative nutrient environment can result from 1) breeding of young dams who compete for nutrients with rapidly growing fetal systems; 2) increased incidences of multiple fetuses or large litters; 3) selection for increased milk production, which competes for nutrients with increased energy demand from fetal and placental growth; or 4) breeding of livestock during high environmental temperatures and pregnancy occurring during periods of poor pasture conditions (Wu et al., 2006; Reynolds et al., 2010). Studies have reported compromised maternal nutrition during gestation can result in increased neonatal mortality, intestinal and respiratory dysfunction, metabolic disorders, decreased postnatal growth rates, and reduced meat quality (Wu et al., 2006). Proper management of cow nutrition during gestation can improve progeny performance and health.

Placental Development

The bovine placenta attaches along the uterine wall at locations known as caruncles. These knob-like structures along the uterine luminal surface serve as attachment sites for the chorionic villi of the fetal placenta known as cotyledons. The caruncle-cotyledonary unit is referred to as a placentome and serves as the primary area of physiological exchange between mother and fetus (Funston et al., 2010a). Establishment of functional uteroplacental and fetal circulation is one of the earliest events during embryonic and placental development (Patten, 1964; Ramsey, 1982) allowing for transportation of all respiratory gas, nutrient, and waste exchanges between maternal and fetal systems (Reynolds and Redmer, 1995; 2001). Transport efficiency is related to uteroplacental blood flow (Reynolds and Redmer, 1995). Although placental growth slows during the last half of gestation, blood flow to the placenta increases three to fourfold from mid to late gestation to support the exponential rate of fetal growth (Rosenfeld et al., 1974; Reynolds et al., 1986; Metcalfe et al., 1988; Ferrell, 1989; Reynolds and Redmer, 1995).

Due to the importance of placental development on fetal nutrient transfer, studies have been conducted to determine how maternal nutrition can influence placental development, or placental programming. Zhu et al. (2007) reported nutrient restriction of beef cows from day 30 to 125 of gestation resulted in reduced ($P < 0.05$) caruncular and cotyledonary weights from nutrient restricted cows compared to control cows, and fetal weights from nutrient restricted cows tended

($P = 0.12$) to be reduced compared to control cows. Following realimentation during day 125 to 250 of gestation, caruncular and cotyledonary weights were still reduced for nutrient restricted cows; however, fetal weight was not different. Vonnahme et al. (2007), using the same cows, reported increased placental angiogenesis as well as angiogenic factor mRNA abundance in the caruncular and cotyledonary tissues at the end of the nutrient restriction period. It was hypothesized the lack of significant fetal weight differences in regard to maternal nutrient restriction may have resulted from the increase in cotyledonary arteriolar density allowing for adequate nutrient transfer (Vonnahme et al., 2007; Zhu et al., 2007).

To measure capillary vascularity of the cotyledon, 4 measurements are collected; capillary area density (**CAD**), a flow-related measure; capillary number density (**CND**), an angiogenesis-related measure; capillary surface density (**CSD**), a nutrient-exchange measure; and area per capillary (**APC**), a capillary density per cross section of muscle area. Vonnahme et al. (2007) reported no difference in these 4 measures from day 30 to day 125 of gestation; however, from day 125 to 250, there were significant differences in CAD, CND, and CSD when comparing control and nutrient restricted cows, suggesting capillary area, numbers, and surface densities had been hindered upon realimentation. Nutrient restriction from day 30 to 125 of gestation did not alter the vasculature of the bovine placenta; however, placental function must have been compromised due to reduced fetal weights.

Fetal Organ Development

Robinson et al. (1977) reported 75% of ruminant fetal growth occurs during the last 2 months of gestation. Due to the minimal nutrient requirement during early gestation, inadequate nutrition during this time was thought to have little significance. However, during the early phase of fetal development critical events for normal conceptus development occur, including differentiation, vascularization, fetal organogenesis, and as previously mentioned, placental development (Funston et al., 2010a).

Fetal organ formation occurs simultaneously to placental development with limb development occurring as early as day 25 of gestation. Following limb development is a sequential development of other organs including the pancreas, liver, adrenal glands, lungs, thyroid, spleen, brain, thymus, and kidneys (Hubbert et al., 1972). Testicle development begins by day 45 in male calves, and by day 50-60 ovarian development begins in female calves. Another important event in female gonadal development occurs approximately day 80 of gestation when oocyte nests break down to form primordial follicles (Nilsson and Skinner, 2009). These follicles represent the oocyte supply available to a female after puberty known as the ovarian reserve and can influence her reproductive lifespan (Hirshfield, 1994). A review by Caton et al. (2007) lists examples of fetal programming in livestock models in individual organs including heart (Han et al., 2004), lung (Gnanalingham et al., 2005), pancreas (Limesand et al., 2005; 2006), kidney (Gilbert et al., 2007), placenta (Reynolds et al., 2006), perirenal fat (McMillin et al., 2004; Matsuaki et al., 2006), and small intestine (Greenwood and Bell, 2003).

Fetal Muscle Development

The fetal stage is also crucial for skeletal muscle development because muscle fiber numbers do not increase after birth (Stickland, 1978; Zhu et al., 2004). Skeletal muscle is particularly vulnerable to nutrient deficiency because it is a lower priority in nutrient partitioning compared with the brain, heart, or other organ systems (Bauman et al., 1982; Close and Pettigrew, 1990); thus, decreased nutrients to the dam during gestation can result in a reduced number of muscle fibers through fetal programming, reducing muscle mass and impacting animal performance. Both muscle fiber number and intramuscular adipocytes, which provide the sites for intramuscular fat accumulation or marbling formation, are influenced during fetal development (Tong et al., 2008; Du et al., 2010).

Figure 1 depicts maternal nutrition effects on fetal skeletal muscle formation and control points in which maternal nutrition has been shown to impact fetal muscle development. Although primary muscle fibers of the bovine fetus form within the first 2 months of gestation (Russell and Oteruelo, 1981), very limited numbers of muscle fibers are formed at this stage; thus, maternal nutrition has little influence on primary muscle formation (Du et al., 2010). During the 2 to 7/8 months of gestation, the majority of muscle fibers form; thus, reducing muscle fiber formation during this stage through any source of stimuli (i.e. maternal nutrition) has long-lasting, irreversible consequences to the offspring (Du et al., 2010). Due to the importance fetal stage plays in adipocyte formation, Du et al. (2010) proposed the prospect of nutritional management altering marbling is greatest for the fetal stage, followed by the neonatal stage, early weaning stage (i.e., 150 to 250 d of age), and finally, weaning and older stages.

Larson et al. (2009) reported increased progeny birth BW from protein supplemented dams, suggesting a potential alteration in fetal muscle growth. Greenwood et al. (2009) reported steers from cows nutritionally restricted during gestation had reduced BW and carcass weight at 30 months of age compared to steers from adequately fed cows. Both Larson et al. (2009) and Greenwood et al. (2009) reported retail yield on a carcass weight basis was greater in steers from nutrient restricted cows, indicating an increased propensity for carcass fatness was not a consequence of nutritional restriction in utero.

Although fetal adipocyte development begins early in gestation, the majority of fetal adipose tissue is not deposited until the final few weeks of gestation (Symonds et al., 2007). Adipose tissue growth occurs through preadipocyte proliferation, impacting formation of new mature adipocytes (hyperplasia), and increasing size and lipid storage capacity of mature adipocytes (hypertrophy). By feeding ewes 150% of NRC nutrient requirements, Tong et al. (2008, 2009) reported increased adipogenesis in fetal skeletal muscle. In a review on fetal programming of skeletal muscle, Du et al. (2010) reported University of Wyoming scientists fed beef cattle 1 of 3 diets from day 60 to 180 of gestation: 100% of NRC (2000) nutrient requirements, 70% of requirements, or 70% of requirements plus supplementation of ruminal bypass protein. Steer progeny from dams fed 70% nutrient requirements plus supplement had numerical decreases in marbling scores when compared to steers from dams fed 100% of requirements. Underwood et al. (2010) also reported increased tenderness in steers from dams grazed on improved pasture compared to steers from dams grazed on native range during mid-gestation.

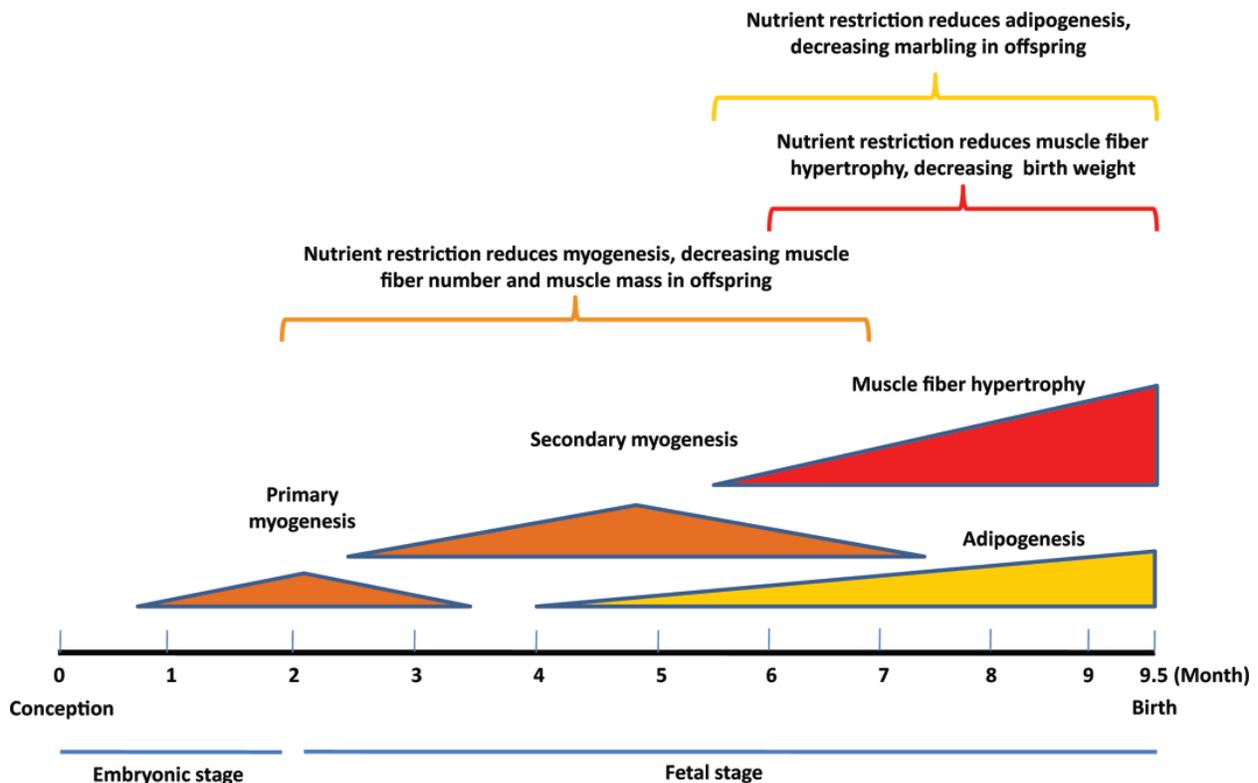


Figure 1. Effects of maternal nutrition on bovine fetal skeletal muscle development. Dates are estimated mainly based on data from sheep, rodents, and humans and represent progression through the various developmental stages. Nutrient restriction during midgestation reduces muscle fiber numbers, whereas restriction during late gestation reduces both muscle fiber sizes and intramuscular adipocyte formation. From Du et al. (2010).

Heifer Progeny Performance

Data regarding the effect of late gestation protein supplementation on heifer progeny performance are reported in Table 1. Martin et al. (2007) conducted a study with cows grazing dormant Sandhills range during late gestation. One group received a 42% CP (DM basis) cube offered 3 times weekly at the equivalent of 1.0 lb/day while another group received no supplement. Calf birth BW between heifer progeny from supplemented and nonsupplemented dams was not different; however, heifer progeny from supplemented cows had increased adjusted 205 day weaning BW, prebreeding BW, BW at pregnancy diagnosis, and improved pregnancy rates compared to heifers from nonsupplemented dams. Martin et al. (2007) also reported after a subset of these heifers were placed in a Calan gate individual feeding system, DMI, ADG, and residual feed intake between heifer progeny from supplemented and nonsupplemented dams was not different.

Funston et al. (2010b), using the same cow herd, offered a distillers based supplement (28% CP, DM basis) 3 times weekly at the equivalent of 1.0 lb/day, or no supplement during late gestation as cows grazed either dormant Sandhills range or corn crop residue. Calf weaning BW was greater ($P = 0.04$) for heifers from protein supplemented dams, whereas Martin et al. (2007) reported a trend ($P = 0.12$) for increased weaning BW for heifers from protein supplemented

dams. Funston et al. (2010b) also reported a decreased age at puberty for heifers from protein supplemented cows and a trend ($P = 0.13$) for higher pregnancy rates when compared to heifers from nonsupplemented dams, possibly related to decreased age at puberty. Similarly, Corah et al. (1975) reported heifers born to primiparous heifers fed 100% of their dietary energy requirement during the last 90 days of gestation were pubertal 19 days earlier than heifers born to primiparous heifers fed 65% of their dietary energy requirement.

Table 1. Effect of maternal protein supplementation on heifer progeny performance

Item	Dietary treatment			
	Martin et al. (2007) ¹		Funston et al. (2010b) ²	
	NS	SUP	NS	SUP
Weaning BW, lb	456	467	492 ^a	511 ^b
Adj. 205-d wt, lb	481 ^a	498 ^b	470	478
DMI, lb/d	14.39	14.88	20.89	20.50
ADG, lb/d	0.90	0.88	1.86 ^x	1.74 ^y
Residual Feed Intake	-0.12	0.07	0.08	-0.04
Age at Puberty, d	334	339	365 ^x	352 ^y
Pregnant, %	80 ^a	93 ^b	83	90

¹NS = dams did not receive protein supplement while grazing dormant Sandhills range during the last third of gestation; SUP = dams were supplemented 3 times per week with the equivalent of 1.0 lb/d of 42% CP cube (DM basis) while grazing dormant Sandhills range during the last third of gestation.

²NS = dams did not receive protein supplement while grazing dormant Sandhills range or corn residue during the last third of gestation; SUP = dams were supplemented 3 times per week with the equivalent of 1.0 lb/d of a 28% CP cube (DM basis) while grazing dormant Sandhills range or corn residue during the last third of gestation.

^{a,b}Means within a study with different superscripts differ ($P \leq 0.05$).

^{x,y}Means within a study with different superscripts differ ($P \leq 0.10$).

Funston et al. (2010b) reported no differences in heifer BW at prebreeding and no differences in calf birth BW, calf production, or second calf rebreeding when comparing heifer progeny from supplemented and nonsupplemented cows. Gunn et al. (1995) reported a decrease in the proportion of singleton, and an increase in the proportion of multiple births over three parities in progeny born to ewes offered a protein supplement while grazing native pastures during the last 100 days of gestation compared to progeny from nonsupplemented ewes. Late gestation supplementation did not alter the proportion of barren ewe progeny (Gunn et al., 1995). Martin et al. (2007) reported a 28% increase in the proportion of heifers calving in the first 21 days of the calving season from protein supplemented dams compared to heifers from nonsupplemented dams. Pryce et al. (2002) reported no difference in progeny heifer reproductive performance when considering dairy cow maternal nutritional status, determined by BCS, DMI, and milk yield of fat and protein.

Steer Progeny Performance

As previously mentioned, studies have reported improved muscle development in steers from adequately fed dams when compared to progeny from nutrient restricted dams. Underwood et al. (2010) reported increased BW gains, final BW, and HCW in steers from cows grazing improved pasture from day 120 to 180 of gestation when compared to progeny from cows grazing native range during that same time (Table 2). Steers from cows grazing improved pasture had increased back fat and tended to have improved marbling scores compared to steers from cows grazing native range.

To determine the effect dietary energy source had on progeny calf performance, Radunz (2009) offered cows 1 of 3 diets during gestation beginning on approximately day 209: hay (fiber), corn (starch), or distillers grains with solubles (fiber plus fat). Corn and distillers grains diets were limit fed to ensure isocaloric intake among treatments. Results indicated reduced birth BW for calves from dams fed grass hay when compared to calves from the other two groups (Table 2), with an increase ($P \leq 0.05$) in calf BW reported through weaning when comparing calves from corn fed dams to hay fed dams. Feedlot performance among treatments was not different; however, calves from hay fed dams required 8 and 10 more days on feed to reach a similar fat thickness when compared to calves from distillers and corn fed dams, respectively.

Table 2. Effect of maternal nutrition on steer progeny performance

Item	Dietary treatment				
	Underwood et al. (2010) ¹		Radunz (2009) ²		
	NR	IP	Hay	Corn	DDGS
Birth BW, lb	85	81	86 ^a	95 ^b	91 ^b
Weaning BW, lb	534 ^a	564 ^b	580 ^a	607 ^b	591 ^{a,b}
ADG, lb/d	3.28 ^a	3.65 ^b	3.37	3.46	3.41
HCW, lb	726 ^a	768 ^b	688	688	675
12-th rib fat, in	0.49 ^a	0.65 ^b	0.48	0.50	0.51
Marbling score ³	420	455	549 ^a	506 ^b	536 ^{ab}

¹NR = dams grazed native range from day 120 to 180 of gestation; IP = dams grazed improved pasture from day 120 to 180 of gestation.

²Hay = dams offered a diet of grass hay beginning on day 209 of gestation; Corn = dams offered limit-fed diet of corn beginning on day 209 of gestation; DDGS = cows offered a limit-fed diet of distillers grains with solubles beginning on day 209 of gestation.

³Where 400 = Small⁰.

^{a,b}Means within a study with different superscripts differ ($P \leq 0.05$).

Stalker et al. (2006, 2007) reported steer progeny from dams supplemented the equivalent of 1.0 lb/day (42% CP, DM basis) cube during late gestation had no difference in calf birth BW when compared to steers from nonsupplemented dams. Conversely, Larson et al. (2009) using the same cow herd, reported an increase in calf birth BW when comparing calves born to dams supplemented the equivalent of 1.0 lb/day (28% CP, DM basis) cube during late gestation to calves from nonsupplemented dams. In the study reported by Stalker et al. (2006), cows were

utilized in a switchback design, whereas cows utilized by Larson et al. (2009) remained on the same treatment over the 3 year study.

Protein supplementation during late gestation increased weaning BW, ADG to weaning, and proportion of calves weaned when comparing calves from supplemented to nonsupplemented dams grazing dormant winter range (Stalker et al., 2006, 2007; Larson et al., 2009; Table 3). Stalker et al. (2006) reported no differences in steer progeny feedlot performance and carcass characteristics when comparing progeny from supplemented and nonsupplemented dams. However, Larson et al. (2009) reported increased ADG, HCW, and marbling scores in steers from supplemented dams. Furthermore, a greater proportion of steers from supplemented dams graded USDA Choice and USDA Choice or greater when compared to steers from nonsupplemented dams. Nonsupplemented cows in Larson et al. (2009) may have been under greater nutritional stress than Stalker et al. (2006) as average weaning date was approximately one month later and possibly had greater impact on fetal development.

Table 3. Effect of maternal protein supplementation of steer progeny performance

Item	Dietary treatment					
	Stalker et al. (2007) ¹		Stalker et al. (2006) ¹		Larson et al. (2009) ²	
	NS	SUP	NS	SUP	NS	SUP
Weaning BW, lb	463 ^a	489 ^b	463 ^a	476 ^b	514 ^a	529 ^b
DMI, lb/d	24.6 ^a	26.6 ^b	18.7	18.8	19.8 ^x	20.3 ^y
ADG, lb/d	3.53	3.70	3.46	3.44	3.66	3.75
Feed:gain	6.97	7.19	5.41	5.46	5.37	5.38
HCW, lb	765 ^a	805 ^b	800	814	805 ^a	822 ^b
Choice, %	--	--	85	96	71	85
Marbling score ³	449	461	467	479	445 ^a	492 ^b

¹NS = dams did not receive protein supplement while grazing dormant Sandhills range during the last third of gestation; SUP = dams were supplemented 3 times per week with the equivalent of 1.0 lb/d of 42% CP cube (DM basis) while grazing dormant Sandhills range during the last third of gestation.

²NS = dams did not receive protein supplement while grazing dormant Sandhills range or corn residue during the last third of gestation; SUP = dams were supplemented 3 times per week with the equivalent of 1.0 lb/d of a 28% CP cube (DM basis) while grazing dormant Sandhills range or corn residue during the last third of gestation.

³Where 400 = Small⁰.

^{a,b}Means within a study with different superscripts differ ($P \leq 0.05$).

^{x,y}Means within a study with different superscripts differ ($P \leq 0.10$).

Influence of Maternal Nutrition on Progeny Health

Several reports have linked maternal nutrition during gestation to calf health, including Corah et al. (1975), indicating increased morbidity and mortality rates in calves born to primiparous heifers receiving 65% of their dietary energy requirement over the last 90 days of gestation compared to calves from primiparous heifers receiving 100% of their energy requirement. One factor contributing to increased morbidity and mortality is decreased birth BW. Calves born to nutrient restricted dams were 4.5 lbs lighter at birth compared to calves from dams receiving

adequate nutrition (Corah et al., 1975). Similarly, Moule (1956) reported as birth BW increases from 4.5 to 9 lb, mortality decreases dramatically in lambs.

Mulliniks et al. (2008) and Larson et al. (2009) indicated reduced proportions of steers treated for respiratory disease in the feedlot from cows supplemented with protein compared to calves from nonsupplemented dams. Stalker et al. (2006) reported increased proportions of live calves weaned to dams offered supplement during late gestation; however, there was no difference in the number of treated calves prior to weaning or in the feedlot. Furthermore, Larson et al. (2009) reported no difference in the number of steer calves treated for respiratory disease prior to weaning. Similarly, Funston et al. (2010b) reported no differences in illness in cohort heifers.

Snowder et al. (2006) reported incidence of disease is more likely after 5 days on feed and remains high through the first 80 days in the feedlot. Furthermore, steers were more likely to become sick compared to heifers in the feedlot. Post-weaning stress is a factor influencing calf health. As mentioned earlier, Funston et al. (2010b) did not report any difference in heifer calf health. These heifers, unlike their steer cohorts, remained at the ranch post-weaning and were maintained on a forage based diet, likely reducing the amount of stress placed on the animal when compared to their steer cohorts who were transported to the feedlot 2 weeks post-weaning and adapted to a concentrate based diet.

Summary

Management of maternal diet beginning during early gestation will ensure proper placental programming resulting in adequate nutrient transfer to the fetus. Maternal nutrition later in gestation has been reported to influence fetal organ development, muscle development, postnatal calf performance, carcass characteristics, and reproduction. Although the mechanisms by which placental and fetal programming occur are not clear, managing resources to ensure proper cow nutrient intake during critical points of gestation can improve calf performance and health.

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Metabolic differences in temperamental Brahman cattle can affect productivity

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Introduction

Many factors may adversely affect the growth and productivity of livestock. These include stressors associated with management practices, such as weaning, handling relative to transportation, and vaccination, that can modulate growth through the production of stress-related hormones (i.e., cortisol, epinephrine, and norepinephrine; Crookshank et al., 1979; Rulofson et al., 1988; Lay et al., 1992; Carrasco and Van de Kar, 2003; Charmandari et al., 2005; Buckham Sporer et al., 2008). As the cost of cattle production continues to increase, it is essential for producers to find ways to decrease input costs in order to increase profit. Temperament is an additional factor that can influence the productivity of cattle. Temperament is defined as the manner in which cattle react to humans or novel environments (Fordyce et al., 1988).

Various methods are used to measure temperament, with the two most commonly used by our laboratories being pen score and exit velocity (see Burdick et al., 2011b for review). Pen score is a subjective method to measure temperament. For this particular measurement, cattle are separated in groups of 3 to 5 animals and their reactivity to a human observer is ranked on a scale of 1, described as calm, docile, and approachable, to 5, described as volatile, very aggressive, and crazy (Hammond et al., 1996). For more information, refer to the BIF Guidelines on pen score. Exit velocity, also referred to as flight speed, is emerging as a more objective measurement of temperament in cattle (Fell et al., 1999; Curley et al., 2006; Müller and Von Keyserlingk, 2006; Vann et al., 2008). Exit velocity (Burrow et al., 1988; Curley et al., 2006) is defined as the rate (in feet/second) at which an animal traverses a specified distance after exiting a squeeze chute. As different aspects of behavior may be measured by different temperament assessment methods (Curley et al., 2006), it is possible that a combined score utilizing multiple methods (i.e. average of pen score and exit velocity to determine a temperament score) may allow more accurate temperament classification. Based on temperament score, cattle can be ranked into temperament groups (i.e., calm, intermediate, and temperamental). A previous study from our group reported the heritability of pen score (0.44), exit velocity (0.28), and temperament score (0.41) in Brahman cattle (Loyd et al., 2011).

Several research groups have demonstrated that temperament can negatively affect various production traits, including live weight, average daily gain, dry matter intake, conception rates,

milk yield, carcass weight, tenderness, rib fat, and bruising score (Hafez and Lindsay, 1965; Fordyce et al., 1985; Fordyce et al., 1988; Burrow and Dillon, 1997; Breuer et al., 2000; Petherick et al., 2003; Prayaga and Henshall, 2005; King et al., 2006; Müller and von Keyserlingk, 2006; Hoppe et al., 2010; Café et al., 2011). Additionally, cattle temperament has been linked to stress responsiveness. Specifically, cattle that are more temperamental have greater circulating concentrations of the adrenal gland derived stress hormones cortisol and epinephrine (Curley et al., 2006; Burdick et al., 2009), which also markedly affect metabolism. The adrenal glucocorticoid cortisol stimulates the production of glucose from substrates such as lactate, glycerol and amino acids (i.e., gluconeogenesis) in the liver, inhibits the uptake of glucose into adipose tissue, and continuously stimulates the breakdown of muscle protein. The adrenal catecholamine epinephrine (i.e., adrenaline) increases plasma concentration of the energy substrates glucose and non-esterified fatty acids (NEFAs; free fatty acids that are not linked to a glycerol molecule) through stimulating the breakdown of glycogen, the molecule by which glucose is stored, and triglycerides. The inherently greater concentrations of metabolically active stress hormones in temperamental cattle may be the basis for how temperament affects metabolic performance during both stress-free and stressful circumstances. The interaction between temperament and metabolism is one area that has yet to be studied in sufficient detail. Herein, we discuss three studies aimed at elucidating the potential influence of temperament on metabolism.

Results and Discussion

A study was designed to determine the effect of temperament on the metabolic response of calves to a glucose tolerance test. During a glucose tolerance test, cattle are administered glucose, and the glucose and insulin responses are monitored. The test is utilized to determine the time it takes for insulin to clear the exogenous glucose, as well as to monitor the relationship between insulin and glucose in order to determine insulin sensitivity or insensitivity. While the test has been utilized in humans as a test for type 2 diabetes, it has also been used in the dairy cattle industry in order to understand the influence of stress and nutritional state on dairy cow milking traits (Lemosquet and Faverdin, 2001). Cortisol plays a major role in glucose metabolism, as discussed above; therefore, it has been hypothesized that the greater basal concentrations of cortisol secreted by temperamental cattle may alter glucose clearance and the insulin response to a glucose tolerance test. For this study, temperament score was determined for 36 Brahman heifers, from which the 6 most temperamental and 6 most calm heifers were utilized for a glucose tolerance test (Bradbury, 2011). During the 90-min period following placement of a jugular catheter and prior to the onset of the glucose tolerance test, temperamental heifers maintained greater plasma concentrations of glucose and cortisol compared to calm heifers ($P < 0.01$ for both glucose and cortisol). Following administration of the glucose bolus, temperamental heifers maintained greater concentrations of cortisol ($P = 0.03$) and glucose ($P < 0.01$; Figure 1) compared to calm heifers. Additionally, there was a time by temperament interaction such that calm heifers had significantly greater concentrations of insulin than

temperamental heifers from 10 to 60 min following administration of the glucose tolerance test ($P < 0.01$; Figure 2). Overall, time to peak insulin concentration, glucose half-life concentration, and glucose half-life time were all greater in temperamental heifers than calm heifers ($P < 0.01$ for all variables). Yet, peak insulin concentration was greater in calm than temperamental heifers ($P = 0.04$). In general, these data demonstrate that temperamental cattle have greater concentrations of cortisol, which remain elevated during periods of stress. Additionally, these data demonstrate that calm heifers were able to clear glucose at a much faster rate than temperamental heifers. Insulin is responsible for increasing the uptake of glucose into adipose and muscle tissue (Hocquette and Abe, 2000). Therefore, temperamental cattle may be more resistant to insulin compared to calm cattle, thus decreasing the amount of glucose that the cattle can absorb and store in muscle, fat, and the liver. As temperament modifies metabolic regulatory responses in heifers, this altered metabolism may partially explain their decreased productivity.

In addition to influencing metabolism, cortisol can also influence the immune response. Elevated cortisol concentration, induced by acute stress (i.e., exposure to a stressor for a short duration of time) is not necessarily detrimental to an animal's health, and may actually enhance immune functions. However, chronic stress, or stress extended over a prolonged period of time, can be detrimental to the health and well-being of livestock. Therefore, it was hypothesized that temperamental cattle would have an altered response to an immune stimulus compared to calm cattle. To test this hypothesis, a study was conducted that utilized calm ($n = 8$), intermediate ($n = 8$), and temperamental ($n = 8$) Brahman bulls, selected based on temperament score from a pool of 60 bulls, in order to determine their response to an immune challenge (i.e., lipopolysaccharide, LPS, a component of the cell wall of gram negative bacteria such as *E. coli*; Burdick et al., 2011a). Prior to administration of LPS, temperamental bulls had greater rectal temperature ($P < 0.01$), and greater cortisol ($P < 0.01$) and epinephrine concentrations ($P < 0.01$). Following administration of LPS, rectal temperature increased in all bulls, with temperamental bulls producing the smallest increase in rectal temperature (i.e., relative to baseline values) compared to calm and intermediate bulls ($P < 0.01$). Sickness behaviors, measured on a scale of 1 (normal maintenance behaviors) to 5 (head distended and lying on side with labored breathing) were also lower in temperamental bulls than intermediate and calm bulls ($P < 0.01$; Figure 3). Therefore, these data suggest that temperamental cattle may display limited behavioral signs of illness, which may prevent proper medical intervention, and increase the risk of transferring pathogens to healthy, calmer cattle. While absolute cortisol concentrations were not different between temperament groups following LPS administration ($P = 0.80$), the change in cortisol relative to baseline concentration (i.e., measured from -2 to 0 h prior to LPS administration) was greater in calm and intermediate bulls than temperamental bulls ($P < 0.01$; Figure 4). The greater cortisol concentrations in temperamental bulls prior to LPS administration may have resulted in the blunted cortisol response observed following LPS administration, which is similar to the results observed by Curley et al. (2008) in which cortisol secretion was stimulated by exogenous administration of adrenocorticotropic hormone (ACTH). Concentrations of plasma epinephrine also remained elevated in temperamental bulls following administration of LPS ($P < 0.05$; Figure

5). In summary, differences exist in the physiological (i.e., rectal temperature and sickness behavior) as well as endocrine (i.e., cortisol and epinephrine) responses of temperamental cattle to an LPS challenge.

The immune system has a high energy demand when activated. It has been estimated that to increase body temperature 1°C an animal must increase its metabolic rate by 10 to 13% (Carroll and Forsberg, 2007). Aside from increasing body temperature, there are additional energy requirements for other immune functions, such as the production of antibodies and acute phase proteins. As demonstrated in the first study, temperament can influence metabolic parameters, including glucose and insulin. These data, together with the immune response data, led our group to hypothesize that differences observed in response to an immune challenge are due to differences in energy availability between calm and temperamental cattle.

To test this hypothesis samples collected during the LPS challenge described above were analyzed for various metabolic parameters. Results from this study indicate that temperamental bulls had an altered metabolic response compared to intermediate and calm bulls (Carroll et al., 2011). Specifically, there was a time by temperament interaction ($P < 0.01$) such that concentrations of glucose increased in response to LPS challenge in calm and intermediate bulls, but there was no increase in glucose concentration observed in temperamental bulls (Figure 6). Additionally, insulin, released in response to increasing blood glucose concentrations, was greater in calm bulls than intermediate and temperamental bulls following administration of LPS ($P < 0.01$). Due to the high concentrations of glucose and insulin observed in calm bulls, it is possible that the calm bulls became insulin resistant, and therefore were unable to properly regulate the uptake of glucose from the circulation and into tissues that required it, which may partially explain the greater amount of sickness behaviors observed in calm bulls. Studies performed in the 1930s and described by Long et al. (1940) found that removal of the adrenal gland, and subsequent decreases in cortisol, caused a decrease in glucose concentrations and a decrease in the ability to store glucose as glycogen in the liver and muscle. It is possible that greater cortisol concentrations observed in the temperamental bulls may make them more resistant to cortisol, as suggested earlier, which may have reduced their subsequent glucose and insulin responsiveness following LPS administration. This is supported by the initial study described above, in which temperamental heifers failed to produce an insulin response to a glucose tolerance test, while maintaining greater concentrations of cortisol compared to calm heifers (Bradbury, 2011).

Temperament also influenced the availability of NEFAs. Specifically, temperamental bulls maintained greater concentrations of NEFA both prior to and following administration of LPS ($P < 0.01$; Figure 7). A greater concentration of NEFA supports a previous report which found that temperamental cattle fail to deposit adequate amounts of fat, and suggests an influence of temperament on adiposity, or fat content (Nkrumah et al., 2007). We concluded that temperamental cattle were utilizing NEFA for energy in the presence of low glucose concentrations, thus preventing the incorporation of fatty acids into triglycerides inside fat cells.

It is interesting to note that greater concentrations of NEFA have been linked to insulin resistance (Lam et al., 2003). Additionally, NEFA concentrations were negatively associated with insulin and glucose concentrations during the LPS challenge, suggesting a negative relationship between insulin and NEFA concentrations. Temperamental cattle also had lower concentrations of blood urea nitrogen (BUN), an indicator of protein break down ($P = 0.01$). This suggests that temperamental bulls did not have to break down muscle protein in order to provide energy during the immune challenge, as did intermediate and calm bulls. Collectively, these data suggest that temperamental cattle may be utilizing NEFA rather than glucose for energy, which may have influenced their response to the LPS challenge.

Together, these data suggest that clear metabolic differences exist between calm and temperamental Brahman calves. The decreased ability to utilize glucose, likely due to a high concentration of cortisol, supports the potential for temperamental cattle to utilize an alternate source of energy when glucose concentrations are low. Therefore, it is likely that temperamental cattle utilize free fatty acids, resulting from the continuous lipolysis of adipose tissue, to fuel tissues and organs that can utilize other energy sources rather than glucose. As temperamental cattle do not deposit fat at the same rate as do calm cattle (Nkrumah et al., 2007), producers may want to feed temperamental cattle differently as they may not reach the same quality grade as calmer cattle. These data go against treating ‘all cattle the same’, as alternative management for temperamental cattle (e.g. not implanting due to the likelihood of decreased fat deposition by temperamental cattle) may decrease input costs. Future research by our research team is focused on determining if alternative management strategies for calm versus temperamental cattle can increase profitability through reducing costs.

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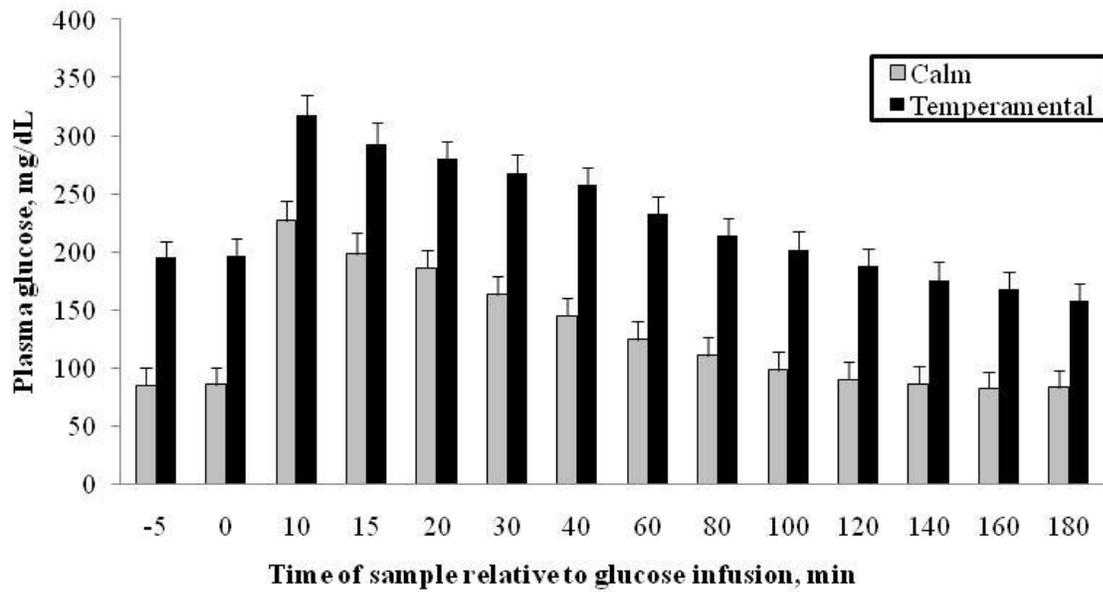


Figure 1. Plasma glucose response to administration of a glucose tolerance test in calm and temperamental Brahman heifers (Bradbury, 2011).

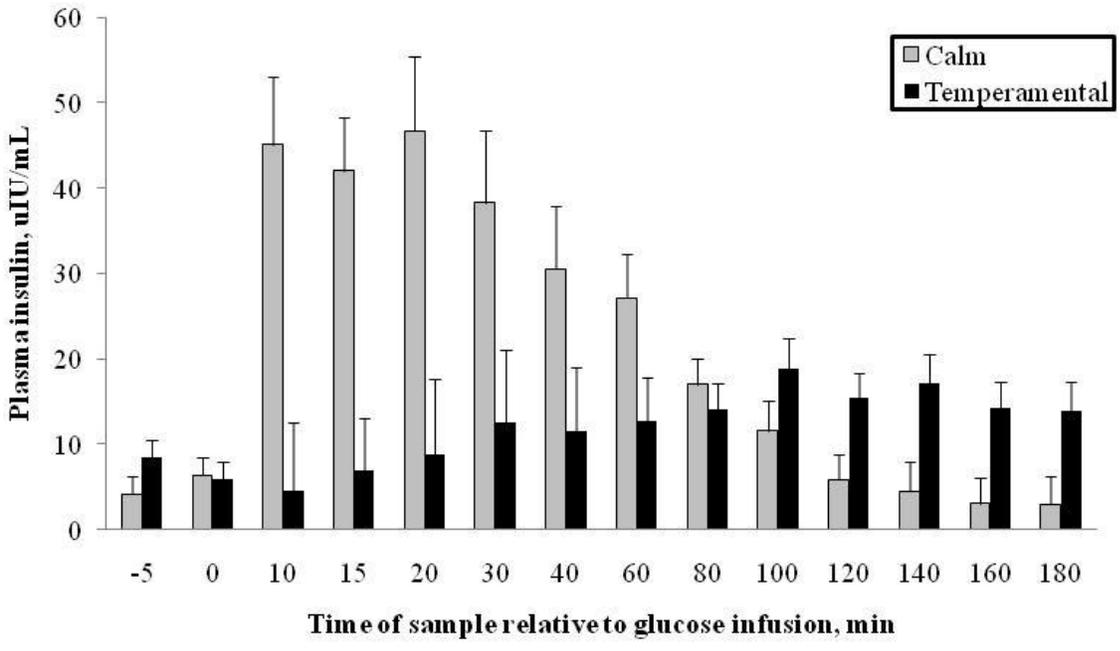


Figure 2. The insulin response to administration of a glucose tolerance test in calm and temperamental Brahman heifers (Bradbury, 2011).

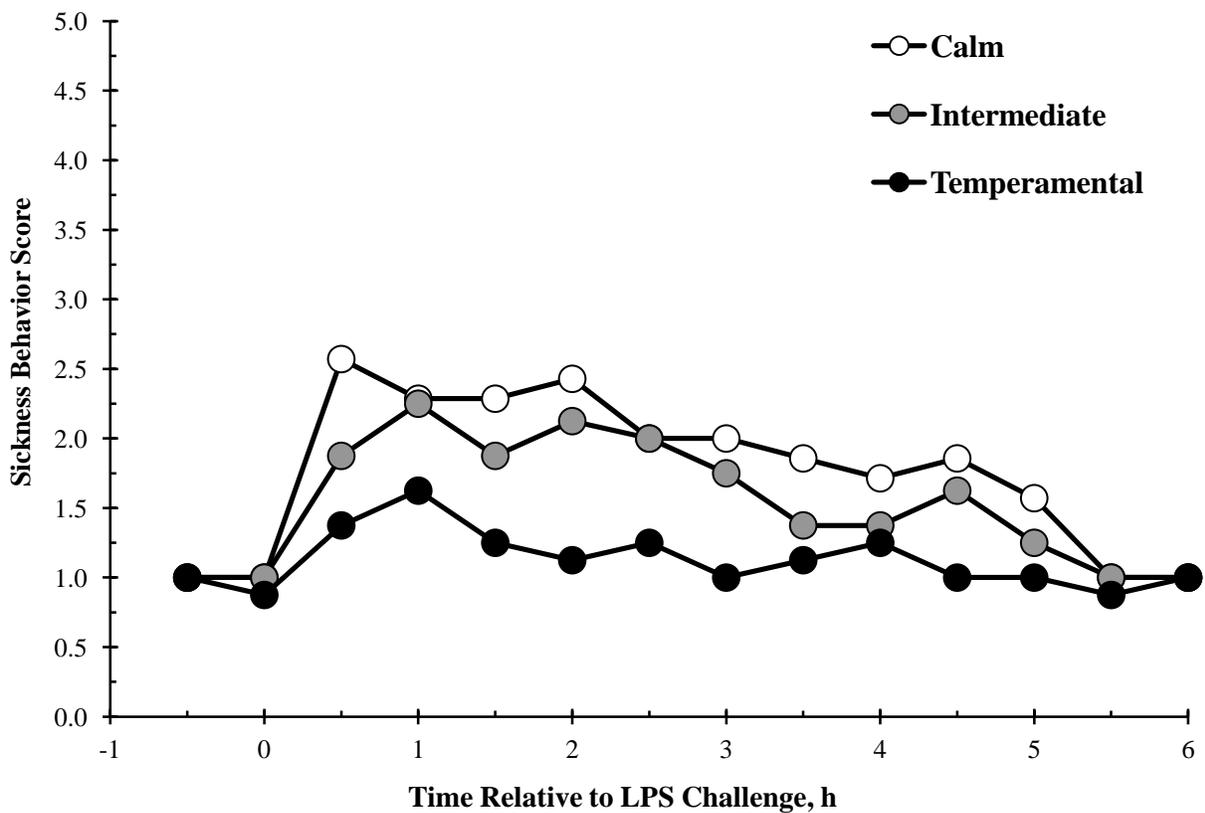


Figure 3. Sickness behavior response to administration of lipopolysaccharide (LPS) in calm, intermediate, and temperamental Brahman bulls (Burdick et al., 2011a).

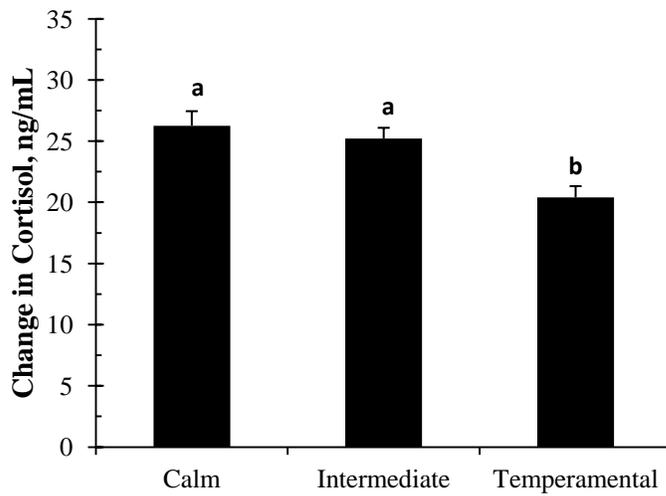


Figure 4. Average change in serum cortisol concentration (relative to an average of baseline cortisol concentrations) following administration of lipopolysaccharide (LPS) in calm, intermediate, and temperamental Brahman bulls (Burdick et al., 2011a). Unlike superscripts represent differences between temperament groups ($P < 0.05$).

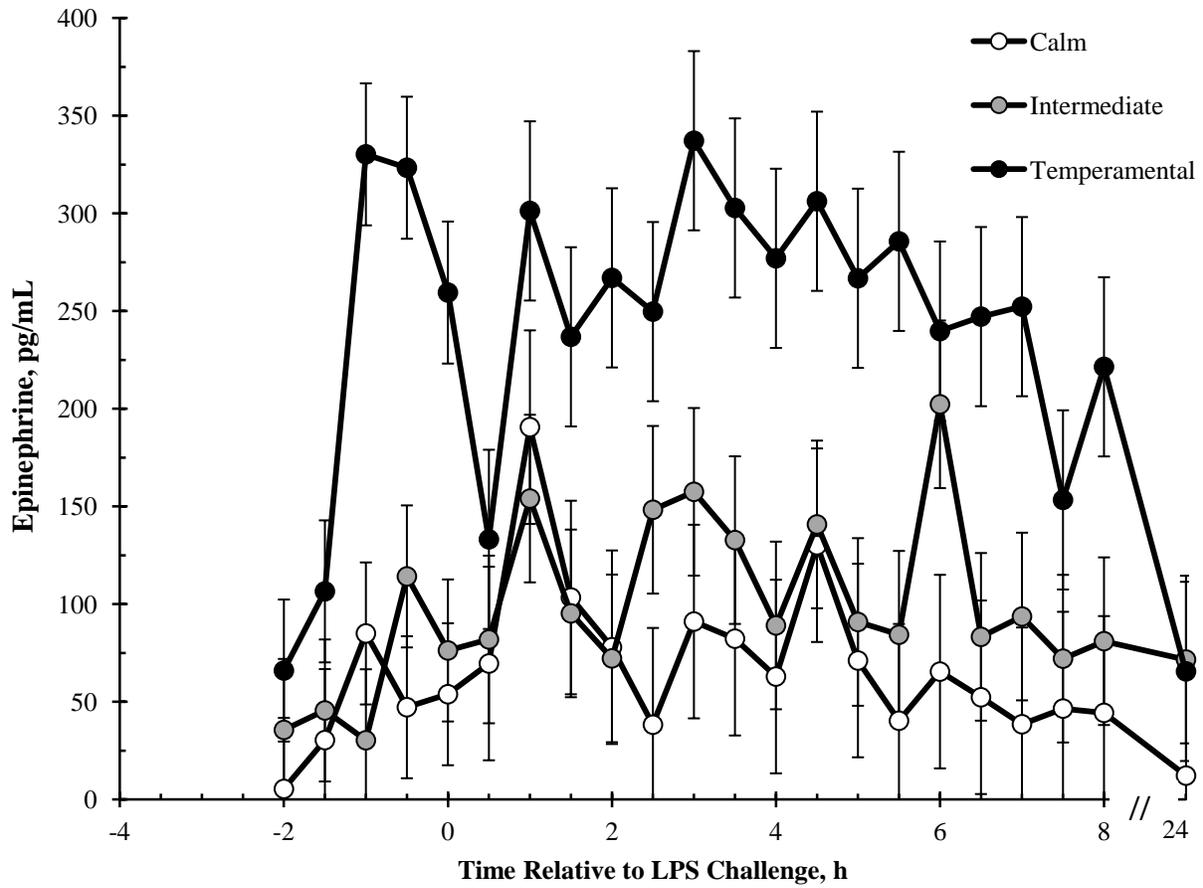


Figure 5. Plasma epinephrine response to administration of lipopolysaccharide (LPS) in calm, intermediate, and temperamental Brahman bulls (Burdick et al., 2011a).

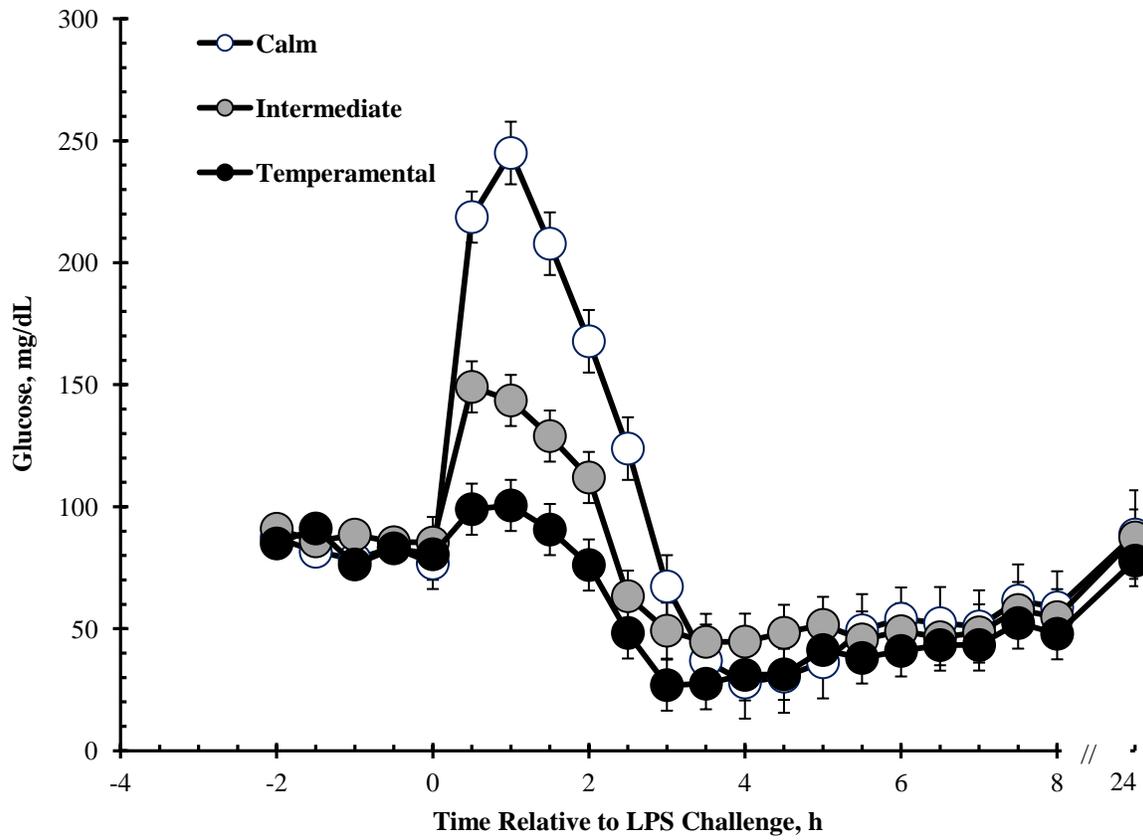


Figure 6. Serum glucose response to administration of lipopolysaccharide (LPS) in calm, intermediate, and temperamental Brahman bulls (Carroll et al., 2011).

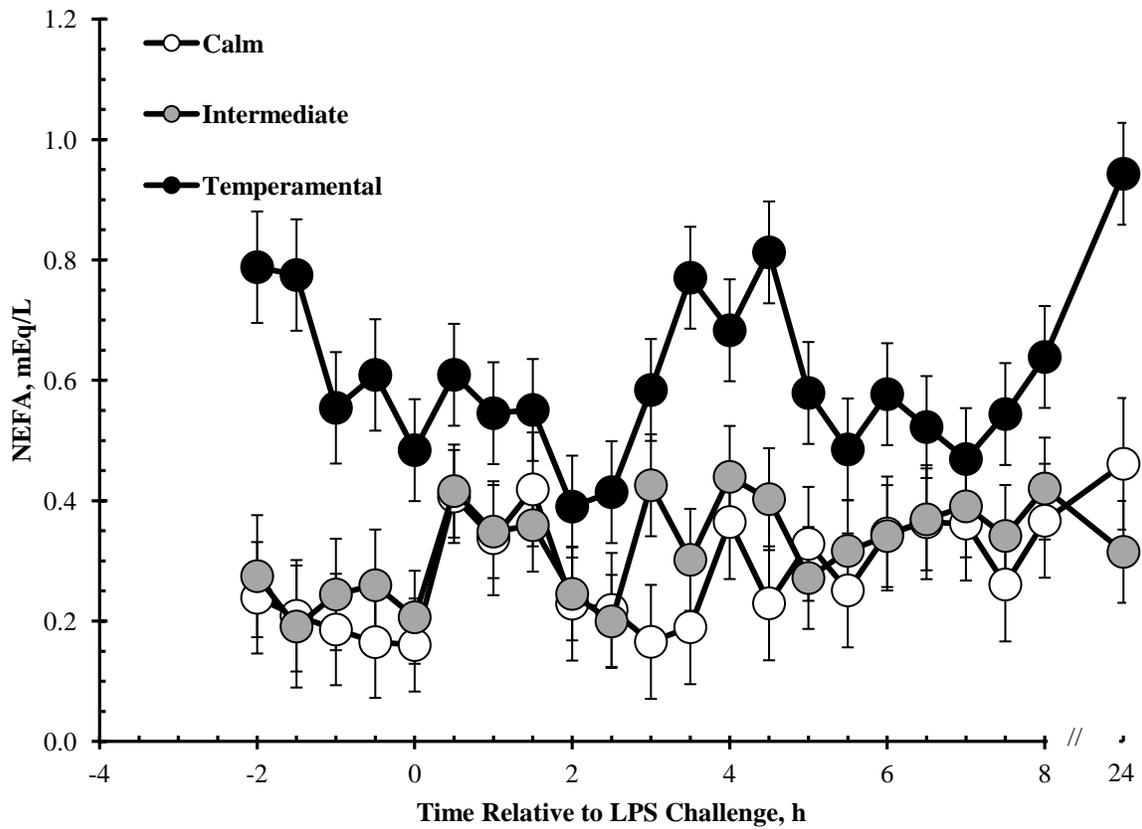


Figure 7. Serum non-esterified fatty acid (NEFA) response to administration of lipopolysaccharide (LPS) in calm, intermediate, and temperamental Brahman bulls (Carroll et al., 2011).

Metabolic Differences in Temperamental Brahman Cattle Can Affect Productivity

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Temperament

- ❑ Temperament in cattle can be defined as the response of an animal to being handled by a human (Fordyce et al., 1982). It is assessed by the way that cattle react to human handling and interaction.

- ❑ Temperament and cattle management
 - ❑ Human interaction is inevitable.
 - ❑ Destructive to themselves, facilities, other animals.

- Cattle temperament can influence many areas of production including reproduction, immunity, and carcass traits.

- ❑ Petherick et al. (2009) reported that fear response can be reduced with proper human handling and association with positive events.
 - ❑ Scores re-evaluated over time did not change, even though fear was sometimes lessened.

- Temperament is predominately innate and heritable in *Bos taurus* cattle (Gauly et al., 2001).

- Heritability of pen score (0.44), exit velocity (0.28), and temperament score (0.41) has been reported in Brahman cattle (Loyd et al., 2011).

Temperament

- ❑ Cattle that are more temperamental:
 - ❑ Tend to have significantly lower body weights than more calm animals (Tulloh, 2004).
 - ❑ Lower BCS, carcass and slaughter weights, dressing percentage (Burrow and Dillon, 1997; Petherick et al., 2002)
 - ❑ Lower ADG and higher shear force values (del Campo et al., 2010)
 - ❑ Decreased tenderness at slaughter (King et al., 2006)

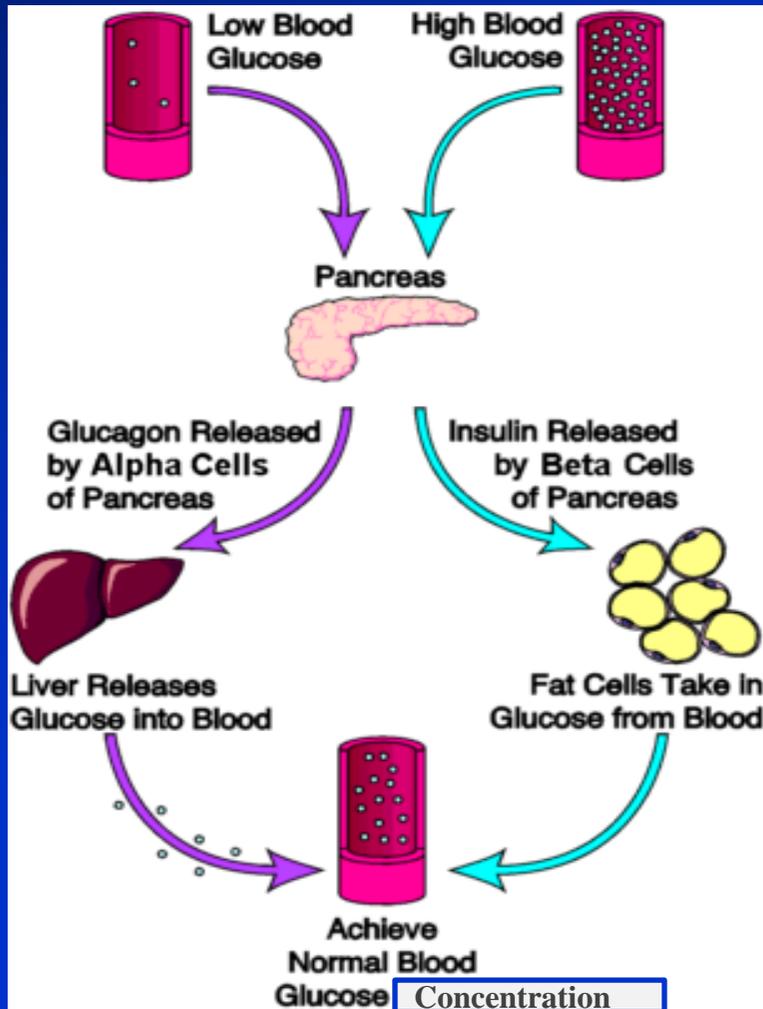
Temperament

- ❑ Animals of different temperaments have diverse functional characteristics of their HPA axis and therefore react to stress differently (Curley et al., 2008).
- ❑ Cattle that are more excitable have greater concentrations of stress hormones such as cortisol and epinephrine than calm cattle, which is correlated to temperament.
(King et al., 2006; Curley et al., 2006, 2008).
- ❑ Cortisol (a glucocorticoid) is known as the hormone of stress.

Glucocorticoids

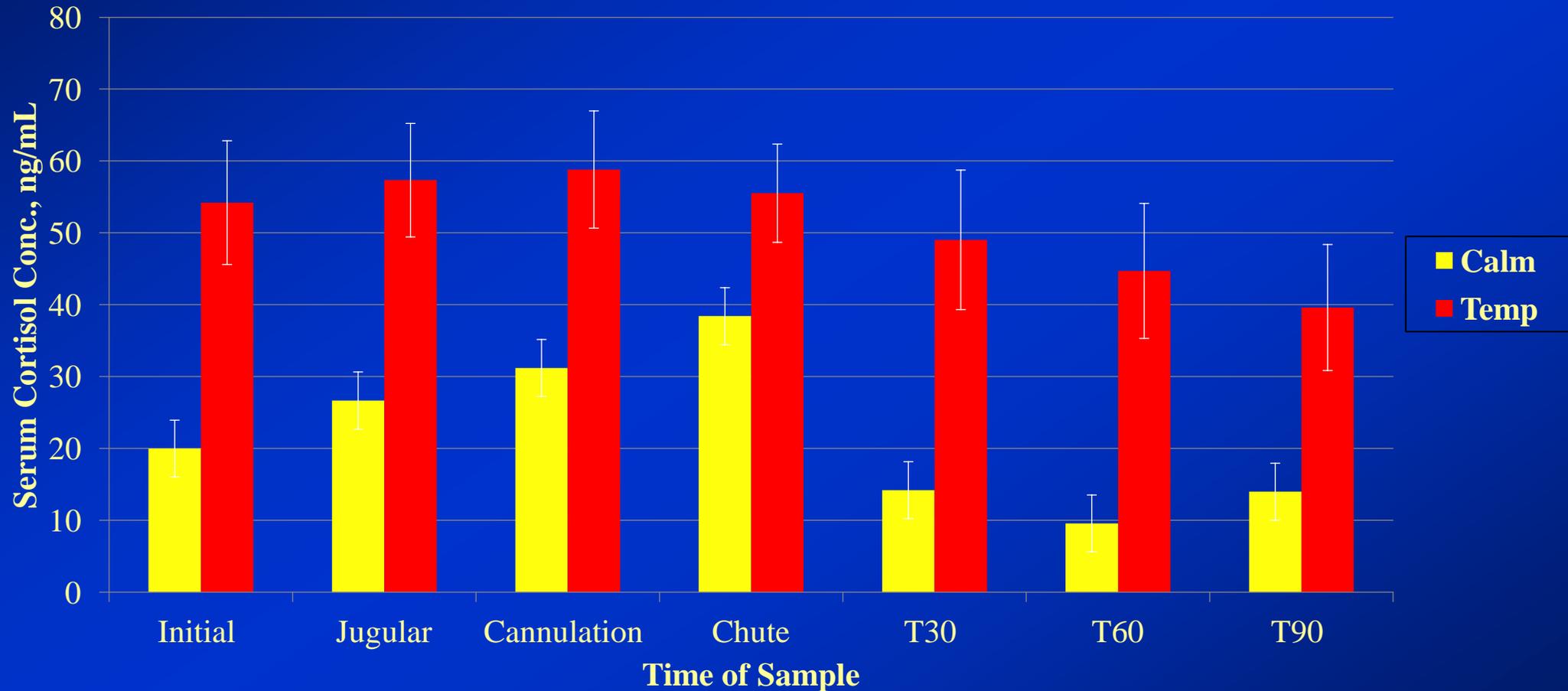
- ❑ Glucocorticoids are steroid hormones that bind to the glucocorticoid receptor, which is present in most animal cells.
- ❑ Cortisol is the most important glucocorticoid in cattle.
- ❑ Metabolism:
 - ❑ Inhibits the uptake of glucose into adipose and muscle tissue.
 - ❑ Stimulation of gluconeogenesis in the liver.
 - ❑ Stimulates fat breakdown in adipose tissue.

Glucose Homeostasis



- Glucose is the most important cellular energy source.
- Insulin is a metabolic hormone that regulates the concentration of glucose in the blood.

Cortisol

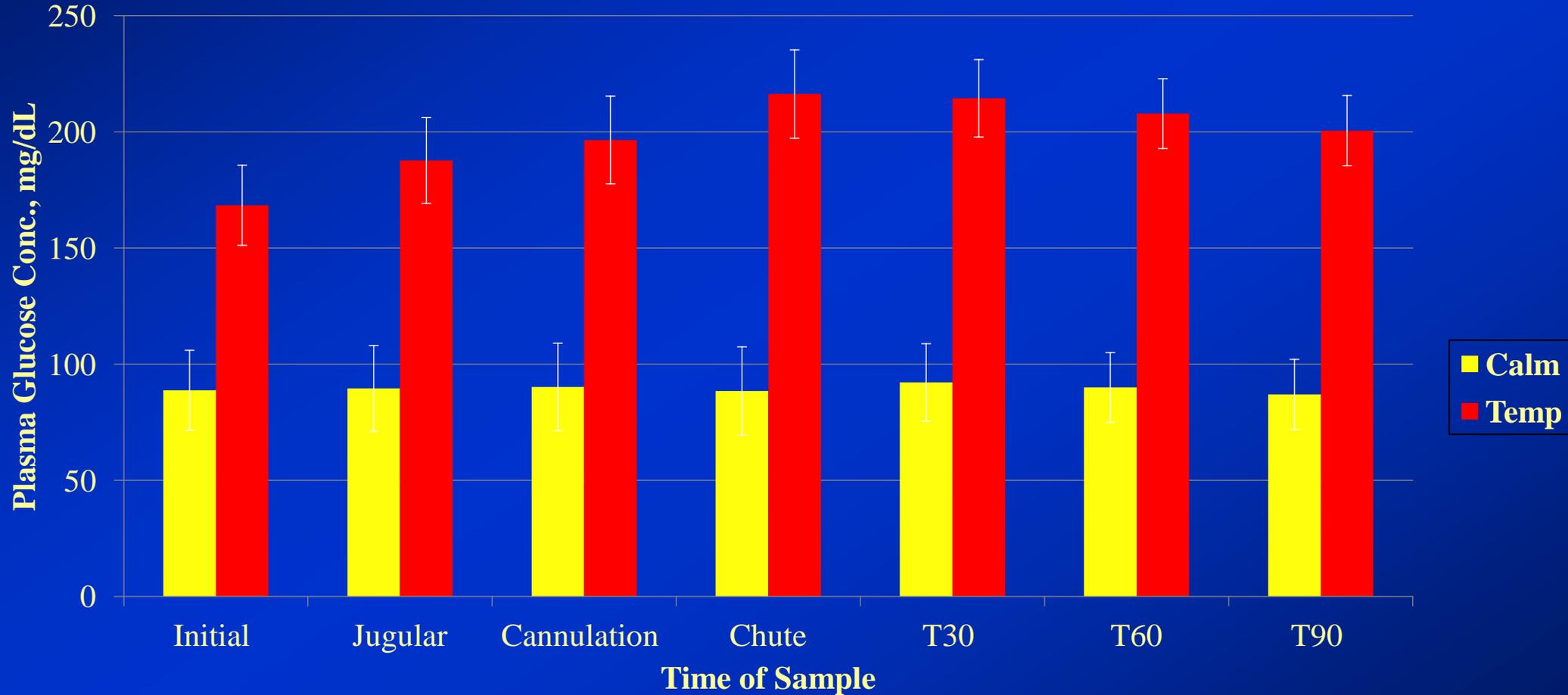


Temp $P=0.0238$

Time $P=0.0002$

TimeXTemp $P=0.2359$

Glucose

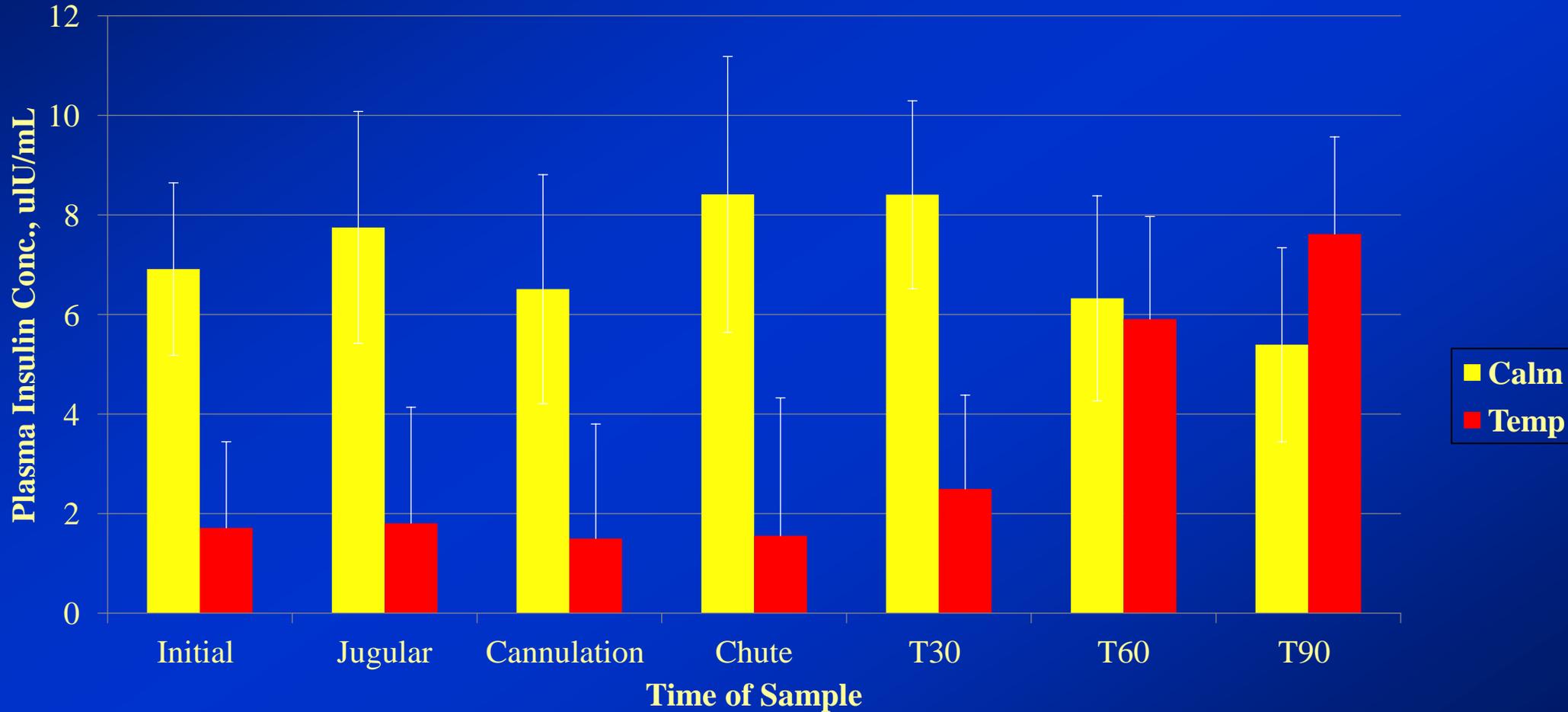


Temp $P=0.0005$

Time $P=0.1521$

TimeXTemp $P=0.1765$

Insulin



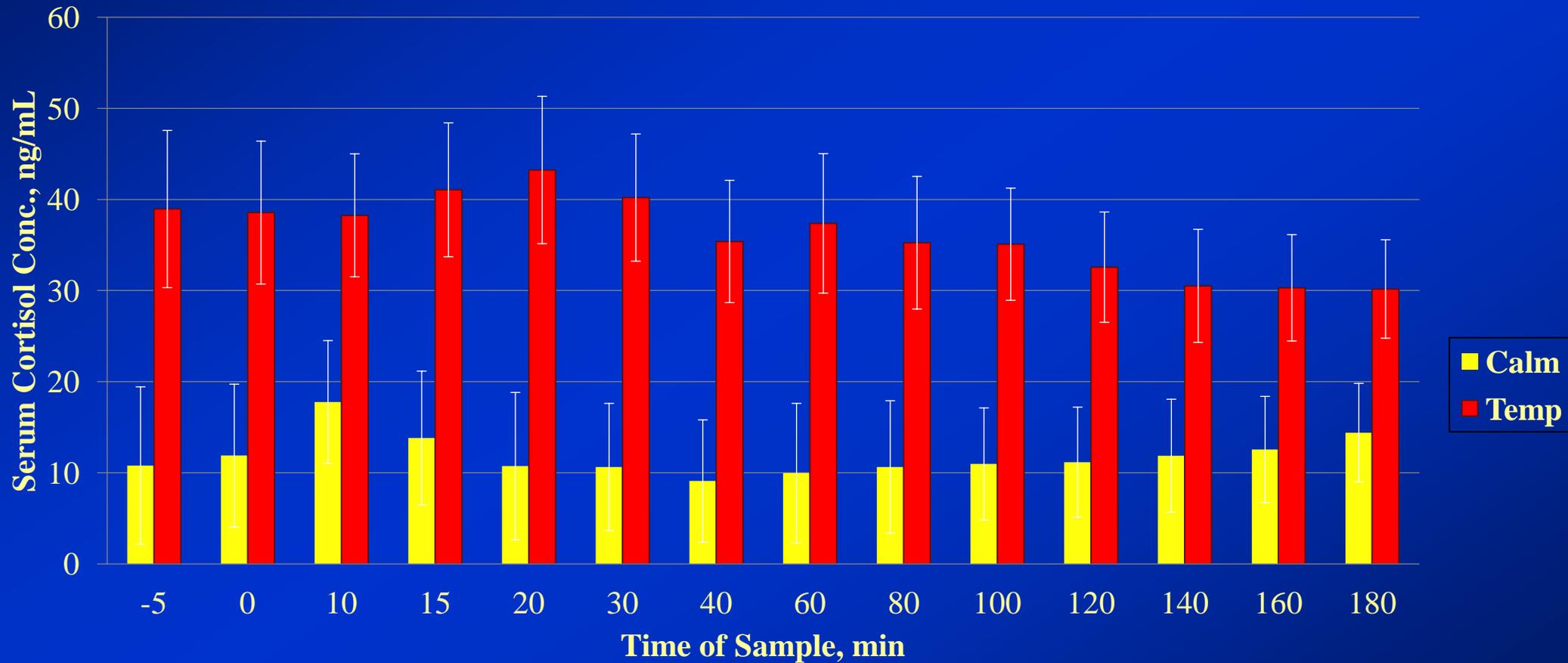
Temp $P=0.1560$

Time $P=0.4235$

123

TimeXTemp $P=0.0434$

Cortisol

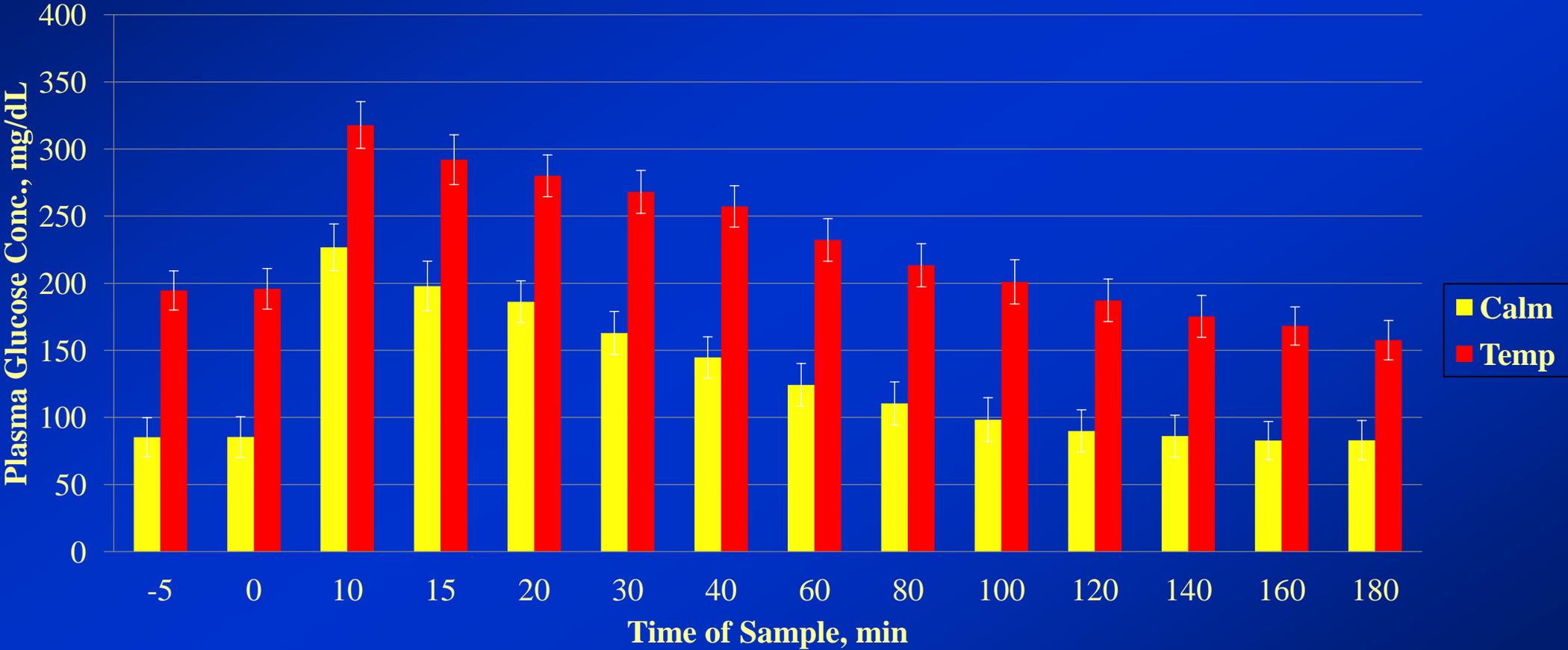


Temp $P=0.0282$

Time $P=0.0099$

TimeXTemp $P=0.0041$

Glucose

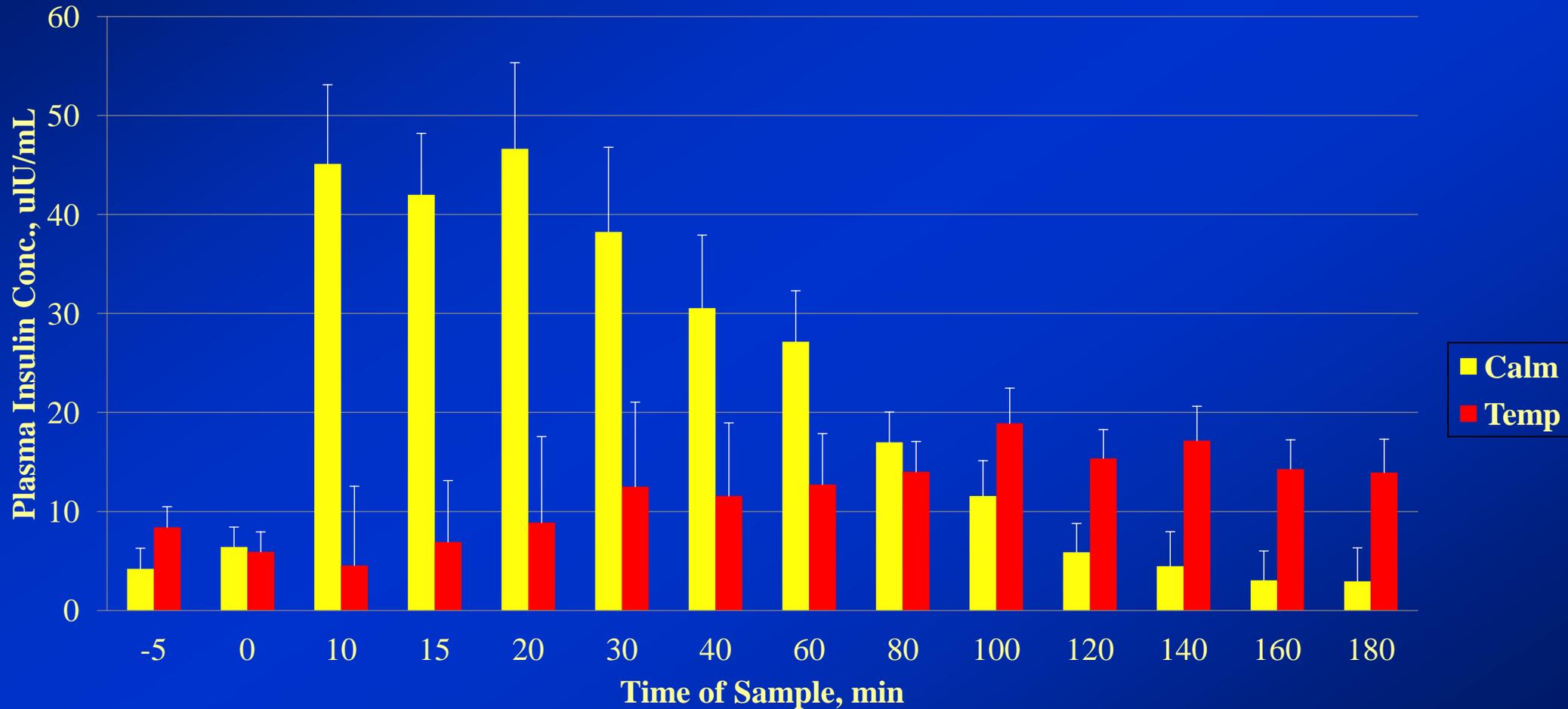


Temp $P=0.0011$

Time $P=0.0001$

TimeXTemp $P=0.0428$

Insulin



Temp $P=0.0793$

Time $P=0.0022$

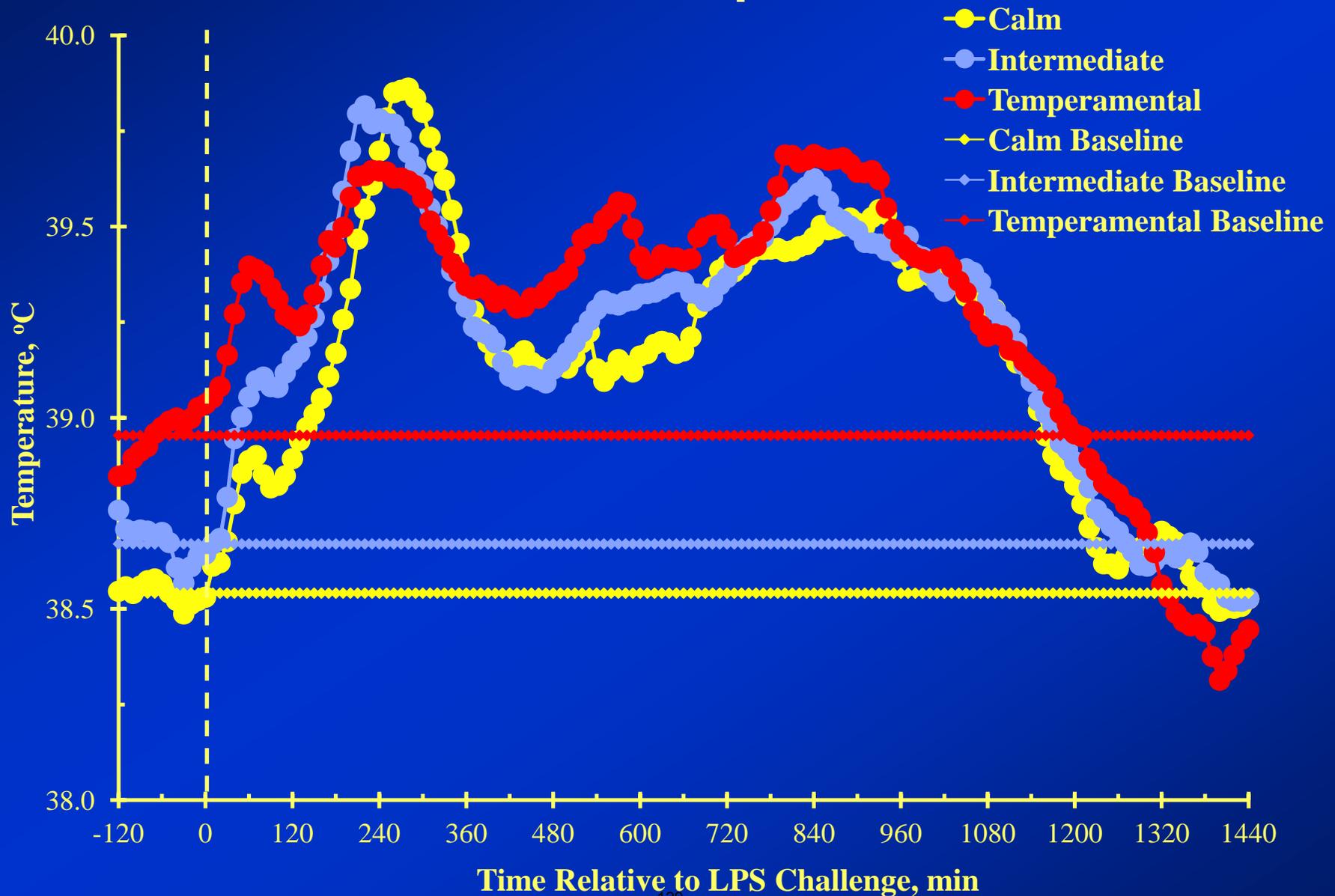
TimeXTemp $P=0.0001$

Conclusions

- ❑ Temperamental cattle have greater concentrations of cortisol, which remain elevated when stressed.
- ❑ Temperamental cattle have higher concentrations of glucose in their blood.
- ❑ Temperament modifies metabolic regulatory responses in heifers and this altered metabolism of temperamental cattle may partially explain their decreased productivity.

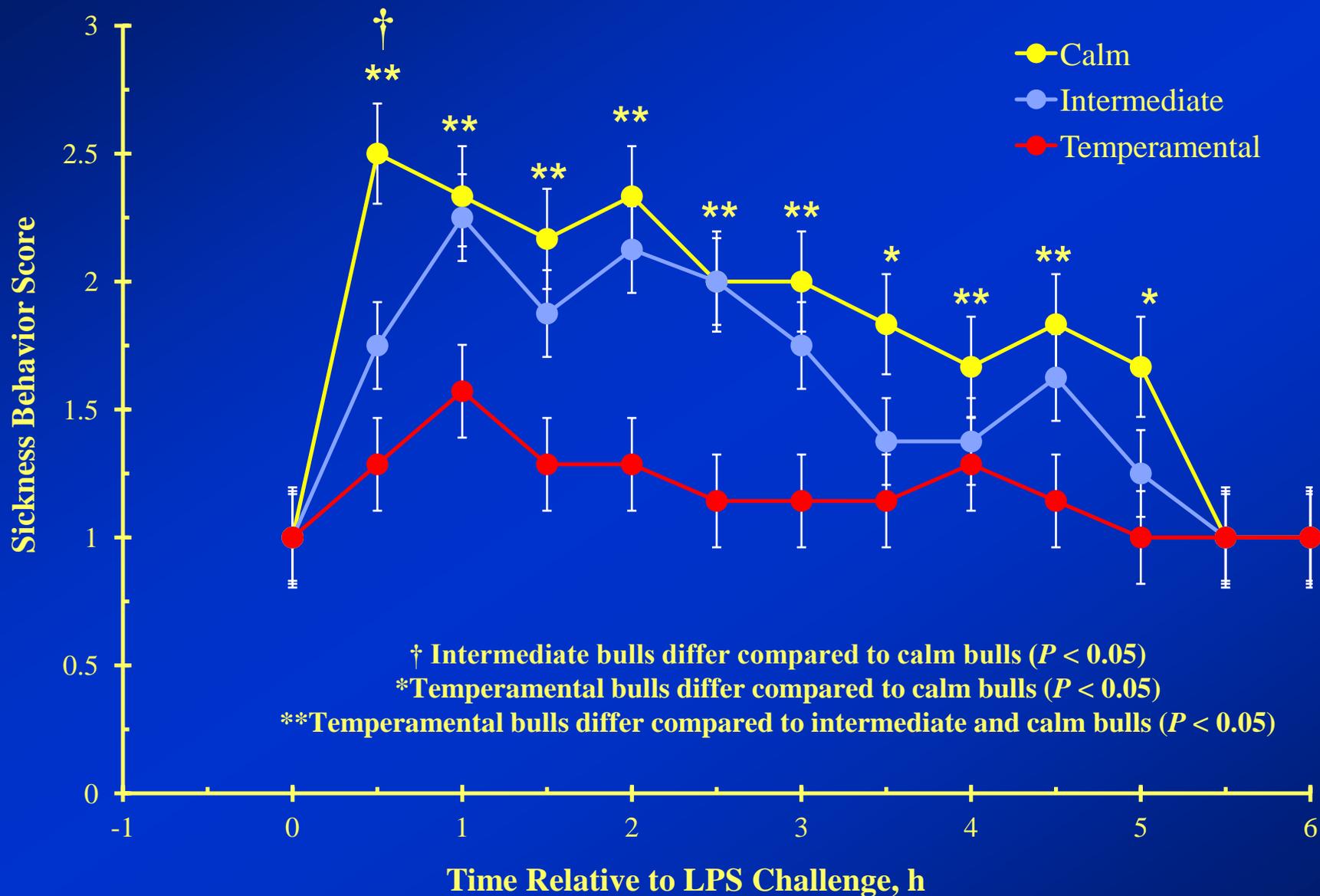
How do temperamental cattle respond to a disease challenge?

Rectal Temperature



Pre and Post-LPS: Temp: $P < 0.001$; Time: $P < 0.001$

Sickness Behavior Scores

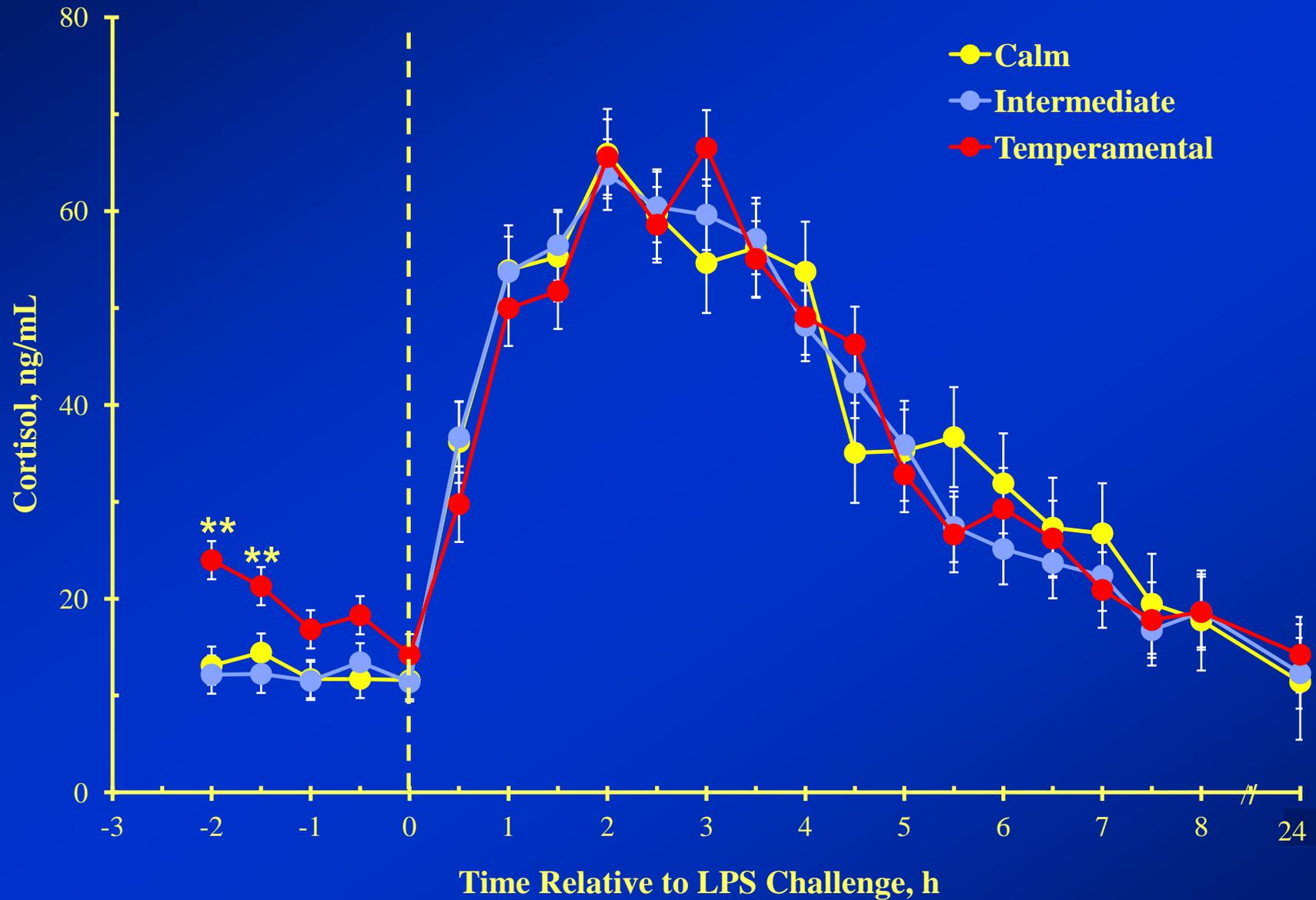


Temp: $P < 0.001$;

Time: $P < 0.001$;

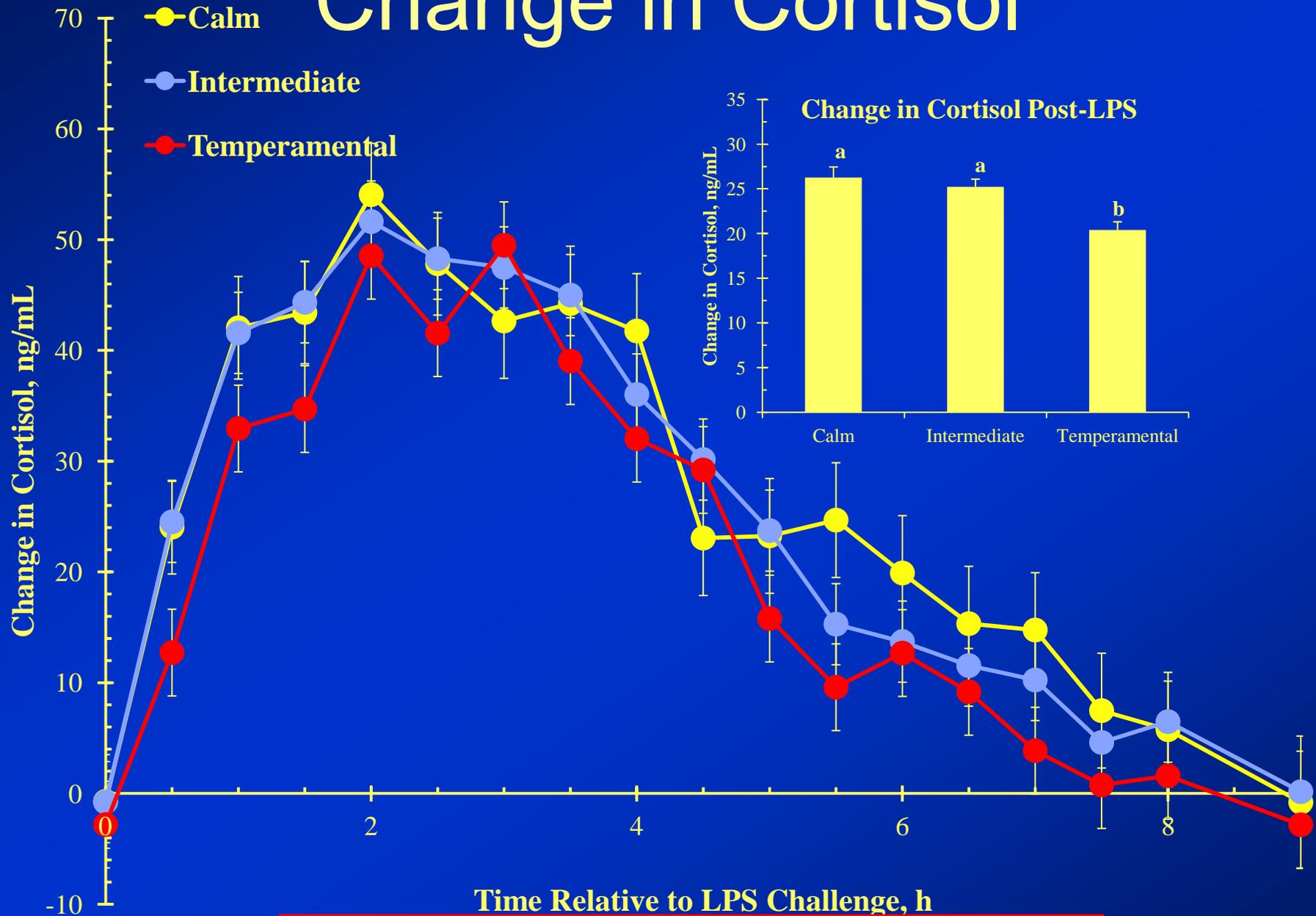
Temp x Time: $P = 0.064$

Cortisol



Pre: Temp: P < 0.01; Time: P = 0.07; | ¹³¹ Post: Temp: P = 0.80; Time: P < 0.01

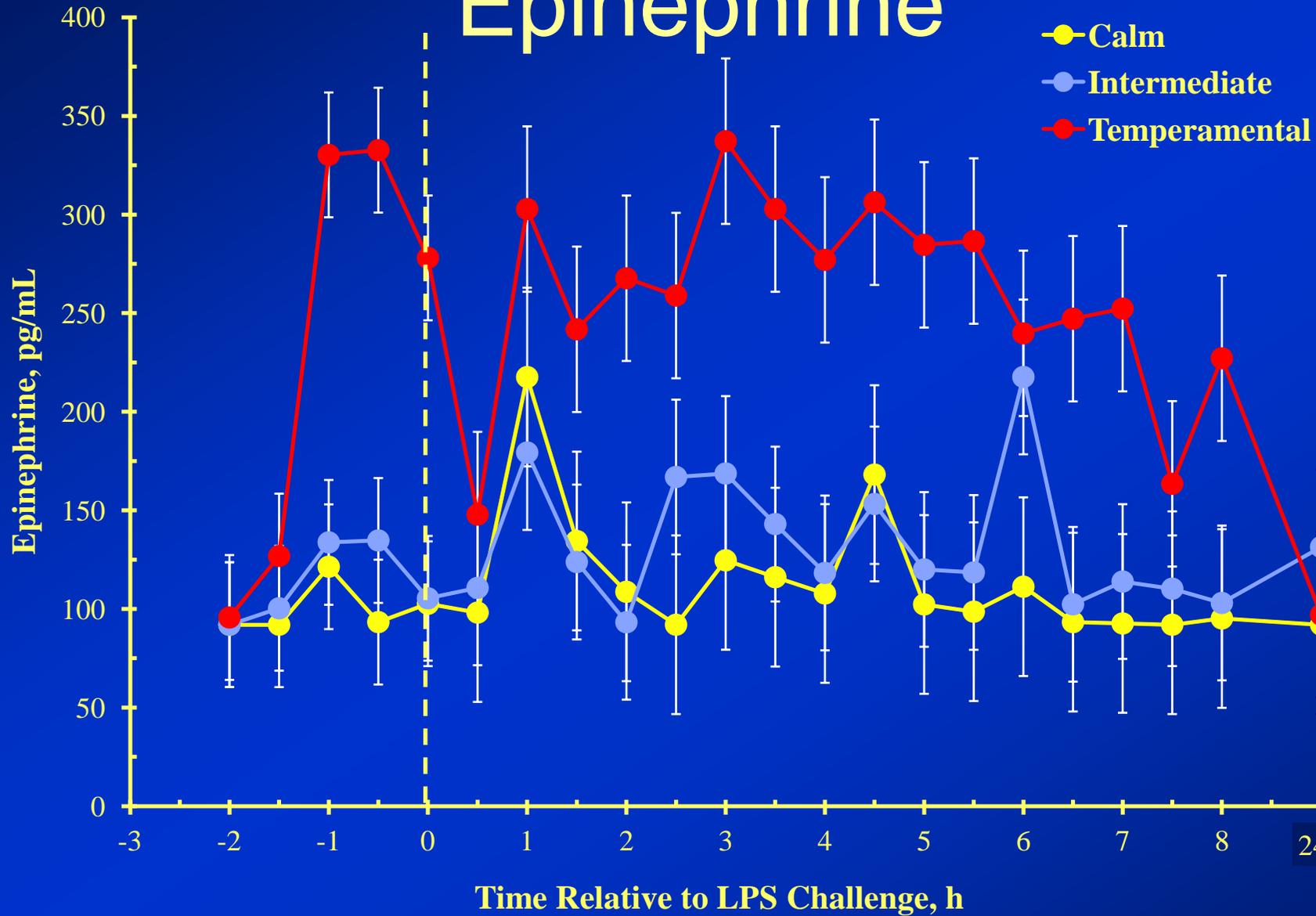
Change in Cortisol



Temp: $P < 0.01$;

Time: $P < 0.01$

Epinephrine



Pre: Temp: $P < 0.01$; Time: $P < 0.01$; Time x Temp: $P = 0.01$

Post: Temp: $P < 0.01$; Time: $P = 0.03$

Results

1. Temperamental bulls had greater pre-LPS rectal temperature but produced a lesser response to LPS.
2. Temperamental bulls displayed less signs of sickness following LPS administration.
3. Relative to baseline values, temperamental bulls produced a lesser cortisol response to LPS.
4. Temperamental bulls produced greater epinephrine pre- and post-LPS.

Conclusions

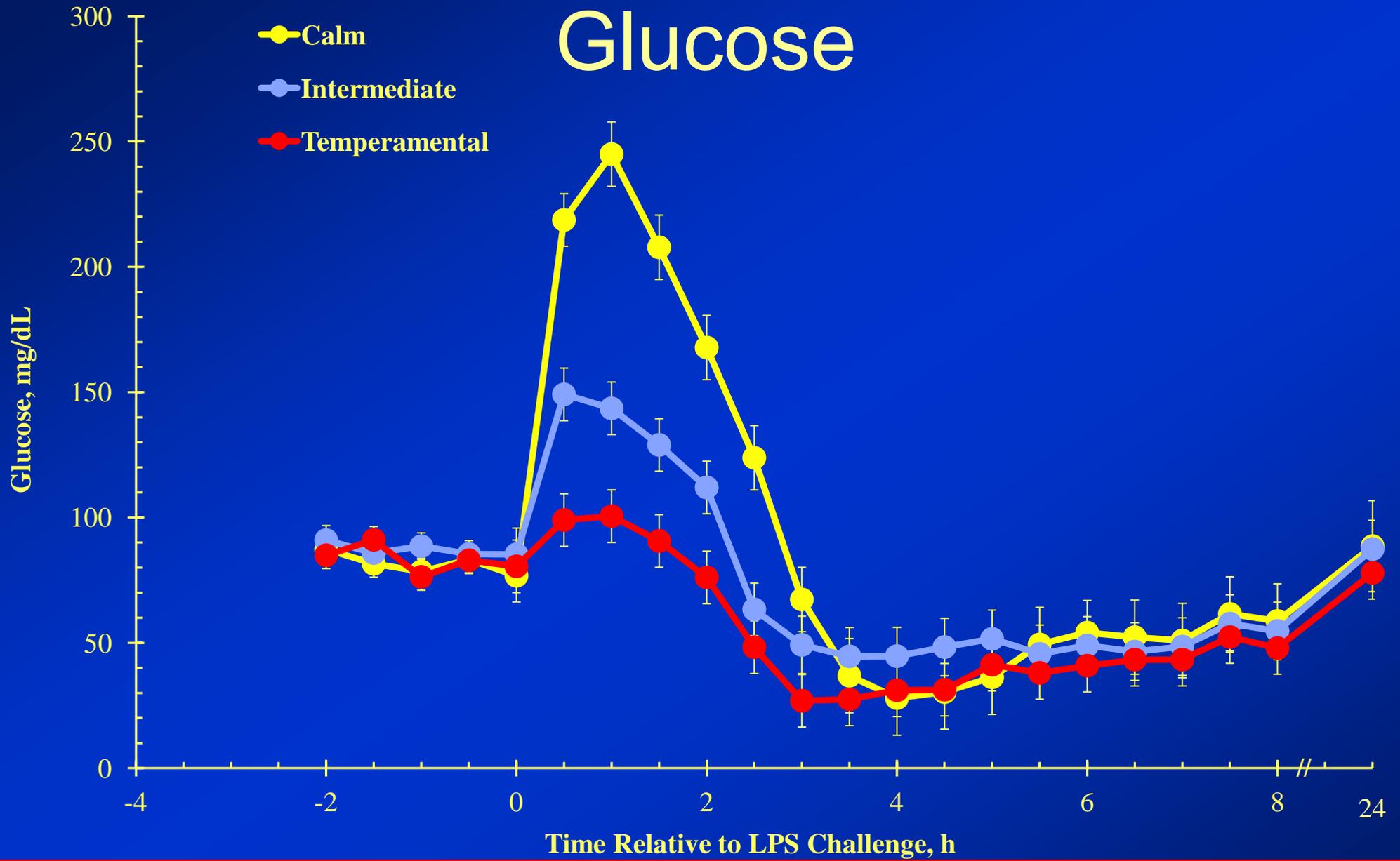
1. Temperament differentially influenced physiological and endocrine responses to LPS challenge.
2. As temperamental cattle do not display as many behavioral signs of sickness, they may increase the risk of infection to calmer cattle.
3. Other factors may be influencing the response of temperamental cattle to LPS.

The immune response has a high energy demand.

Hypothesis:

Differences observed in response to an immune challenge are due to differences in energy availability between calm and temperamental cattle.

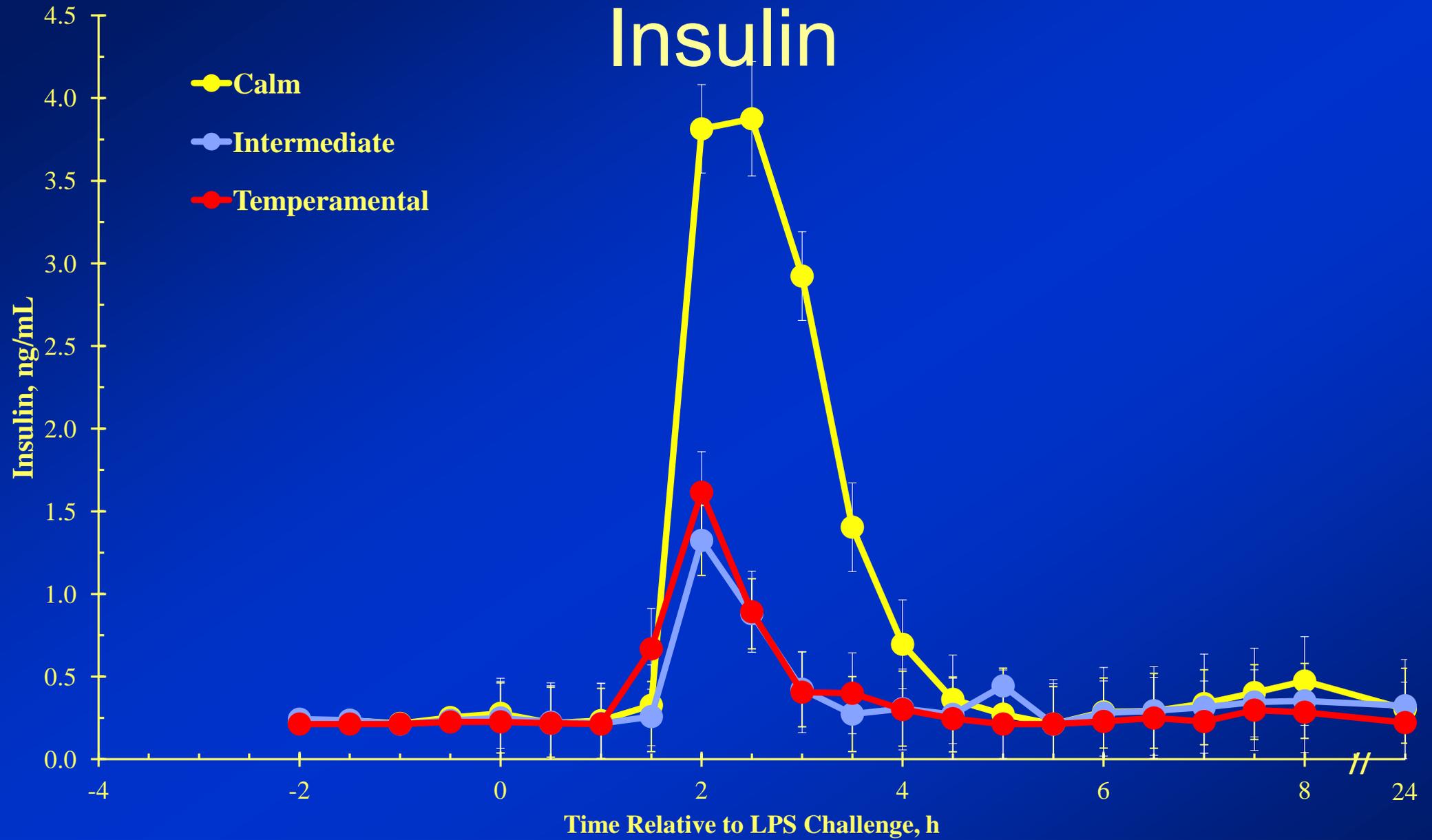
Glucose



Pre: Temp: $P = 0.40$; Time: $P = 0.47$

Post: Temp: $P < 0.01$; Time: $P = 0.03$; Time x Temp: $P < 0.01$

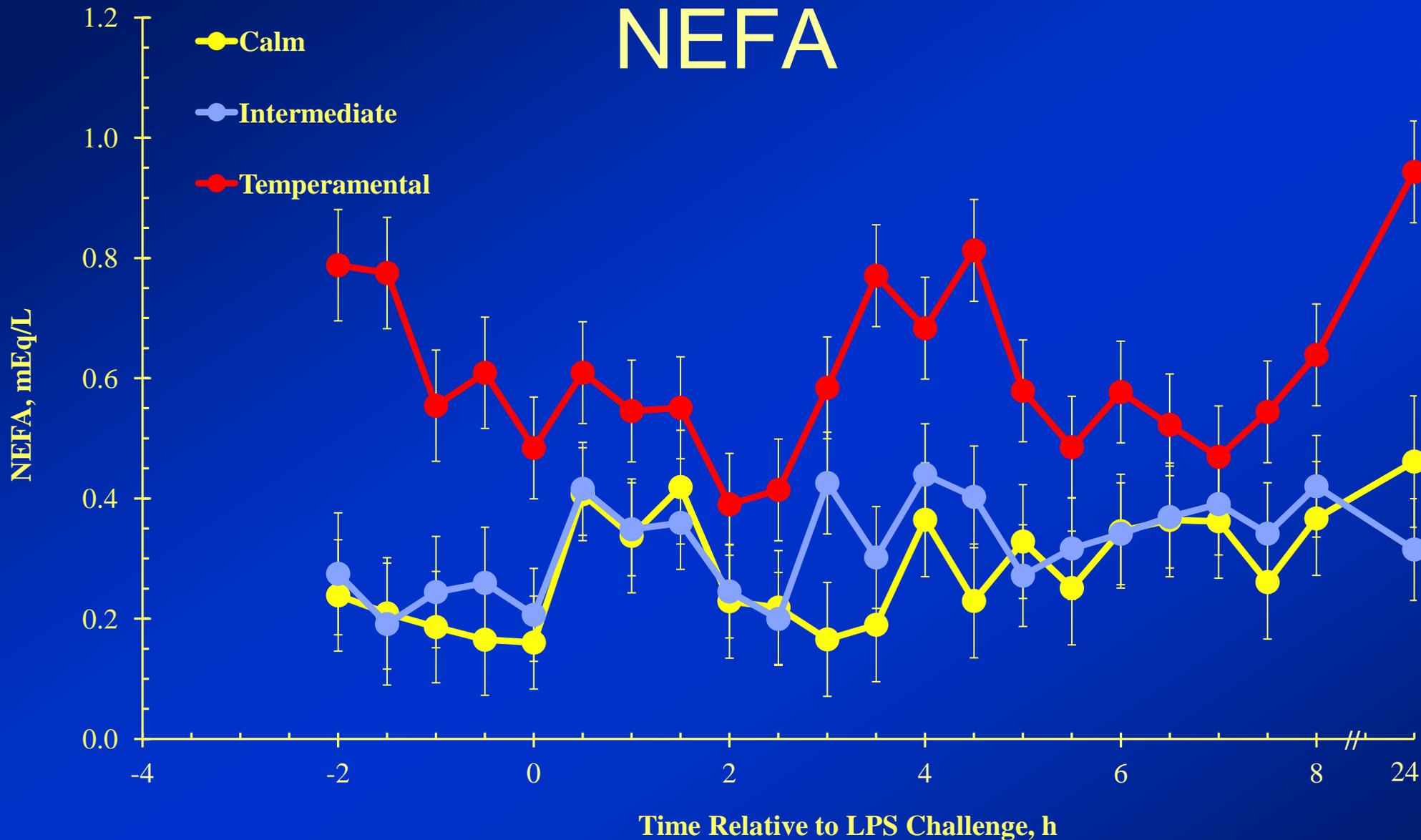
Insulin



Pre: Temp: $P = 0.02$; Time: $P < 0.02$

Post: Temp: $P < 0.01$; Time: $P < 0.01$; Time x Temp: $P < 0.01$

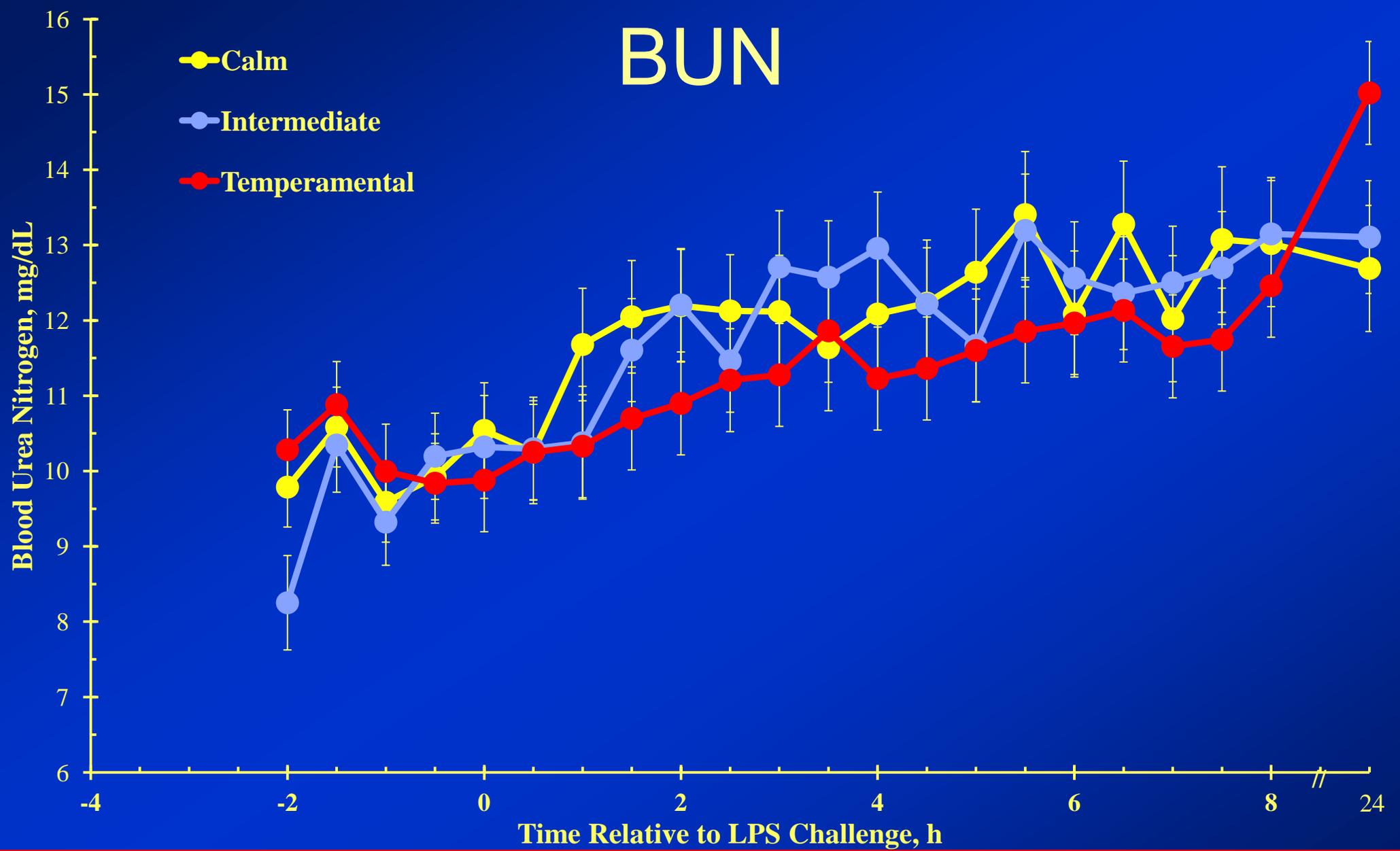
NEFA



Pre: Temp: $P < 0.01$; Time: $P = 0.51$

Post: Temp: $P < 0.01$; Time: $P < 0.01$

BUN



Pre: Temp: $P = 0.22$; Time: $P = 0.08$

Post: Temp: $P = 0.01$; Time: $P < 0.01$

Results

1. Glucose increased in response to LPS in calm and intermediate bulls.
2. Insulin release was greater in calm bulls following LPS.
3. Concentrations of NEFA were greater before and after LPS in temperamental bulls.
4. Concentrations of blood urea nitrogen were lower in temperamental bulls.

Conclusions

1. Calm bulls became insulin resistant following LPS challenge.
2. Elevated cortisol and epinephrine before LPS challenge of temperamental bulls may reduce subsequent glucose responsiveness.
3. Temperamental bulls use NEFA for energy as they have less glucose available.

Metabolic differences exist between temperaments in cattle.

Separate management strategies
should be devised for
temperamental cattle to decrease
input costs and maximize profit.

QUESTIONS?



MEAN EPDs REPORTED BY DIFFERENT BREEDS

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

It is useful for producers to compare the EPDs of potential breeding animals with their breed average. The current EPDs from the most recent genetic evaluations of 25 breeds are presented in this report. Mean EPDs for growth traits are shown in Table 1 (25 breeds), for other production traits in Table 2 (16 breeds), and for carcass and composition traits in Table 3 (20 breeds). Several breeds also have EPDs that are unique to their breed; these EPDs are presented in Table 4.

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

This list is likely incomplete; evaluations for some breeds are not widely reported. If you see a breed missing and would like to report the average EPDs for that breed, please contact Larry (Larry.Kuehn@ars.usda.gov) or Mark (Mark.Thallman@ars.usda.gov).

Table 1. Birth year 2009 average EPDs from 2011 evaluations for growth traits

Breed	Birth Weight (lb)	Weaning Weight (lb)	Yearling Weight (lb)	Maternal Milk (lb)	Total Maternal (lb)
Angus	1.8	47	85	22	
Black Hereford	3.1	42	65.1	13.8	34.8
Hereford	3.6	44	73	17	39
Murray Grey	3.4	20	30	4	13
Red Angus	-0.1	32	60	17	33
Red Poll	1.7	14	23	6	
Shorthorn	2.4	15.0	24.4	2.2	9.7
South Devon	2.6	40.5	75.8	23	43.2
Beefmaster	0.3	8	13	2	
Braford	1.0	9	14	2	7
Brahman	1.7	14.7	23.5	6.3	
Brangus	0.7	23.0	41.7	10.8	22.3
Red Brangus	1.6	13.2	20.6	5.2	11.8
Santa Gertrudis	0.6	5.0	7.0	0.0	3.0
Senepol	1.0	11	16	5	10.4
Simbrah	2.3	28.4	46.3	2.8	17.1
Braunvieh	2.8	40.9	63.5	34.5	55.0
Charolais	0.6	24.2	42.6	6.8	18.9
Chianina	2.0	36.8	68.7	12.8	31.8
Gelbvieh	1.2	40.0	74.4	16.7	36.8
Limousin	1.5	45.4	83.0	20.9	
Maine-Anjou	1.7	39.4	78.1	19.6	
Salers	1.8	41.3	79.4	20.1	40.7
Simmental	0.7	30.8	56.3	3.4	18.8
Tarentaise	1.9	16	28.6	0.6	

Table 2. Birth year 2009 average EPDs from 2011 evaluations for other production traits

Breed	Calving Ease Direct (%)	Calving Ease Maternal (%)	Scrotal Circ (cm)	Docility Score	Mature Weight (lb)	Heifer Pregnancy (%)	Stayability (%)
Angus	5	8	0.45	10	37.5	8.0	
Hereford	0.4	0.9	0.7		85		
Murray Grey	-0.7	-0.3	0.10		46		
Red Angus	5	4				10	10
Shorthorn	-1.9	-1.8					
South Devon			0				
Beefmaster			0.2				
Brangus			0.65				
Simbrah	2.7	5.7					
Braunvieh	0.12	-0.81					
Charolais	2.8	3.7	0.61				
Gelbvieh	107	103	0.3				5.8
Limousin	8.4	4.7	0.4	18.5			
Salers	0.2	0.3	0.3	8			23.3
Simmental	7.5	10.3		9.6			18.0
Tarentaise	-1.2	0.6					

Table 3. Birth year 2009 average EPDs from 2011 evaluations for carcass and composition traits

Breed	Carcass Wt (lb)	Retail Product (%)	Yield Grade	Carcass			Rump fat (in)	WBSF (lb)
				Marbling Score	Ribeye Area (in ²)	Fat Thickness (in)		
Angus	22			0.43	0.32	0.009		
Hereford				0.04	0.25	0.001		
Murray Grey	26	0.3		0.0	0.08	0.00	0.00	
Red Angus	36		-0.003	0.07	0.07	0.00		
Shorthorn	3.9			-0.01	0.05	-0.012		
South Devon	24.7	0.8		0.3	0.21	0.01		
Beefmaster				0.00 ^a	0.03 ^a	0.01 ^a	0.01 ^a	
Braford	6			0.01	0.05	0.012		
Brahman	5.9	0.0		0.00	0.04	-0.002		-0.01
Brangus	14.8			0.01 ^b	0.29 ^b	-0.002 ^b		
Santa Gertrudis	2			0.00	0.02	0.00		
Simbrah	-6.3		0.03	0.01	-0.14	0.006		-0.03
Braunvieh	31.6			0.41	0.73	-0.092		
Charolais	14.5			0.03	0.20	0.000		
Chianina	4.7	-0.14		0.25	0.03	0.02		
Gelbvieh	12.4 ^c			-0.03 ^c	0.13 ^c			
Limousin	24.2		-0.05	-0.04	0.53			
Maine-Anjou	-0.3	0.28		0.22	0.16	0.00		
Salers	20.5	0.0		0.2	0.02	0.00		
Simmental	-2.9		-0.04	0.17	0.19	0.012		-0.31

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

^bReported on an ultrasound scale (IMF% instead of marbling score) but calculated using ultrasound and carcass data in a multi-trait model

^cAdjusted to a fat-constant endpoint

Table 4. Birth year 2009 average EPDs from 2011 evaluations for other traits unique to individual breeds

Angus	Residual Average Daily Gain (lb)	Mature Height (in)	Yearling Height (in)	Cow Energy Value (\$)	Weaned Calf Value (\$)	Feedlot Value (\$)	Grid Value (\$)	Beef Value (\$)
	0.12	0.4	0.35	-2.05	26.66	26.64	25.79	55.50
Hereford	Baldy Maternal Index (\$)	Brahman Influence Index (\$)	Certified Hereford Beef Index (\$)	Calving Ease Index (\$)				
	17	15	20	15				
Red Angus	Mature Cow Maintenance (Mcal/mo)							
	4							
Gelbvieh	Feedlot Merit (\$)	Carcass Value (\$)	Gestation Length (d)	Days to Finish (d)				
	9.39	14.85	-1.0	2.3				
Limousin	Mainstream Terminal Index (\$)							
	43.4							
Simmental	All Purpose Index (\$)	Terminal Index (\$)	Simbrah	All Purpose Index (\$)	Terminal Index (\$)			
	105.4	61.7		64.3	50.4			
Murray Grey	600-d wt (lb)	Gestational length (d)	Days to calving (d)					
	45	-0.1	-0.6					

ACROSS-BREED EPD TABLES FOR THE YEAR 2012 ADJUSTED TO BREED DIFFERENCES FOR BIRTH YEAR OF 2010

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Summary

Factors to adjust the expected progeny differences (EPD) of each of 18 breeds to the base of Angus EPD are reported in the column labeled 6 of Tables 1-7 for birth weight, weaning weight, yearling weight, maternal milk, marbling score, ribeye area, and fat thickness, respectively. An EPD is adjusted to the Angus base by adding the corresponding across-breed adjustment factor in column 6 to the EPD. It is critical that this adjustment be applied only to Spring 2012 EPD. Older or newer EPD may be computed on different bases and, therefore, could produce misleading results. When the base of a breed changes from year to year, its adjustment factor (Column 6) changes in the opposite direction and by about the same amount.

Breed differences are changing over time as breeds put emphasis on different traits and their genetic trends differ accordingly. Therefore, it is necessary to qualify the point in time at which breed differences are represented. Column 5 of Tables 1-7 contains estimates of the differences between the averages of calves of each breed born in year 2010. Any differences (relative to their breed means) in the samples of sires representing those breeds at the U.S. Meat Animal Research Center (USMARC) are adjusted out of these breed difference estimates and the across-breed adjustment factors. The breed difference estimates are reported as progeny differences, e.g., they represent the expected difference in progeny performance of calves sired by average bulls (born in 2010) of two different breeds and out of dams of a third, unrelated breed. In other words, they represent half the differences that would be expected between purebreds of the two breeds.

Introduction

This report is the year 2012 update of estimates of sire breed means from data of the Germplasm Evaluation (GPE) project at USMARC adjusted to a year 2010 basis using EPD from the most recent national cattle evaluations. The 2010 basis year is chosen because yearling records for weight and carcass traits should have been accounted for in EPDs for progeny born in 2010 in the Spring 2012 EPD national genetic evaluations. Factors to adjust Spring 2012 EPD of 18 breeds to a common base were calculated and are reported in Tables 1-3 for birth weight (BWT), weaning weight (WWT), and yearling weight (YWT) and in Table 4 for the maternal milk (MILK) component of maternal weaning weight (MWWT). Tables 5-7 summarize the factors for marbling score (MAR), ribeye area (REA), and fat thickness (FAT).

The across-breed table adjustments apply **only** to EPD for most recent (spring, 2012) national cattle evaluations. Serious errors can occur if the table adjustments are used with earlier or later EPD which may have been calculated with a different within-breed base.

The following describes the changes that have occurred since the update released in 2011

(Kuehn et al., 2011):

New samplings of sires in the USMARC GPE program continued to increase progeny records for 16 of the 18 breeds involved in the across-breed EPD program. Approximately 60 progeny per breed were added to the evaluation (birth weight). These additional progeny improve the accuracy of breed differences estimated at USMARC (column 3 in Tables 1-7) particularly for breeds with less data in previous GPE cycles (e.g., Santa Gertrudis, Chiangus). Sires continue to be sampled on a continuous basis, now for each of the 18 breeds in the across-breed EPD program. There are still not enough daughters produced from these new samplings of sires to significantly impact maternal milk estimates. Factors estimated for Santa Gertrudis and Chiangus remain the most susceptible to changes from year-to-year because of increases in progeny number representing greater proportions of their sample. For instance, breed of sire estimates for Santa Gertrudis (yearling weight) and Chiangus (carcass traits) represented some of the largest breed solution estimate changes from last year's analysis.

Other significant changes were largely due to changes in national cattle evaluations for individual breeds. Bases shifts (columns 1 and 2, Tables 1-7) were observed in Braunvieh for most traits. Large mean EPD changes (column 1, Tables 1-7) were also observed in Chiangus and Salers for marbling score, Angus for ribeye area, and Red Angus and Chiangus for fat thickness. Beyond the effects of some of these shifts, most changes were relatively minor relative to Kuehn et al. (2011). In general base shifts only affect the adjustment factors (column 6, Tables 1-7); however, this year changes in Braunvieh also affected their estimated sire breed difference relative to Angus (Column 5, Tables 1-7) because the base shift did not change the mean sire EPDs of USMARC bulls (Column 2, Tables 1-7) to the extent of the mean breed EPD.

Materials and Methods

All calculations were as outlined in the 2010 BIF Guidelines. The basic steps were given by Notter and Cundiff (1991) with refinements by Núñez-Dominguez et al. (1993), Cundiff (1993, 1994), Barkhouse et al. (1994, 1995), Van Vleck and Cundiff (1997–2006), and Kuehn et al. (2007-2011). Estimates of variance components, regression coefficients, and breed effects were obtained using the MTDFREML package (Boldman et al., 1995). All breed solutions are reported as differences from Angus. The table values of adjustment factors to add to within-breed EPD are relative to Angus.

Models for Analysis of USMARC Records

An animal model with breed effects represented as genetic groups was fitted to the GPE data set (Arnold et al., 1992; Westell et al., 1988). In the analysis, all AI sires (sires used via artificial insemination) were assigned a genetic group according to their breed of origin. Due to lack of pedigree, dams mated to the AI sires and natural service bulls mated to F₁ females were also assigned to separate genetic groups (i.e., Hereford dams were assigned to different genetic groups than Hereford AI sires). Cows from Hereford selection lines (Koch et al., 1994) were used in Cycle IV of GPE and assigned into their own genetic groups. Through Cycle VIII, most dams were from Hereford, Angus, or MARCIII (1/4 Angus, 1/4 Hereford, 1/4 Pinzgauer, 1/4 Red Poll) composite lines. In order to be considered in the analysis, sires had to have an EPD for

the trait of interest. All AI sires were considered unrelated for the analysis in order to adjust resulting genetic group effects by the average EPD of the sires.

Fixed effects in the models for BWT, WWT (205-d), and YWT (365-d) included breed (fit as genetic groups) and maternal breed (WWT only), year and season of birth by GPE cycle by age of dam (2, 3, 4, 5-9, >10 yr) combination (228), sex (heifer, bull, steer; steers were combined with bulls for BWT), a covariate for heterosis, and a covariate for day of year at birth of calf. Models for WWT also included a fixed covariate for maternal heterosis. Random effects included animal and residual error except for the analysis of WWT which also included a random maternal genetic effect and a random permanent environmental effect.

For the carcass traits (MAR, REA, and FAT), breed (fit as genetic groups), sex (heifer, steer) and slaughter date (229) were included in the model as fixed effects. Fixed covariates included slaughter age and heterosis. Random effects were animal and residual error. To be included, breeds had to report carcass EPD on a carcass basis using age-adjusted endpoints, as suggested in the 2010 BIF Guidelines.

The covariates for heterosis were calculated as the expected breed heterozygosity for each animal based on the percentage of each breed of that animal's parents. In other words, it is the probability that, at any location in the genome, the animal's two alleles originated from two different breeds. Heterosis is assumed to be proportional to breed heterozygosity. For the purpose of heterosis calculation, AI and dam breeds were assumed to be the same breed and Red Angus was assumed the same breed as Angus. For purposes of heterosis calculation, composite breeds were considered according to nominal breed composition. For example, Brangus (3/8 Brahman, 5/8 Angus) × Angus is expected to have 3/8 as much heterosis as Brangus × Hereford.

Variance components were estimated with a derivative-free REML algorithm with genetic group solutions obtained at convergence. Differences between resulting genetic group solutions for AI sire breeds were divided by two to represent the USMARC breed of sire effects in Tables 1-7. Resulting breed differences were adjusted to current breed EPD levels by accounting for the average EPD of the AI sires of progeny/grandprogeny, etc. with records. Average AI sire EPD were calculated as a weighted average AI sire EPD from the most recent within breed genetic evaluation. The weighting factor was the sum of relationship coefficients between an individual sire and all progeny with performance data for the trait of interest relative to all other sires in that breed.

For all traits, regression coefficients of progeny performance on EPD of sire for each trait were calculated using an animal model with EPD sires excluded from the pedigree. Genetic groups were assigned in place of sires in their progeny pedigree records. Each sire EPD was 'dropped' down the pedigree and reduced by ½ depending on the number of generations each calf was removed from an EPD sire. In addition to regression coefficients for the EPDs of AI sires, models included the same fixed effects described previously. Pooled regression coefficients, and regression coefficients by sire breed were obtained. These regression coefficients are monitored as accuracy checks and for possible genetic by environment interactions. The pooled regression coefficients were used as described in the next section to adjust for differences in management at USMARC as compared to seedstock production (e.g.,

YWT of males at USMARC are primarily on a slaughter steer basis, while in seedstock field data they are primarily on a breeding bull basis). For carcass traits, MAR, REA, and FAT, regressions were considered too variable and too far removed from 1.00. Therefore, the regressions were assumed to be 1.00 until more data is added to reduce the impact of sampling errors on prediction of these regressions. However, the resulting regressions are still summarized.

Records from the USMARC GPE Project are not used in calculation of within-breed EPD by the breed associations. This is critical to maintain the integrity of the regression coefficient. If USMARC records were included in the EPD calculations, the regressions would be biased upward.

Adjustment of USMARC Solutions

The calculations of across-breed adjustment factors rely on breed solutions from analysis of records at USMARC and on averages of within-breed EPD from the breed associations. The basic calculations for all traits are as follows:

USMARC breed of sire solution (1/2 breed solution) for breed i (USMARC (i)) converted to an industry scale (divided by b) and adjusted for genetic trend (as if breed average bulls born in the base year had been used rather than the bulls actually sampled):

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

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

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

where,

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

EPD(i)_{YY} is the average within-breed 2012 EPD for breed i for animals born in the base year (YY, which is two years before the update; e.g., YY = 2010 for the 2012 update),

EPD(i)_{USMARC} is the weighted (by total relationship of descendants with records at USMARC) average of 2012 EPD of bulls of breed i having descendants with records at USMARC,

b is the pooled coefficient of regression of progeny performance at USMARC on EPD of sire (for 2010: 1.18, 0.83, 1.06, and 1.19 BWT, WWT, YWT, and MILK, respectively; 1.00 was applied to MAR, REA, and FAT data),

i denotes sire breed i, and

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

Results

Heterosis

Heterosis was included in the statistical model as a covariate for all traits. Maternal heterosis was also fit as a covariate in the analysis of weaning weight. Resulting estimates were 1.30 lb, 13.40 lb, 16.83 lb, 0.021 marbling score units (i.e. $4.00 = S1^{00}$, $5.00 = Sm^{00}$), 0.25 in^2 , and 0.043 in for BWT, WWT, YWT, MAR, REA, and FAT respectively. These estimates are interpreted as the amount by which the performance of an F_1 is expected to exceed that of its parental breeds. The estimate of maternal heterosis for WWT was 13.14 lb.

Across-breed adjustment factors

Tables 1, 2, and 3 (for BWT, WWT, and YWT) summarize the data from, and results of, USMARC analyses to estimate breed of sire differences on a 2010 birth year basis. The column labeled 6 of each table corresponds to the Across-breed EPD Adjustment Factor for that trait. Table 4 summarizes the analysis of MILK. Tables 5, 6, and 7 summarize data from the carcass analyses (MAR, REA, FAT). Because of the accuracy of sire carcass EPDs and the greatest percentage of data being added to carcass traits, sire effects and adjustment factors are more likely to change for carcass traits in the future.

Column 5 of each table represents the best estimates of sire breed differences for calves born in 2010 on an industry scale. These breed difference estimates are reported as progeny differences, e.g., they represent the expected difference in progeny performance of calves sired by average bulls (born in 2010) of two different breeds and out of dams of a third, unrelated breed. Thus, they represent half the difference expected between purebreds of the respective breeds.

In each table, breed of sire differences were added to the raw mean of Angus-sired progeny born 2006 through 2011 at USMARC (Column 4) to make these differences more interpretable to producers on scales they are accustomed to.

Figures 1-4 illustrate the relative genetic trends of most of the breeds involved (if they submitted trends) adjusted to a constant base using the adjustment factors in column 6 of Tables 1-7. These figures demonstrate the effect of selection over time on breed differences; breeders within each breed apply variable levels of selection toward each trait resulting in reranking of breeds for each traits over time. These figures and Column 5 of Tables 1-7 can be used to identify breeds with potential for complementarity in mating programs.

Across-breed EPD Adjustment Factor Example

Adjustment factors can be applied to compare the genetic potential of sires from different breeds. Suppose the EPD for yearling weight for a Simmental bull is +52.1 (which is below the year 2010 average of 56.3 for Simmental) and for a Gelbvieh bull is +84.0 (which is above the year 2010 average of 74.4 for Gelbvieh). The across-breed adjustment factors in the last column of Table 3 are 22.4 for Simmental and -13.5 for Gelbvieh. Then the adjusted EPD for the Simmental bull is $52.1 + 22.4 = 74.5$ and for the Gelbvieh bull is $84.0 + (-13.5) = 70.5$. The expected yearling weight difference when both are mated to another breed of cow, e.g., Angus,

would be $74.5 - 70.5 = 4.0$ lb. The differences in true breeding value between two bulls with similar within-breed EPDs are primarily due to differences in the genetic base from which those within-breed EPDs are computed.

Birth Weight

The range in estimated breed of sire differences for BWT (Table 1, column 5) ranged from 0.5 lb for Red Angus to 7.4 lb for Charolais and 11.0 lb for Brahman. Angus continued to have the lowest estimated sire effect for birth weight (Table 1, column 5). The relatively heavy birth weights of Brahman-sired progeny would be expected to be offset by favorable maternal effects reducing birth weight if progeny were from Brahman or Brahman cross dams which would be an important consideration in crossbreeding programs involving Brahman cross females. Changes in breed of sire effects were generally small, less than 1.5 lb for all breeds relative to last year's update (Kuehn et al., 2011).

Weaning Weight

All of the 17 sire breed differences (Table 2, column 5) were within 5 lb of the values reported by Kuehn et al. (2011). Changes in breed effects caused by new sampling of GPE bulls seem to be stabilizing for both birth weight and weaning weight.

Yearling Weight

Breed of sire effects for yearling weight were also similar to Kuehn et al. (2011) in general. All but three of the estimates were within 6 lb of last year's estimates. The estimated Santa Gertrudis breed difference increased by 9.1 lb and the Maine Anjou difference decreased by 8.1 lb likely due to increased sampling and progeny. The Braunvieh breed of sire difference also decreased by 11.8 lb; however, this change seems to primarily be attributable to changes in the Braunvieh sire evaluation due to the breed mean and the mean EPD of USMARC sampled Braunvieh sires both having changed considerably from last year. Angus continued to have the greatest rate of genetic change for yearling weight, causing all breed of sire differences relative to Angus to decrease at least slightly.

Maternal Milk

Changes to the maternal milk breed of sire differences (Table 4, column 5) were generally small. All changes were less than 6 lb difference from those reported in 2011. However, the breed solution estimates (Table 4, column 3) are expected to change the most in future updates as GPE heifers from each of the 18 breeds being continuously sampled are developed and bred. As this occurs, we expect to be able to produce adjustment factors for maternal milk for Santa Gertrudis and Chiangus.

Marbling

Marbling score was again highest in Angus followed closely by South Devon (0.08 score units lower). Most changes relative to last year's update were minor with the exception of Braunvieh and Salers (genetic evaluation changes) and Chiangus (USMARC breed solution; due

to increase numbers of progeny sampled). Continental breeds continue in general to be lower for marbling score relative to Angus (most more than 0.5 score units lower).

Ribeye Area

Continental breeds had higher ribeye area estimates relative to the British breeds (Table 6, column 5) as would be expected. However, differences relative to Angus decrease because of a large change in the mean ribeye area EPD for Angus (0.11 sq in larger). Braunvieh also changed due to genetic evaluation differences relative to last year. Increased sampling of Chiangus steers in GPE has shown them to be quite similar to Angus (only 0.11 sq in larger as a sire breed on average)

Fat Thickness

Progeny of Continental breeds again had 0.1 to 0.2 in less fat at slaughter than British breeds (Table 7, Column 5). All other breeds were leaner than Angus. Charolais, Salers, Maine Anjou, and Simmental were predicted to be the leanest breeds among the 12 breeds analyzed for carcass traits. Limousin was not included in the FAT analysis because they do not report an EPD for FAT. Changes in breed of sire effects relative to Angus were all minor compared to the previous year (Kuehn et al., 2011) except for Braunvieh whose breed mean EPD changed relative to last year's analysis by a significant amount (decreased by almost 0.2 in while the average of the bulls used at USMARC only decrease by approximately 0.1 in).

Accuracies and Variance Components

Table 8 summarizes the average Beef Improvement Federation (BIF) accuracy for bulls with progeny at USMARC weighted appropriately by average relationship to animals with phenotypic records. South Devon bulls had relatively small accuracy for all traits as did Hereford and Brahman bulls. Charolais and Gelbvieh bulls had low accuracy for yearling weight and milk. Accuracies for carcass traits, as expected, were considerably lower than accuracies for growth traits in general. The sires sampled recently in the GPE program have generally been higher accuracy sires, so the average accuracies should continue to increase over the next several years.

Table 9 reports the estimates of variance components from the animal models that were used to obtain breed of sire and breed of MGS solutions. Heritability estimates for BWT, WWT, YWT, and MILK were 0.59, 0.18, 0.46, and 0.16, respectively. Heritability estimates for MAR, REA, and FAT were 0.49, 0.48, and 0.41, respectively.

Regression Coefficients

Table 10 updates the coefficients of regression of records of USMARC progeny on sire EPD for BWT, WWT, and YWT which have theoretical expected values of 1.00. The standard errors of the specific breed regression coefficients are large relative to the regression coefficients. Large differences from the theoretical regressions, however, may indicate problems with genetic evaluations, identification, or sampling. The pooled (overall) regression coefficients of 1.18 for BWT, 0.83 for WWT, and 1.06 for YWT were used to adjust breed of sire solutions to the base

year of 2010. These regression coefficients are reasonably close to expected values of 1.0. Deviations from 1.00 are believed to be due to scaling differences between performance of progeny in the USMARC herd and of progeny in herds contributing to the national genetic evaluations of the 18 breeds. Breed differences calculated from the USMARC data are divided by these regression coefficients to put them on an industry scale. A regression greater than one suggests that variation at USMARC is greater than the industry average, while a regression less than one suggests that variation at USMARC is less than the industry average. Reasons for differences in scale can be rationalized. For instance, cattle at USMARC, especially steers and market heifers, are fed at higher energy rations than some seedstock animals in the industry. Also, in several recent years, calves have been weaned earlier than 205 d at USMARC, likely reducing the variation in weaning weight of USMARC calves relative to the industry.

The coefficients of regression for MILK are also shown in Table 10. Several sire (MGS) breeds have regression coefficients considerably different from the theoretical expected value of 1.00 for MILK. Standard errors, however, for the regression coefficients by breed are large except for Angus and Hereford. The pooled regression coefficient of 1.19 for MILK is reasonably close to the expected regression coefficient of 1.00.

Regression coefficients derived from regression of USMARC steer progeny records on sire EPD for MAR, REA, and FAT are shown in Table 11. Each of these coefficients has a theoretical expected value of 1.00. Compared to growth trait regression coefficients, the standard errors even on the pooled estimates are high, though they have decreased from the previous year. While REA and FAT are both close to the theoretical estimate of 1.00, we continued to use the theoretical estimate of 1.00 to derive breed of sire differences and EPD adjustment factors. Pooled regression estimates for these two traits may be used in future updates.

Prediction Error Variance of Across-Breed EPD

Prediction error variances were not included in the report due to a larger number of tables included with the addition of carcass traits. These tables were last reported in Kuehn et al. (2007; available online at <http://www.beefimprovement.org/proceedings.html>). An updated set of tables is available on request (Larry.Kuehn@ars.usda.gov).

Implications

Bulls of different breeds can be compared on a common EPD scale by adding the appropriate across-breed adjustment factor to EPD produced in the most recent genetic evaluations for each of the 18 breeds. The across-breed EPD are most useful to commercial producers purchasing bulls of two or more breeds to use in systematic crossbreeding programs. Uniformity in across-breed EPD should be emphasized for rotational crossing. Divergence in across-breed EPD for direct weaning weight and yearling weight should be emphasized in selection of bulls for terminal crossing. Divergence favoring lighter birth weight may be helpful in selection of bulls for use on first calf heifers. Accuracy of across-breed EPD depends primarily upon the accuracy of the within-breed EPD of individual bulls being compared.

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Table 1. Breed of sire solutions from USMARC, mean breed and USMARC EPD used to adjust for genetic trend to the year 2010 base and factors to adjust within breed EPD to an Angus equivalent – BIRTH WEIGHT (lb)

Breed	Number		Ave. Base EPD		Breed Soln at USMARC (vs Ang) (3)	BY 2010 Sire Breed Average (4)	BY 2010 Sire Breed Difference ^a (5)	Factor to adjust EPD To Angus (6)
	AI Sires	Direct Progeny	Breed 2010 (1)	USMARC Bulls (2)				
Angus	128	1735	1.8	1.8	0.0	89.8	0.0	0.0
Hereford	135	2176	3.6	2.3	3.8	94.3	4.5	2.7
Red Angus	42	574	-0.1	-1.2	-0.7	90.3	0.5	2.4
Shorthorn	47	406	2.3	1.4	6.6	96.3	6.5	6.0
South Devon	15	153	2.6	2.0	5.2	94.8	5.0	4.2
Beefmaster	38	343	0.3	1.0	7.0	95.0	5.2	6.7
Brahman	55	653	1.7	0.6	11.7	100.8	11.0	11.1
Brangus	40	336	0.7	1.0	3.5	92.4	2.6	3.7
Santa Gertrudis	21	218	0.6	0.9	7.7	96.0	6.2	7.4
Braunvieh	30	405	2.9	4.3	4.4	92.1	2.2	1.2
Charolais	95	1019	0.6	0.2	8.2	97.2	7.4	8.6
Chiangus	24	218	2.0	2.7	5.0	93.2	3.4	3.3
Gelbvieh	72	939	1.2	1.2	4.1	93.3	3.5	4.0
Limousin	62	1009	1.5	0.7	3.2	93.3	3.5	3.8
Maine Anjou	37	407	1.7	3.9	7.3	93.8	4.0	4.1
Salers	50	405	1.8	2.5	3.0	91.6	1.8	1.8
Simmental	66	969	0.7	1.7	6.0	93.9	4.1	5.2
Tarentaise	7	199	1.9	1.9	2.1	91.6	1.8	1.7

Calculations:

$$(4) = (3) / b + [(1) - (2)] + (\text{Recent Raw Angus Mean: } 89.8 \text{ lb}) \text{ with } b = 1.11$$

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

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

^aThe breed difference estimates represent half the differences that would be expected between purebreds of the two breeds.

Table 2. Breed of sire solutions from USMARC, mean breed and USMARC EPD used to adjust for genetic trend to the year 2010 base and factors to adjust within breed EPD to an Angus equivalent – WEANING WEIGHT (lb)

Breed	Number		Ave. Base EPD		Breed Soln	BY 2010	BY 2010	Factor to adjust EPD To Angus (6)
	AI Sires	Direct Progeny	Breed 2010 (1)	USMARC Bulls (2)	at USMARC (vs Ang) (3)	Sire Breed Average (4)	Sire Breed Difference ^a (5)	
Angus	128	1598	47.0	26.3	0.0	582.0	0.0	0.0
Hereford	133	2014	44.0	27.0	-1.7	576.2	-5.8	-2.8
Red Angus	42	556	31.9	26.3	-0.5	566.3	-15.7	-0.6
Shorthorn	45	385	15.0	13.8	2.7	565.7	-16.3	15.7
South Devon	15	134	40.5	23.7	0.5	578.7	-3.3	3.2
Beefmaster	38	334	8.0	13.5	18.7	578.3	-3.7	35.3
Brahman	55	566	14.7	7.5	19.6	592.2	10.2	42.5
Brangus	40	324	23.0	21.8	7.1	571.0	-11.0	13.0
Santa Gertrudis	21	211	5.0	8.3	16.4	577.7	-4.3	37.7
Braunvieh	30	383	40.9	45.1	-0.4	556.7	-25.3	-19.2
Charolais	94	921	24.2	13.4	22.6	599.3	17.3	40.1
Chiangus	24	204	36.8	37.3	-3.2	556.9	-25.1	-14.9
Gelbvieh	71	880	40.0	33.1	10.4	580.8	-1.2	5.7
Limousin	62	928	45.4	29.6	2.0	579.5	-2.5	-0.9
Maine Anjou	37	377	39.4	41.3	1.6	561.4	-20.6	-13.0
Salers	50	383	41.3	32.8	2.8	573.2	-8.8	-3.1
Simmental	65	883	30.8	26.5	20.9	590.7	8.7	24.9
Tarentaise	7	191	16.0	-5.6	1.0	584.1	2.1	33.1

Calculations:

$$(4) = (3) / b + [(1) - (2)] + (\text{Raw Angus Mean: } 561.3 \text{ lb}) \text{ with } b = 0.83$$

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

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

^aThe breed difference estimates represent half the differences that would be expected between purebreds of the two breeds.

Table 3. Breed of sire solutions from USMARC, mean breed and USMARC EPD used to adjust for genetic trend to the year 2010 base and factors to adjust within breed EPD to an Angus equivalent – YEARLING WEIGHT (lb)

Breed	AI Sires	Number Direct Progeny	Ave. Base EPD		Breed Soln	BY 2010	BY 2010	Factor to adjust EPD To Angus (6)
			Breed 2010 (1)	USMARC Bulls (2)	at USMARC (vs Ang) (3)	Sire Breed Average (4)	Sire Breed Difference ^a (5)	
Angus	127	1437	85.0	48.3	0.0	1036.8	0.0	0.0
Hereford	128	1836	73.0	44.5	-25.4	1004.6	-32.1	-20.1
Red Angus	37	460	59.6	46.7	-14.4	999.4	-37.4	-12.0
Shorthorn	44	314	24.4	21.0	12.8	1015.6	-21.2	39.4
South Devon	15	134	75.8	50.4	-4.5	1021.3	-15.5	-6.3
Beefmaster	26	170	13.0	22.8	7.4	997.3	-39.5	32.5
Brahman	44	450	23.5	11.6	-33.9	980.0	-56.7	4.8
Brangus	25	168	41.7	40.1	5.5	1006.9	-29.8	13.5
Santa Gertrudis	17	135	7.0	11.1	-3.5	992.7	-44.1	33.9
Braunvieh	23	312	63.5	71.6	-16.2	976.7	-60.0	-38.5
Charolais	92	803	42.6	25.2	25.1	1041.2	4.4	46.8
Chiangus	17	140	68.7	66.9	-13.5	989.1	-47.6	-31.3
Gelbvieh	65	784	74.4	61.1	-0.8	1012.7	-24.1	-13.5
Limousin	55	812	83.0	58.3	-26.2	1000.0	-36.7	-34.7
Maine Anjou	36	294	78.1	84.5	1.8	995.3	-41.4	-34.5
Salers	47	305	79.4	60.9	-1.9	1016.8	-19.9	-14.3
Simmental	63	756	56.3	49.1	24.5	1030.5	-6.3	22.4
Tarentaise	7	189	28.6	-3.6	-32.6	1001.6	-35.2	21.2

Calculations:

(4) = (3) / b + [(1) – (2)] + (Raw Angus Mean: 1000.1 lb) with b = 1.06

(5) = (4) – (4, Angus)

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

^aThe breed difference estimates represent half the differences that would be expected between purebreds of the two breeds.

Table 4. Breed of maternal grandsire solutions from USMARC, mean breed and USMARC EPD used to adjust for genetic trend to the year 2010 base and factors to adjust within breed EPD to an Angus equivalent – MILK (lb)

Breed	AI Sires	Number		Ave. Base EPD		Breed Soln at USMARC (vs Ang) (3)	BY 2010 Sire Breed Average (4)	BY 2010 Sire Breed Difference ^a (5)	Factor to adjust EPD To Angus (6)
		Direct Gpr	Direct Progeny	Breed 2010 (1)	USMARC Bulls (2)				
Angus	123	2788	609	22.0	13.1	0.0	570.2	0.0	0.0
Hereford	120	3530	769	17.0	9.6	-24.1	548.5	-21.7	-16.7
Red Angus	31	519	140	17.4	14.2	-2.4	562.5	-7.7	-3.1
Shorthorn	34	283	88	2.2	4.3	10.8	568.3	-1.9	17.9
South Devon	14	373	70	23.0	19.1	4.4	568.8	-1.3	-2.3
Beefmaster	22	273	54	2.0	-1.6	-8.2	558.0	-12.2	7.8
Brahman	40	791	199	6.3	4.8	16.7	576.9	6.7	22.4
Brangus	21	252	46	10.8	3.4	-3.5	565.8	-4.4	6.8
Braunvieh	16	560	110	34.5	33.8	24.2	582.3	12.2	-0.4
Charolais	79	1268	284	6.8	5.2	-2.6	560.7	-9.5	5.7
Gelbvieh	55	1251	273	16.7	16.8	20.5	578.5	8.3	13.6
Limousin	47	1389	291	20.1	18.0	-5.2	559.1	-11.1	-9.2
Maine Anjou	27	546	104	19.6	23.1	6.3	563.2	-7.0	-4.7
Salers	37	380	107	20.1	21.4	12.8	570.7	0.5	2.4
Simmental	59	1387	287	3.4	5.6	14.6	571.4	1.2	19.8
Tarentaise	6	367	80	0.6	5.3	18.6	572.2	2.0	23.4

Calculations:

(4) = (3) / b + [(1) – (2)] + (Raw Angus Mean: 561.3lb) with b = 1.19

(5) = (4) – (4, Angus)

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

^aThe breed difference estimates represent half the differences that would be expected between purebreds of the two breeds.

Table 5. Breed of sire solutions from USMARC, mean breed and USMARC EPD used to adjust for genetic trend to the year 2010 base and factors to adjust within breed EPD to an Angus equivalent – MARBLING (marbling score units^a)

Breed	AI Sires	Number Direct Progeny	Ave. Base EPD		Breed Soln	BY 2010	BY 2010	Factor to adjust EPD To Angus (6)
			Breed 2010 (1)	USMARC Bulls (2)	at USMARC (vs Ang) (3)	Sire Breed Average (4)	Sire Breed Difference ^b (5)	
Angus	109	646	0.43	0.18	0.00	5.92	0.00	0.00
Hereford	125	860	0.04	-0.01	-0.53	5.19	-0.73	-0.34
Red Angus	36	160	0.07	0.11	-0.04	5.59	-0.34	0.03
Shorthorn	43	183	-0.01	0.01	-0.30	5.34	-0.58	-0.14
South Devon	13	49	0.30	-0.08	-0.21	5.84	-0.08	0.05
Santa Gertrudis	18	75	0.00	-0.01	-0.86	4.82	-1.10	-0.67
Braunvieh	27	164	0.41	0.39	-0.46	5.23	-0.69	-0.67
Charolais	41	189	0.03	-0.04	-0.68	5.05	-0.87	-0.46
Chiangus	19	84	0.25	0.19	-0.41	5.32	-0.60	-0.42
Limousin	54	322	-0.04	-0.08	-0.96	4.75	-1.17	-0.70
Maine Anjou	36	165	0.22	0.14	-0.83	4.92	-1.01	-0.79
Salers	42	151	0.20	-0.37	-0.66	5.58	-0.34	-0.11
Simmental	63	346	0.17	0.10	-0.63	5.11	-0.81	-0.55

Calculations:

(4) = (3) / b + [(1) – (2)] + (Raw Angus Mean: 5.67) with b = 1.00

(5) = (4) – (4, Angus)

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

^a4.00 = S1⁰⁰, 5.00 = S_m⁰⁰

^bThe breed difference estimates represent half the differences that would be expected between purebreds of the two breeds.

Table 6. Breed of sire solutions from USMARC, mean breed and USMARC EPD used to adjust for genetic trend to the year 2010 base and factors to adjust within breed EPD to an Angus equivalent – RIBEYE AREA (in²)

Breed	Number		Ave. Base EPD		Breed Soln	BY 2010	BY 2010	Factor to
	AI Sires	Direct Progeny	Breed 2010 (1)	USMARC Bulls (2)	at USMARC (vs Ang) (3)	Sire Breed Average (4)	Sire Breed Difference ^a (5)	adjust EPD To Angus (6)
Angus	109	647	0.32	0.05	0.00	12.96	0.00	0.00
Hereford	125	860	0.25	-0.04	-0.21	12.77	-0.18	-0.11
Red Angus	36	160	0.07	-0.17	-0.32	12.60	-0.35	-0.10
Shorthorn	43	183	0.05	0.01	0.13	12.86	-0.10	0.17
South Devon	13	49	0.21	0.21	0.31	12.99	0.04	0.15
Santa Gertrudis	18	76	0.02	0.01	-0.23	12.46	-0.49	-0.19
Braunvieh	27	164	0.73	0.79	0.96	13.59	0.64	0.23
Charolais	41	190	0.20	0.08	0.95	13.76	0.81	0.92
Chiangus	19	85	0.03	0.10	0.45	13.06	0.11	0.40
Limousin	54	323	0.53	0.29	1.30	14.24	1.28	1.07
Maine Anjou	36	165	0.16	0.17	1.00	13.67	0.72	0.88
Salers	42	152	0.02	0.03	0.73	13.40	0.45	0.75
Simmental	63	347	0.19	0.02	0.89	13.75	0.79	0.92

Calculations:

(4) = (3) / b + [(1) – (2)] + (Raw Angus Mean: 12.69 in²) with b = 1.00

(5) = (4) – (4, Angus)

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

^aThe breed difference estimates represent half the differences that would be expected between purebreds of the two breeds.

Table 7. Breed of sire solutions from USMARC, mean breed and USMARC EPD used to adjust for genetic trend to the year 2010 base and factors to adjust within breed EPD to an Angus equivalent – FAT THICKNESS (in)

Breed	AI Sires	Number Direct Progeny	Ave. Base EPD		Breed Soln	BY 2010	BY 2010	Factor to adjust EPD To Angus (6)
			Breed 2010 (1)	USMARC Bulls (2)	at USMARC (vs Ang) (3)	Sire Breed Average (4)	Sire Breed Difference ^a (5)	
Angus	109	647	0.009	0.000	0.000	0.587	0.000	0.000
Hereford	125	860	0.001	-0.003	-0.056	0.526	-0.061	-0.053
Red Angus	36	160	0.000	-0.008	-0.042	0.544	-0.043	-0.034
Shorthorn	43	183	-0.012	-0.004	-0.152	0.418	-0.169	-0.148
South Devon	13	49	0.010	0.008	-0.103	0.477	-0.110	-0.111
Santa Gertrudis	18	76	0.000	0.004	-0.110	0.463	-0.124	-0.115
Braunvieh	27	164	-0.092	-0.106	-0.200	0.391	-0.196	-0.095
Charolais	41	190	0.000	0.000	-0.222	0.356	-0.231	-0.222
Chiangus	19	85	0.024	0.016	-0.141	0.445	-0.142	-0.157
Maine Anjou	36	165	0.003	-0.023	-0.233	0.371	-0.216	-0.210
Salers	42	152	0.000	-0.005	-0.216	0.368	-0.219	-0.210
Simmental	63	347	0.012	0.013	-0.203	0.375	-0.212	-0.215

Calculations:

(4) = (3) / b + [(1) – (2)] + (Raw Angus Mean: 0.578 in) with b = 1.00

(5) = (4) – (4, Angus)

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

^aThe breed difference estimates represent half the differences that would be expected between purebreds of the two breeds.

Table 8. Mean weighted^a accuracies for birth weight (BWT), weaning weight (WWT), yearling weight (YWT), maternal weaning weight (MWWT), milk (MILK), marbling (MAR), ribeye area (REA), and fat thickness (FAT) for bulls used at USMARC

Breed	BWT	WWT	YWT	MILK	MAR	REA	FAT
Angus	0.79	0.76	0.70	0.71	0.51	0.50	0.48
Hereford	0.65	0.61	0.60	0.57	0.24	0.38	0.28
Red Angus	0.92	0.91	0.91	0.88	0.80	0.80	0.80
Shorthorn	0.81	0.80	0.73	0.78	0.61	0.60	0.54
South Devon	0.37	0.41	0.37	0.44	0.02	0.05	0.05
Beefmaster	0.86	0.89	0.87	0.75			
Brahman	0.66	0.67	0.59	0.60			
Brangus	0.87	0.81	0.79	0.68			
Santa Gertrudis	0.85	0.82	0.78		0.31	0.52	0.44
Braunvieh	0.54	0.47	0.36	0.40	0.10	0.13	0.08
Charolais	0.79	0.73	0.64	0.67	0.48	0.50	0.45
Chiangus	0.82	0.79	0.79		0.52	0.51	0.55
Gelbvieh	0.82	0.77	0.63	0.66			
Limousin	0.93	0.90	0.84	0.84	0.74	0.74	
Maine Anjou	0.78	0.77	0.75	0.75	0.35	0.35	0.35
Salers	0.83	0.82	0.77	0.81	0.23	0.27	0.31
Simmental	0.94	0.94	0.94	0.92	0.81	0.80	0.81
Tarentaise	0.96	0.95	0.95	0.94			

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

Table 9. Estimates of variance components (lb²) for birth weight (BWT), weaning weight (WWT), yearling weight (YWT), and maternal weaning weight (MWWT) and for marbling (MAR; marbling score units²), ribeye area (REA; in⁴), and fat thickness (FAT; in²) from mixed model analyses

Analysis	Direct		
	BWT	WWT ^a	YWT
Direct			
Animal within breed (19 breeds)	72.31	489.62	3669.03
Maternal genetic within breed (17 breeds)		433.09	
Maternal permanent environment		724.34	
Residual	50.53	1213.12	4324.94
Carcass Direct			
	MAR	REA	FAT
Animal within breed (12-13 breeds)	0.279	0.660	0.0100
Residual	0.294	0.728	0.0144

^aDirect maternal covariance for weaning weight was -83.33 lb²

Table 10. Pooled and within-breed regression coefficients (lb/lb) for weights at birth (BWT), 205 days (WWT), and 365 days (YWT) of F₁ progeny and for calf weights (205 d) of F₁ dams (MILK) on sire expected progeny difference and by sire breed

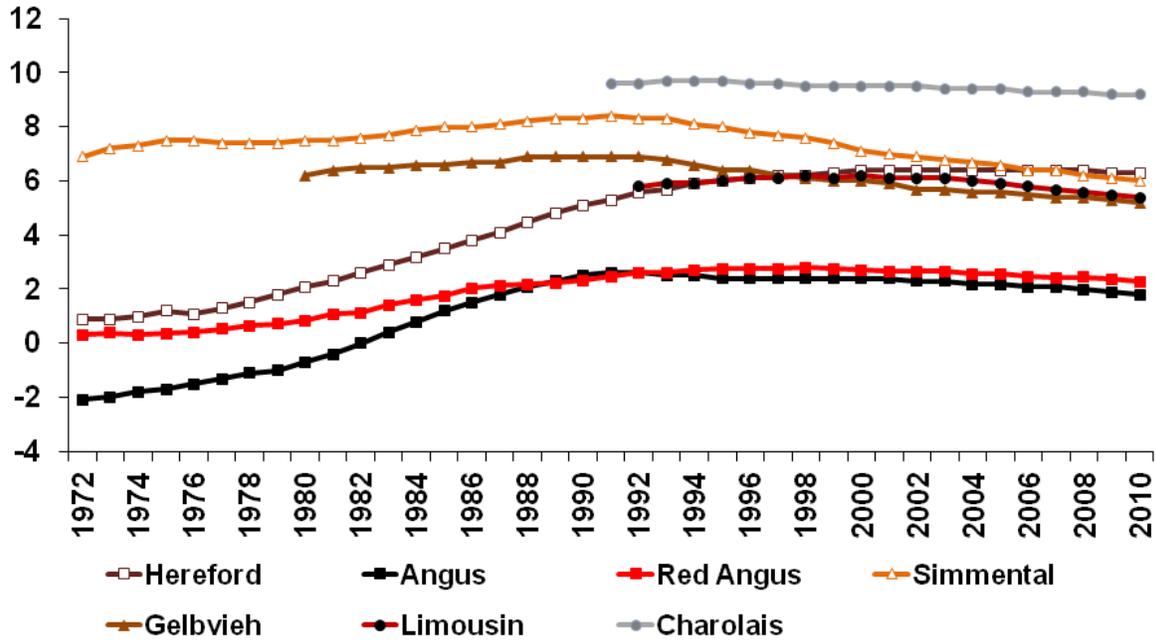
	BWT	WWT	YWT	MILK
Pooled	1.18 ± 0.04	0.83 ± 0.04	1.06 ± 0.05	1.19 ± 0.08
Sire breed				
Angus	1.05 ± 0.10	0.83 ± 0.08	1.26 ± 0.08	1.14 ± 0.16
Hereford	1.19 ± 0.07	0.76 ± 0.05	1.03 ± 0.06	1.08 ± 0.16
Red Angus	1.25 ± 0.16	0.72 ± 0.16	0.56 ± 0.20	1.59 ± 0.34
Shorthorn	0.48 ± 0.24	0.79 ± 0.24	0.69 ± 0.29	0.95 ± 0.93
South Devon	-0.22 ± 0.63	0.02 ± 0.56	-0.01 ± 0.48	-0.22 ± 1.54
Beefmaster	2.07 ± 0.37	1.19 ± 0.31	1.02 ± 0.50	3.94 ± 0.72
Brahman	2.11 ± 0.22	1.02 ± 0.21	1.23 ± 0.24	0.34 ± 0.51
Brangus	1.54 ± 0.28	0.45 ± 0.31	0.80 ± 0.42	0.45 ± 0.77
Santa Gertrudis	4.51 ± 0.87	1.44 ± 0.39	0.45 ± 0.42	
Braunvieh	0.80 ± 0.28	1.39 ± 0.31	0.95 ± 0.45	2.99 ± 1.06
Charolais	1.14 ± 0.13	0.95 ± 0.12	0.82 ± 0.13	1.16 ± 0.30
Chiangus	1.88 ± 0.35	0.73 ± 0.35	0.79 ± 0.46	
Gelbvieh	1.04 ± 0.14	0.96 ± 0.17	1.19 ± 0.18	1.32 ± 0.46
Limousin	0.94 ± 0.12	0.98 ± 0.10	1.17 ± 0.13	1.45 ± 0.29
Maine Anjou	1.47 ± 0.20	0.56 ± 0.27	0.71 ± 0.32	1.07 ± 0.52
Salers	1.28 ± 0.25	0.91 ± 0.34	0.51 ± 0.31	1.75 ± 0.51
Simmental	1.21 ± 0.17	1.52 ± 0.15	1.43 ± 0.15	0.75 ± 0.39
Tarentaise	1.50 ± 1.37	0.70 ± 0.61	1.49 ± 0.84	1.00 ± 0.93

Table 11. Pooled and within-breed regression coefficients marbling (MAR; score/score), ribeye area (REA; in²/in²), and fat thickness (FAT; in/in) of F₁ progeny on sire expected progeny difference and by sire breed

	MAR	REA	FAT
Pooled	0.60 + 0.05	0.91 + 0.07	1.18 + 0.10
Sire breed			
Angus	1.00 + 0.10	1.03 + 0.17	1.40 + 0.17
Hereford	0.54 + 0.18	0.60 + 0.15	1.02 + 0.21
Red Angus	0.59 + 0.19	1.15 + 0.27	0.64 + 0.50
Shorthorn	1.75 + 0.34	1.25 + 0.62	2.22 + 0.55
South Devon	-0.61 + 0.67	1.64 + 3.21	5.60 + 4.58
Santa Gertrudis	-0.18 + 1.12	1.07 + 0.54	1.44 + 0.68
Braunvieh	0.80 + 0.55	0.12 + 0.28	0.35 + 0.44
Charolais	1.07 + 0.29	1.44 + 0.32	1.60 + 0.53
Chiangus	0.70 + 0.25	0.61 + 0.51	0.05 + 0.60
Limousin	1.25 + 0.41	1.34 + 0.19	
Maine Anjou	0.10 + 0.40	-1.03 + 0.63	1.03 + 0.74
Salers	0.05 + 0.09	2.38 + 0.77	1.03 ± 0.93
Simmental	0.78 + 0.21	0.73 + 0.18	1.83 ± 0.45

Figure 1. Relative genetic trends for birth weight (lb) of the seven most highly used beef breeds (1a) and all breeds that submitted 2012 trends (1b) adjusted for birth year 2010 using the 2012 across-breed EPD adjustment factors.

1a.



1b.

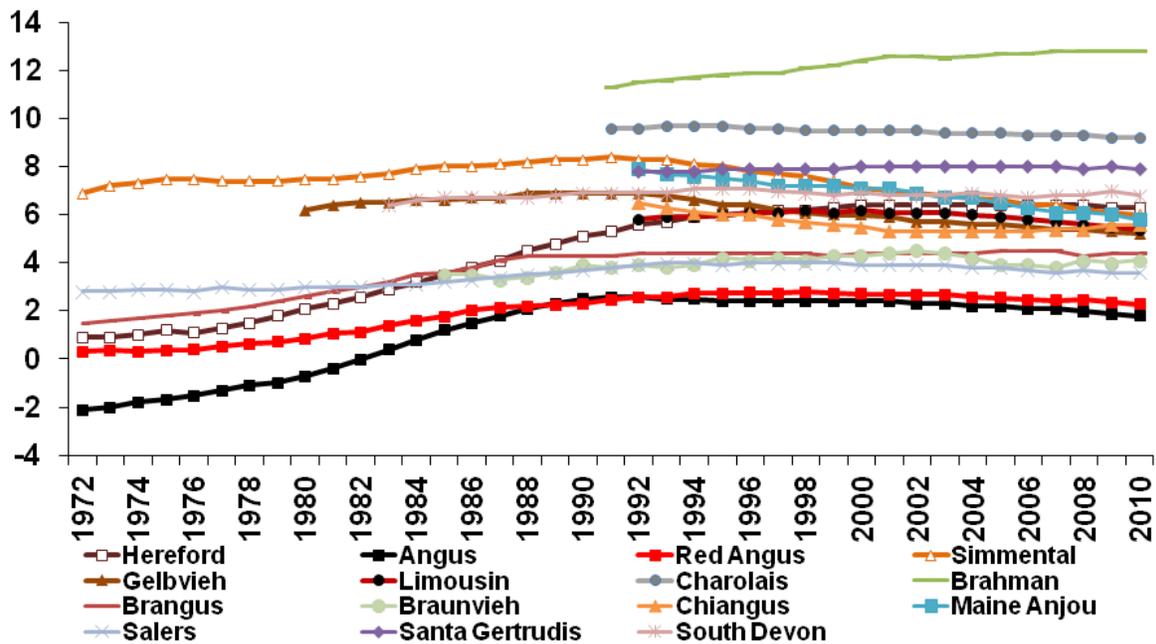
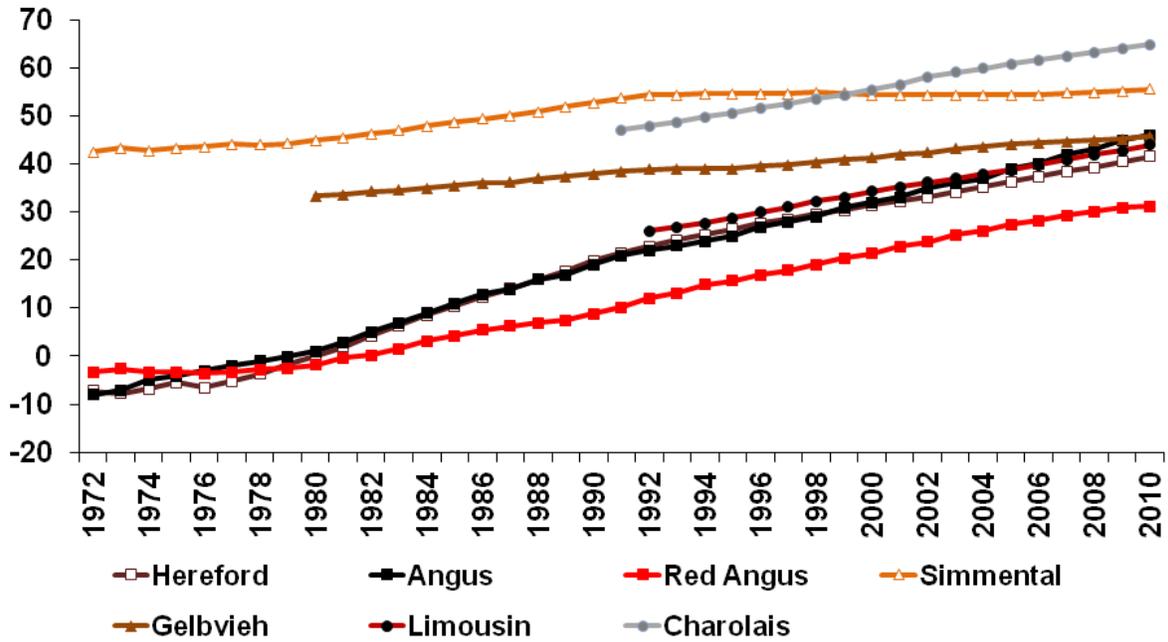


Figure 2. Relative genetic trends for weaning weight (lb) of the seven most highly used beef breeds (2a) and all breeds that submitted 2012 trends (2b) adjusted for birth year 2010 using the 2012 across-breed EPD adjustment factors.

2a.



2b.

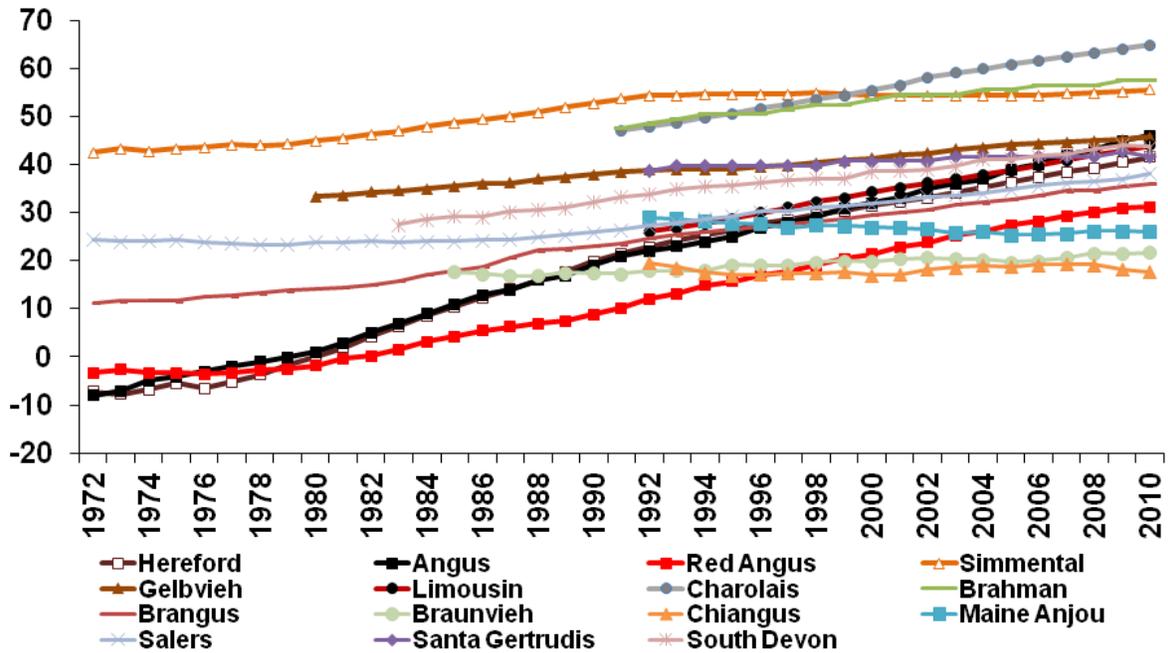
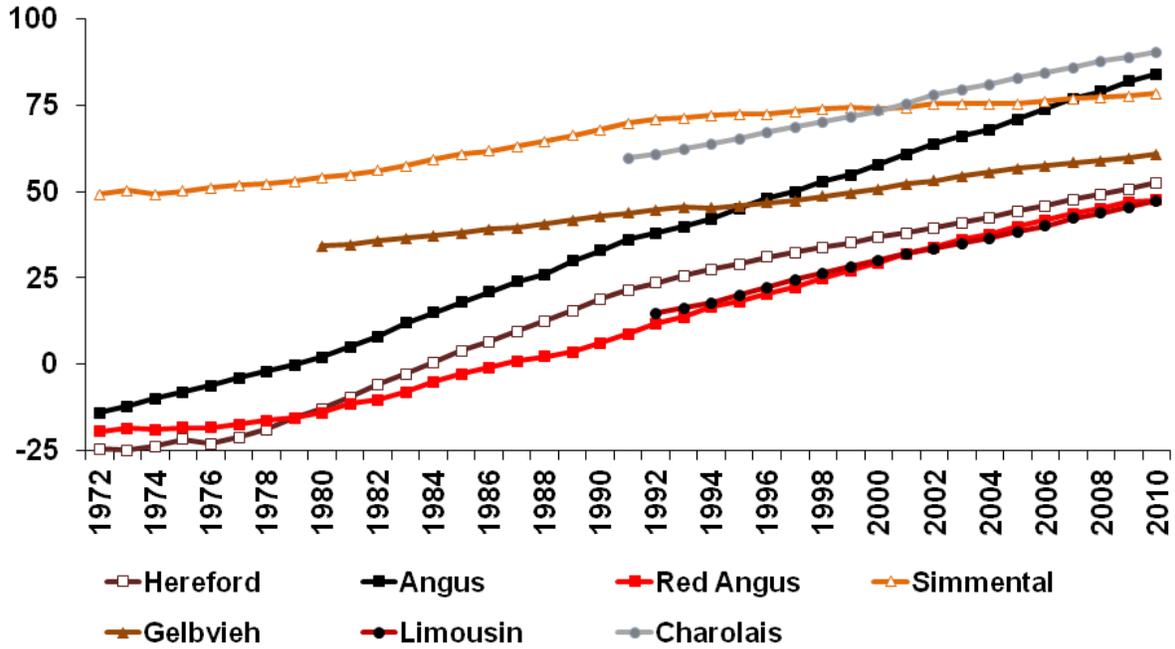


Figure 3. Relative genetic trends for yearling weight (lb) of the seven most highly used beef breeds (3a) and all breeds that submitted 2012 trends (3b) adjusted for birth year 2010 using the 2012 across-breed EPD adjustment factors.

3a.



3b.

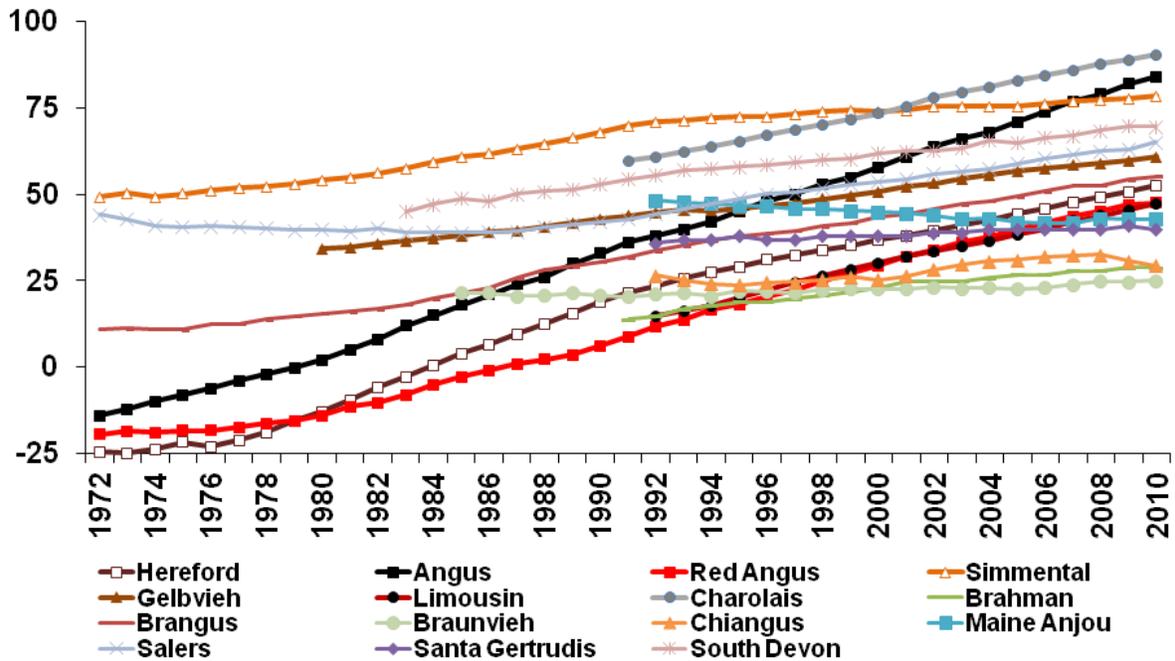
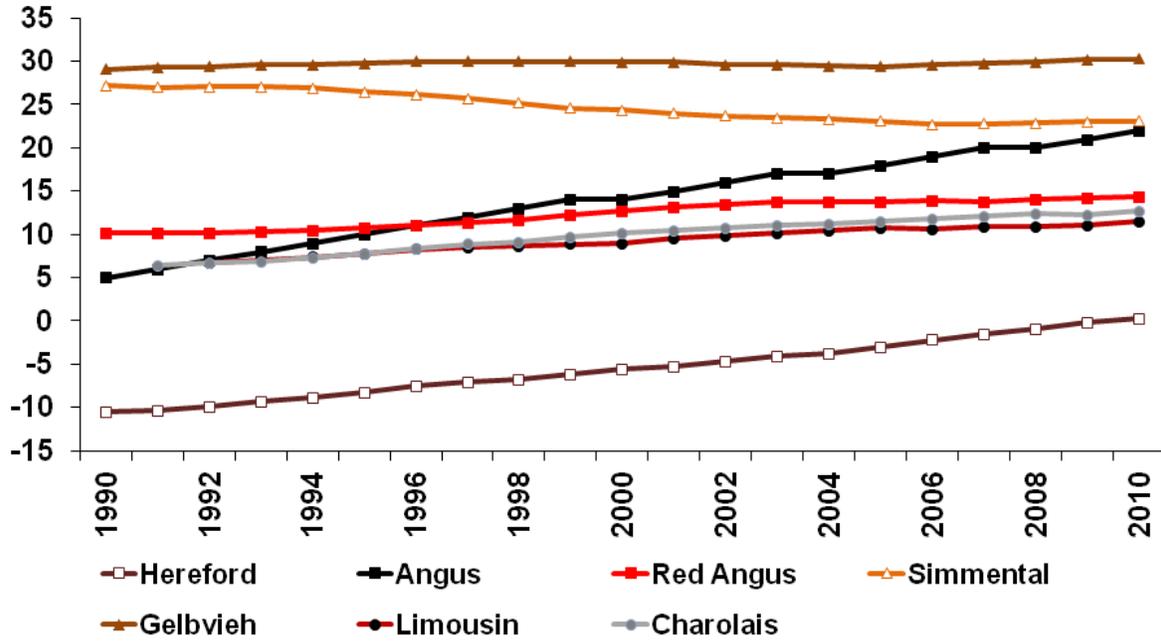
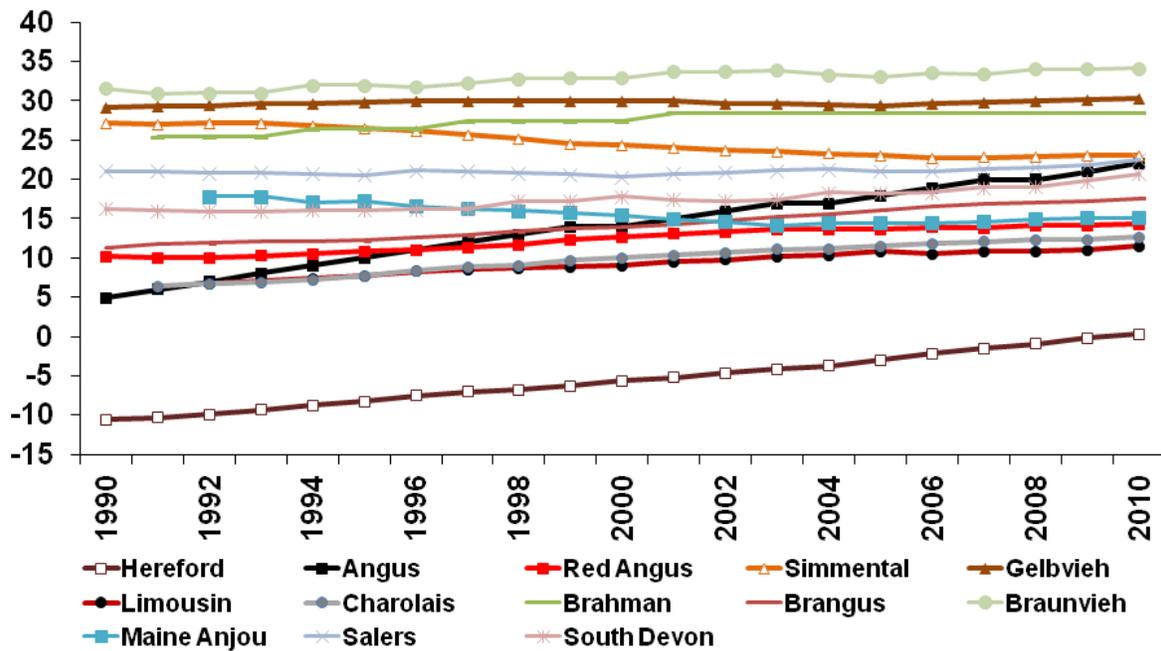


Figure 4. Relative genetic trends for maternal milk (lb) of the seven most highly used beef breeds (4a) and all breeds that submitted 2012 trends (4b) adjusted for birth year 2010 using the 2012 across-breed EPD adjustment factors.

4a.



4b.



"Genetic Components of Fitness and Adaptation: Body Temperature Regulation".

Introduction

Beef production is unique in that animals are kept in an extensive environment with minimal environmental modifications, unlike what is seen in dairy, swine and poultry production. Thus, cattle are reared in environments that differ remarkably in temperature, humidity, and wind speed which have forced cattle to adapt in order to survive in these diverse environments. Examples of breed adaptation include the Nellore breed in South America which is well suited to tropical environments or the Scottish Highland breed which is well suited to the opposite extreme. As a consequence of this extreme adaptation in one direction, heat or cold tolerant breeds are more sensitive to environmental extremes in the opposite direction. Suboptimal body temperature regulation during periods of extreme temperature events has deleterious effects on multiple aspects of production including growth, feed efficiency, reproduction, and animal welfare (McDowell, 1972; Hahn, 1999). Currently breeders mitigate the risks associated with heat or cold stress by using knowledge of breed strengths relative to heat or cold tolerance but direct selection of animals within breeds is currently not possible.

The investigation of genetic components of environmental (temperature) tolerance or adaptation could allow for the development of novel indicator traits that can aid in the selection for Economically Relevant Traits (ERT) such as fertility, disease resistance, and feed efficiency across varying environments. Furthermore Physiological Indicator Traits (PIT) associated with body temperature regulation, including blood hormones or heat shock protein response, could be used as an indicator for ERT. Alternatively, susceptibility to environmental stress may be decreased by identifying and selecting for animals within a population that have a larger genetic threshold for heat and/or cold extremes, instead of relying on inherent breed differences. Knowledge of genetic components of body temperature could also be used to improve the efficiency and fitness of animals through environmental specific management decisions.

Literature Review

Modes of heat exchange from the animal to the environment:

A beef cow has an average body temperature ranging from 38.55 to 38.6°C and a rise or fall of 1°C or less in body temperature is sufficient to produce detectable changes in a number of physiological processes (McDowell, 1972). To maintain this temperature in such narrow limits requires sensitive and immediate acting heat exchange mechanisms. An animal is said to be in its thermoneutral zone when it is in a temperature range that requires the least thermoregulatory effort and temperature regulation is achieved by non-evaporative physical processes alone (Hillman, 2009). The thermoneutral zone is bounded by a lower critical temperature and upper critical temperature and once past this point the animal is under heat or cold stress. When an animal is in its thermoneutral zone the variance across animals in body temperature is small and as the temperature exceeds an animal's lower or upper temperature threshold the variance increases due to differences across animals in their ability to cope with heat or cold stress (Hahn *et al.*, 1990). These differences in thermoregulatory ability are manifested through the complex interaction between anatomical, physiological, and behavioral factors, which are dependent on the life stage, nutrition, genetics, previous degree of heat or cold stress, and health of the animal (McDowell, 1972; Hahn, 1999).

Behavior changes are the first mechanism to account for the heat lost or gained. If behavioral changes don't minimize the heat lost or gained, non-evaporative physical processes that involve the exchange of heat between an animal and its environment are used, which include conduction, radiation, and convection. Resistance to conductive (i.e. heat exchange from particle to particle) heat transfer is proportional to the temperature gradients between the core and outer extremities or the outer extremities and environment (Finch, 1986). As an animal increases in weight its ability to dissipate core heat outward decreases linearly and it becomes more susceptible to heat stress while decreasing its susceptibility to cold stress (Finch, 1985). During cold stress conditions an animal is trying to retain its core body heat, while the environment is acquiring it due to the differing temperature gradients. The animal accounts for this loss of heat by increasing its maintenance energy requirements in order to produce extra heat at a rate of 1% for each 1 °C reduction in effective temperature below its lower threshold

temperature (Hicks, 2007). In heat stress conditions convection (i.e. heat exchange through a liquid or gas) is accomplished by the redirection of blood flow to the extremities or lungs and its effectiveness is dependent on multiple factors including physical properties of the hair coat and size of the animal. When an animal is first exposed to an adverse environment it reacts initially by activation or acceleration of non-evaporative processes to remain at thermal equilibrium and is defined as short-term adaptive changes (McDowell, 1972; Nienaber and Hahn, 2007). If non-evaporative physical processes fail to keep an animal at thermal equilibrium, evaporative processes take over (McDowell, 1972; Hahn, 1999).

Evaporation is the vaporization of water from the body surface and respiratory tract. Resistance to evaporative heat transfer is a function of the gradient through which the water vapors move (Finch, 1986). Evaporative heat transfer is not dependent on the temperature gradient, which becomes important when the environment is warmer than the animal body temperature and would result in the inward flow of heat from the environment to the animal (Davis *et al.*, 2003). Animal factors that affect the efficiency of evaporative heat loss from the skin surface are sweat gland density, function and morphology, hair coat density, length, and color and regulation of epidermal vascular supply (Carvalho *et al.*, 1995; Collier *et al.*, 2008). A rise in respiratory heat loss through panting is one of the first physical signs of an animal experiencing heat stress (Nienaber and Hahn, 2007).

As a consequence of the animal's inability to regulate its body temperature, inefficient measures commence that involve a decrease in production. One of them being a decrease in feed efficiency due to more energy being used for thermoregulatory processes. Also, a heat or cold stressed animal's immune system becomes suppressed and their cellular proteins lose their structure and function causing an increased susceptibility to sickness. These negative consequences cause a decrease in overall growth rate due to energy being used for processes other than growth, which cause an animal to spend more days on feed. Lastly, from a reproductive standpoint, cold or heat stress has deleterious effects on female and male fertility (Hahn, 1999).

After 2 to 4 days of heat or cold exposure, depending on the individual animal and the degree of heat or cold exposure, mobilization of heat dissipation or retention functions

(physiological coping) has progressed to the point that acclimation is apparent (Hahn *et al.*, 1990). Phenotypic acclimation is defined as the “within lifetime phenotypic response” to environmental stress and is a homeorhetic process driven by the endocrine system (Collier *et al.*, 2008). An animal can attain heat or cold tolerance through previous generations of artificial/natural selection or within its lifetime by using alternative pathways that have varying penalties on productivity.

Historically, heat tolerant research has involved comparing and understanding the phenotypic and genetic differences within and between heat-tolerant *Bos indicus* cattle and heat-intolerant *Bos taurus* cattle in controlled or natural environments (Finch, 1985; Finch, 1986; Brown-Brandl *et al.*, 2004; Gaughan *et al.*, 2009). Previous cold tolerance research was concerned with understanding the effects of adverse cold conditions on various production traits using cold tolerant *Bos taurus* cattle (Young, 1983; Hicks, 2007). Multiple indicator traits taken at a single time point or across multiple time points have been used to assess the ability of an animal to regulate its body temperature in extreme hot or cold environments. Some examples include panting score, tympanic temperature, respiration rate (Gaughan *et al.*, 2009), rectal temperature, sweating rate (Finch, 1986), radiotelemetry (Lefcourt and Adams, 1996; Lefcourt and Adams, 1998) and dry matter intake (DMI) (Young, 1983). Due to the fact that body temperature is a continuous function of time, multiple measurements need to be taken to fully describe the circadian rhythm of cattle. Under conditions of minimal heat stress the rhythm is similar across animals, but as the animal is under heat or cold stress the phase, mean temperature, and amplitude get disrupted and the degree of disruption is animal specific (Lefcourt and Adams, 1996; Lefcourt and Adams, 1998).

The degree of disruption can be quantified on an individual animal basis and used as a means of selection by using various phenotypes that indicate the degree of heat or cold stress. Within herd selection for decreased susceptibility to heat or cold stress would broaden the temperature threshold for a herd, which in turn would reduce the occurrence of the deleterious effects during heat or cold stress conditions. This was looked at by Gaughan *et al.* (2009) using panting score along with a heat load index to score individual animals on their ability to cope with heat stress. This approach can be problematic given that an animal’s

tolerance threshold can be influenced by many non-genetic factors, making it difficult to isolate specific genetic differences in thermoregulatory ability based solely on phenotypic measurements (Scharf *et al.*, 2010). Furthermore, it is a challenge to attain phenotypes that measure the ability of an animal to cope with heat or cold stress in a production setting.

An alternative approach would be to isolate genetic variants causing animals within a population to be less sensitive to heat or cold extremes using a component of body temperature as a phenotype. An example of this is illustrated by Howard *et al.* (2011) who found that a genotype by environment interaction existed between the myostatin mutation and a component of body temperature during periods of extreme winter and summer weather conditions. It was found that during heat stress conditions homozygote normal animals were numerically more sensitive to increased environmental temperatures in comparison to animals that were homozygote for the myostatin mutation. Alternatively during cold stress conditions animals that were homozygote for the myostatin mutation were numerically more sensitive to decreased environmental temperatures in comparison to homozygote normal animals (Howard *et al.* 2011).

Knowledge of a gene having variable effects on the phenotype depending on the environment would be beneficial for cattle feeders to implement management strategies based on the genotype of the individual/group. Additionally, breeders can select for genotypes that have increased levels of fitness given the predicted production environment of their customers or own location. The methodology used by Howard *et al.* (2011) can be transferred to other genetic variants or genetic backgrounds that are more conducive to mainstream US beef production and the results could be used to select or better manage cattle based on their genetic temperature threshold.

Genetic parameters for body temperature and relationship to other production traits:

The heritability of various indicators of body temperature regulation during periods of heat stress has been heavily studied in tropical adapted breeds while minimal research has been conducted during cold stress conditions. Burrow (2001) found a heritability of 0.17 for repeated measurements of log transformed rectal temperature on a composite breed of tropical cattle when ambient temperatures exceeded 30°C. In the same study a favorable

genetic and phenotypic relationship was found between rectal temperature and weights and period weight gains from -0.08 to -0.49 and -0.05 to -0.20, respectively. Low to moderate favorable genetic relationships between rectal temperatures and pregnancy status of first 3 parities (-0.16) and days to calving once the bull entered (0.16) has been shown to exist (Burrow, 2001). Turner (1984 and 1982) found a heritability of 0.33 and 0.25 in *Bos indicus*, *Bos taurus* and crossbred lines for repeated measurements of log transformed rectal temperature when the daily maximum ambient temperature was approximately 30°C. A highly favorable genetic correlation (-0.76) between log transformed rectal temperature and fertility, measured as success or failure in producing a calf at term has been shown to exist (Turner, 1982). Da Silva *et al.* (1973) found heritability estimates for the tropically adapted Canchin breed of 0.11 (0.16) and 0.44 (0.27) for initial and increase in rectal temperature during a heat stress event. Mackinnon *et al.* (1991) found a heritability of 0.19 for *Bos indicus*, *Bos taurus* and crossbred lines on a single record rectal temperature when the daily maximum ambient temperature was approximately 30°C. From these studies it has been established that there is a genetic component to the ability of an animal to regulate its body temperature (h^2 of 0.11 to 0.44) through the use of various indicator traits. The genetic correlation between components of body temperature regulation and ERT were favorable, suggesting measures of body temperature could serve as useful indicators to improve various ERT.

Use of genomics in the improvement of quantitative traits in beef cattle:

The traits of economic importance in beef cattle are for the most part quantitative or complex in nature. The classical model of quantitative traits states the phenotypic value is controlled by an infinite number of genes each with an infinitesimal effect as well as by non-genetic or environmental factors (Fisher, 1930). Under this model it is nearly impossible to establish the genotypes of all loci that affect a trait thus a prediction of the total effect of all the genes an animal carries is calculated (estimated breeding value). Traditionally, predictions have been based on the use of dense phenotypes containing the animals and relatives with prior knowledge of the heritability for the particular trait. This approach has been effective and tremendous genetic and phenotypic gains have occurred for a number of economically relevant traits.

This reliance on dense recording of phenotypes is not the most effective for traits that are sex specific (milk yield), measured late in life (longevity), expensive to measure (e.g. methane production, disease resistance, etc.), can only be measured after harvest (meat quality), or have a low heritability (fertility) (Dekkers and Hospital, 2001). In order to increase the accuracy of selection for these traits based on traditional selection schemes requires progeny or sib-testing practices, which increases the generation interval. For these particular traits the accuracy of selection can be increased and generation interval decreased by the use of genomic information to supplement traditional information, which in turn will increase the annual rate of genetic change (Meuwissen *et al.*, 2001). Since the ability to regulate body temperature during hot and cold conditions is difficult and expensive to measure it serves as a trait that would benefit from selection based on genomics. Genomics can be used to locate genomic regions within a population that make an animal less sensitive to heat or cold extremes and then select individuals based on the marker-(s) identified.

The sequencing of the bovine genome uncovered a large number of single nucleotide polymorphisms (SNP), which allowed dense high-throughput genotyping platforms to become commercially available. The use of this information via SNP assays of varying sizes (i.e. 384, 50K, etc.) has allowed for genomic predictors such as Molecular Breeding Values (MBV) to be estimated. MBV for traits where phenotypes are collected on a regular basis (i.e. birth, weaning and yearling weight) has been integrated into National Cattle Evaluation (NCE) for some breeds with others rapidly working towards this end. The challenge lies in the development and implementation of genomic selection (GS) for traits where the phenotype is not measured on a regular basis. Unfortunately, many of these traits (fertility, feed efficiency, adaptation, disease resistance) are of paramount importance to the beef industry. Genomic information used to enhance traditional NCE will become more important in the future to aid in developing selection tools for novel traits as those listed above where phenotypic data is sparse at best.

This technology can be transferred to aid in the management of cattle. This is known as Marker-Assisted Management (MAM) and it consists of using the results of DNA-marker tests to predict future phenotypes of the animal being tested and sort individual cattle into

management groups that are most likely to achieve specific endpoints (Van Eenennaam, 2012). This allows cattle feeders to more efficiently optimize carcass endpoints (i.e. target backfat, weight or quality grade) by deciding how long to feed or whether to use growth-promoting technologies on a group of animal's based on genomic information. Another viable option for MAM is to optimize individual animal fitness by placing animals in an environment that matches up with their upper and lower threshold temperature. MAM allows improved feedlot efficiency by placing animals in a location and feeding them at a specific time of year based on their temperature threshold, which results in faster growth rate and increased feed efficiency due to less energy being used for thermoregulatory processes.

Economically Relevant Traits and Physiological Indicator Traits:

The vast majority of EPD computed in NCE today do not directly affect profit, but are correlated with traits that affect profit. As an example, birth weight and scrotal circumference are measured not because a producer gets more or less money for the weight of his cattle at birth or the scrotal circumference of his bulls, rather these indicator traits are used to indicate the genetic merit of an animal for another trait, in this case calving ease and daughter age at puberty (Golden *et al.*, 2000). The traits we are trying to improve and that are directly associated with a specific cost of production or an income stream are labeled as economically relevant traits (ERT) (Golden *et al.*, 2000). Examples of ERT include heifer pregnancy rate, sale weight, or cow maintenance feed requirement. The importance of indicator traits to predict the genetic merit of ERT is realized for ERT that are unobservable, difficult to obtain/identify a phenotype, expensive to measure, or has a low heritability and the indicator trait is genetically correlated with the ERT. The efficacy of selection is improved by the increase in accuracy for the ERT, which in turn increases the rate of genetic improvement (Golden *et al.*, 2000).

A way to quantify the genetic superiority of an individual for a complex ERT is to combine a suite of practical phenotypes with the proper weighting that accurately predict the ERT. A reductionist approach to improving complex traits allows for the use of practical phenotypes that together may explain the ERT that is highly accurate and robust. Examples of practical phenotypes include traits that can be measured early in life, are inexpensive to measure, have a higher heritability than the ERT, and are genetically correlated with the trait of

interest. An additional approach would be to use physiological indicator traits (PIT) or traits that are expected to be closely related to physiological processes that are components of the trait of interest (Thallman, 2008). This approach takes advantage of the fact that genes related to the physiological process have genetic polymorphisms that affect the ERT and selection for these will in turn positively impact the trait of interest. Potential PIT could be processes that are associated with body temperature regulation (i.e. Heat Shock Proteins, hormone levels, etc.), disease resistance (i.e. red blood cells, or immunological blood factors, etc.), and feed efficiency (hormone levels, enzyme levels, etc.). Another benefit of developing genomic selection tools for PIT is that they could be measured with less error as compared to complex phenotypes such as feed efficiency or fertility, potentially allowing for genomic predictors of high accuracy for PIT.

Conclusions and Implication to Genetic Improvement of Beef Cattle

Suboptimal body temperature regulation has been shown to have negative effects on efficiency of production including growth, feed efficiency, reproduction, and animal welfare (McDowell, 1972; Hahn, 1997). The vast diversity between breeds in their ability to cope with heat or cold stress and the deleterious effects of suboptimal body temperature regulation on multiple economic production traits suggest that inherent differences in body temperature regulation could serve as useful indicator traits to improve the adaptation of animals and efficiency of beef production. Decreased sensitivity to thermal stress events allows for high levels of production to be sustained in the midst of extreme stress events which have positive affects in all areas of production.

The response of animals during times of extreme temperature stress events can be used as an indicator trait to improve ERT across varying environments. PIT associated with body temperature regulation, including blood hormones or heat shock protein response, can be used as an indicator trait in tandem with others in order to estimate the genetic value of an individual for a complex ERT that is a combination of multiple production traits. Knowledge of an animal's genetic threshold paves the way for the implementation of cold or heat stress management practices. Based on an animal's genetic makeup, it could be determined that they would excel if placed on feed in a given region during a specific time of year.

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Advances in the study of genomic prediction and their relevance to the beef cattle industry

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Introduction

Molecular markers can be used to predict genomic breeding values (**DGV**), termed genomic prediction, by exploiting population-wide linkage disequilibrium between QTL and markers distributed throughout the genome as first proposed by Meuwissen *et al.* (2001). This process involves using a population of genotyped and phenotyped individuals as a reference population or training set (**TS**) to estimate DNA marker effects which can be used to predict DGV in another genotyped population. DGV may be combined with parent average information to create genomic estimated breeding values (**GEBV**) using selection index methodology (VanRaden *et al.* 2009, Lund *et al.* 2009, Guo *et al.* 2010) to improve the accuracy of genomic prediction. To confirm genomic prediction accuracy, validation studies are generally performed using a separate phenotyped and genotyped population (Hayes *et al.* 2009a, Luan *et al.* 2009, Su *et al.* 2010); however, estimates of genomic prediction accuracy in the validation population will depend on its genetic relationship to the TS (Habier *et al.* 2007, Habier *et al.* 2010). Therefore, validation populations should be selected such that they are representative of the target population in which genomic selection will be applied. The application of genomic prediction enabled selection, or genomic selection (**GS**), represents a challenge for the U.S. beef cattle industry, as it has fewer populations suitable for use as TS and is composed of many sub-populations of varied breed composition, in terms of number of breeds, levels of admixture, and distribution across industry sectors. As genomic predictions become available for application within certain influential beef breeds (e.g. Angus: Northcutt 2011, Saatchi *et al.* 2011; and Hereford: AHA 2011), lingering concerns are the usefulness of single breed prediction to admixed commercial populations and the potential for accurate across-breed genomic prediction. To address this question, it is necessary to review the progress made in the development and implementation of genomic selection and detail the factors which contribute to genomic prediction accuracy, both within and across populations.

Review of literature

Factors affecting genomic prediction accuracy

The accuracy of genomic prediction depends on several parameters (Hayes & Goddard 2008, Goddard 2009): the extent of linkage disequilibrium (LD), TS size, the heritability of trait, and the distribution of QTL effects. Goddard (2009) expressed the accuracy of genomic prediction for an individual without as phenotype (r) as:
$$r = \frac{\sigma_u^2}{\sigma_u^2 + \frac{L}{4N_e}} \sqrt{h^2}$$
, with σ_e^2 where σ_e^2 is the residual variance and σ_u^2 is the genetic locus variance, N =TS size, and L is the length of the genome in Morgans, h^2 is the heritability, and N_e is the effective population size, and M_e is the effective number of segregating chromosomal segments. While Goddard (2009) approximated M_e as $2N_eL/\ln(4N_eL)$ where N_e is defined as previously and L is the length of the genome in Morgans, Clark *et al.* (2012) found that this definition overestimated baseline genomic prediction accuracy and that defining M_e as $2N_eL$ was more consistent with simulation results.

Figure 1 depicts the relationship between TS size (N) and genomic prediction accuracy based on this definition for a theoretical trait with σ_e^2 equal to 1, L equal to 30, N_e equal to 200 (black) or 300 (gray), and heritability h^2 equal to 0.10 (Δ), 0.30 (\diamond), or 0.60 (\circ). To illustrate the effect of increasing TS size, accuracy increases 0.05-0.10 when TS increases from 2,000 animals to 3,600 animals, depending on the effective population size and the heritability of the trait. This is consistent with results from Holstein populations, using an expected N_e of 64-90 (de Roos *et al.* 2008). VanRaden *et al.* (2009) reported that genomic prediction accuracy increased linearly with increased TS size in the range of 1,151-3,576 Holstein bulls (specifically, accuracy increased from 0.35 to 0.53 for a trait with a heritability of 0.2). Hayes *et al.* (2009a) reported that in Genetic Australia's 2003 progeny test, a low heritability trait with fewer TS records (332) generated lower accuracies (BLUP 0.42, Bayes A 0.37). This is also consistent with the results of Saatchi *et al.* (2011) in U.S. Angus data using 698-3,231 records per trait; an average estimated genomic prediction accuracy of 0.41, assuming an N_e of 200 for U.S. Angus cattle, is consistent with the published estimate of 0.44 derived using a K-means clustering approach for validation. Using a study performed in layer chickens, genomic prediction accuracy increased with increasing TS size across five generations; however, increase in accuracy was not linear, with the largest gains attributed to increasing TS from 295 to 618 animals, and more modest gains from increasing up to 1,563 genotyped animals (Wolc *et al.* 2011).

Marker density, linkage disequilibrium, and genetic relationship

For genomic prediction, it is important to implement careful management of informative SNP markers and genotype density, genotyping sufficient markers to maximize genomic prediction accuracy considering that some proportion of markers will be removed during quality control. At this time, the most common array used in genomic prediction analyses in cattle is the Illumina Bovine SNP50 BeadChip (Bovine SNP50; Matukumalli *et al.* 2009; Illumina Inc., San Diego, CA), which became commercially available in 2008 and contains up to 58,336 SNP markers, depending on version number. However, most studies using this assay do not consider all of these markers to be informative in a given population or breed. For example, markers may be excluded from analysis if they are unreliable (e.g. exhibit frequent parent-progeny conflicts, have low call rates, etc.), redundant (e.g. collinear with other SNP markers), or exhibit minor allele frequency (MAF) that is too low (usually in the range of 0.01-0.05). For example, using Holstein, Jersey, and Brown Swiss cattle genotypes, Wiggans *et al.* (2010) concluded that, of the markers on the Bovine SNP50, 16.6% were unreliable, 3.0% were redundant, and an additional 6.0% had low minor allele frequency (<0.01) in these breeds, leaving only 75% of the markers genotyped considered informative for genomic analyses. The number of unreliable markers is assay- and sample quality-dependent, and the number of redundant and low MAF markers will depend on genetic variability in the population of interest relative to marker density. The proportion of low MAF SNP in the Bovine SNP50 reported by Wiggans *et al.* (2010) is similar to estimates reported in other cattle breeds. McKay *et al.* (2007) reported that low MAF SNP (<0.05) represented 5-20% of markers surveyed in 8 cattle breeds (Nelore, Brahman, Japanese Black, Angus, Limousin, Dutch Black and White Dairy, Holstein, and Charolais). Using combined criteria of call rate ($\geq 90\%$), MAF ($\geq 1\%$), and Hardy-Weinberg equilibrium Chi-square statistic (≤ 300 ; 1 df) for autosomal and pseudoautosomal markers, Saatchi *et al.* (2011) excluded 9,360 of 54,442 loci (17%) for genomic analysis of 3,570 Angus cattle, leaving approximately ~5K fewer markers than was estimated to be necessary for genomic analysis of Australian Angus cattle (de Roos *et al.* 2008).

Ideally, high density genotypes used for genomic analysis should include markers that are in consistent linkage disequilibrium (LD) with QTL influencing a trait of interest. In larger or more diverse populations, higher density genotypes and greater TS are required to accurately estimate marker effects (de Roos *et al.* 2009, Hayes *et al.* 2009b, Ibáñez-Escriche *et al.* 2009). Using 33 microsatellite markers, Huang *et al.* (2008) estimated that only 11% of the total genetic variation was shared between 16 breeds of Scottish, French, Spanish, or Alpine geographic origin. Using

50K density, reports of the extent of LD between markers (and between markers and potential QTL) has varied, depending on population. Meuwissen *et al.* (2001) demonstrated the potential for highly accurate genomic prediction assuming an r^2 (Hill & Robertson 1968) equal to 0.2, which is inconsistent with the values reported in linkage disequilibrium studies of multi-breed cattle populations. Kelly *et al.* (2008) reported that in a population of 374 multi-breed beef cattle (crossbred cows bred to purebred sires derived from Angus, Simmental, Limousin, Charolais, and Piedmontese breeds), average gap size between informative SNP on the Bovine SNP50 was 58kb, and to achieve LD similar to that assumed by Meuwissen *et al.* (2001), average gap size would need to be 30-35kb (with resultant r^2 0.21 ± 0.26). This is similar to the findings of Lu *et al.* (2009), who reported that in a population of 60 Angus, 43 Piedmontese, and 400 crossbred beef cattle, the average gap size was 60kb with highly correlated phase within 60kb regions between breeds ($r=0.78-0.82$) and rapid LD decay as distance between markers increased (average r^2 drops from 0.31 for markers 0-30kb distant to 0.15 for markers 60-100kb distant). McKay *et al.* (2007) reported that while markers from 0-5kb distant ranged in r^2 from $\sim 0.3-0.6$ depending on breed, average r^2 for inter-marker distances of 5-100kb declined to $\sim 0.15-0.2$. In Dutch and Australian Holstein-Friesian, Australian Angus, and New Zealand Friesian and Jersey cattle, de Roos *et al.* (2008) reported average r^2 of 0.35 for inter-marker distances of 0-10kb, which declined to 0.22 for 20-40kb and 0.14 for 40-100kb. To achieve average r^2 equal to 0.2, de Roos *et al.* estimated that 43-75K SNP (50K for Australian Angus) would be required within breed and ~ 300 K SNP for across-breed analysis, which is substantially more than is available using the Bovine SNP50.

This issue may be corrected by using higher density genotyping arrays. Two HD arrays have been released for bovine genomics analysis, the Illumina High-Density Bovine BeadChip Array (BovineHD; 777,962 SNP) and the Affymetrix Axiom Genome-Wide BOS 1 Array (BOS1; Affymetrix Inc., Santa Clara, CA; 648,874 SNP). Data published by Illumina and Affymetrix, respectively, suggest that the increased marker density of these arrays improves genomic coverage (Illumina 2010, Affymetrix 2011). In Angus, the number of informative SNP on the BovineHD array increases 11-fold relative to the Bovine SNP50. As the Bovine SNP50 did not have proportionally as many SNP that were polymorphic in indicine breeds, these breeds exhibit larger increases in effective marker density ($\sim 13-14$ -fold for Nelore, Brahman, and Gir breeds). In total, it was estimated that 651,994 SNP on the Illumina BovineHD BeadChip SNP are informative in taurine breeds, and 538,517 SNP are informative in indicine breeds. In comparison, Affymetrix reported that six taurine breeds have >0.88 genome coverage, and three

indicine breeds have 0.79–0.87 genome coverage using the BOS1 array. In terms of the number of informative SNP available after quality control, Rincon *et al.* (2011), in a preliminary study of 16 Holstein and Jersey cattle genotyped using the BovineHD and the BOS1 arrays, removed few SNP from either array due to unreliability (0.6% and 4.9%, respectively, had low call rate, <0.9) but relatively larger proportions of the SNP dataset were redundant (49.5% and 21.1%, respectively, had LD $r^2 \geq 0.9$). This is consistent with the findings of Harris and Johnson (2010), that increasing SNP density from 20K to 1000K in simulation increased LD between flanking markers and QTL but also increased the number of uninformative SNP.

It is important to exclude collinear SNP as their inclusion in genomic selection analyses may result in the prediction of random error in the training phenotypes or allow a single QTL to be attributed to a number of highly correlated SNP, both of which are expected to reduce genomic prediction accuracy and its persistency across generations. This was confirmed by Schulz-Streeck *et al.* (2011), who found that pre-selection of markers to exclude those with negligible or inconsistent effects (using either ridge regression or spatial models) increased genomic prediction accuracy in simulation. As referred to above, the BovineHD and BOS1 arrays may yield 200–300K informative SNP for genomic analysis in small populations and/or few breeds (Rincon *et al.* 2011) and two–three fold more in larger, more diverse populations (Illumina, 2010). This density reduces average gap size significantly (based on Rincon *et al.* 2011, to 11–12kb), improving average r^2 between adjacent markers. Extensive testing of genomic selection methods using these high density arrays have not yet been published; however, Hayes *et al.* (2011) reported improved across-breed accuracy in Holstein and Jersey cattle using the BovineHD array.

Though increasing marker density to obtain high LD between markers and QTL is optimal, a counter-argument is that LD does not need to be present to generate accurate genomic prediction. Habier *et al.* (2007) demonstrated that genomic prediction accuracy could be non-zero and positive even when there was no LD between markers and QTL present in the population simulated, as accuracy is generated by markers which capture either persistent association with QTL (LD) or additive genetic relationship, defined as twice the coefficient of coancestry (Malécot, 1948). This was shown mathematically by Gianola *et al.* (2009), where the mean genetic variance for a given locus, σ_u^2 , was defined as: $\sigma_u^2 = 2\theta p q$ where σ_a^2 is the genetic variance, θ is the additive substitution effect expressed as a deviation from the mean, and p and q are the allele frequencies at a particular locus. Hence, even when the value of the

substitution effect is zero, the locus variance may be non-zero. One way to conceptualize the method by which this could occur is to consider the regression of family means on within-family allele frequency, which would improve the prediction of family means but not Mendelian sampling terms (Jannink, 2010), thus compromising the ability of genomic selection to improve genetic gain without increasing inbreeding by facilitating discrimination between siblings prior to phenotyping or progeny testing. This was confirmed in simulation by de Roos *et al.* (2011), as the rate of inbreeding strongly increased when young animals selected based on GEBV were allowed to be used for breeding.

However, genomic prediction accuracy contributed by markers which capture additive genetic relationship but are in linkage equilibrium with QTL will decay with increasing genetic distance between the training and target populations, and conversely, accuracy due to linkage disequilibrium with QTL will be more persistent across generations. As a result, genomic prediction accuracy that is due to LD can be more persistent over time than traditional EBV accuracy (Wolc *et al.* 2011, Pszczola *et al.* 2012); however genomic selection will cause genomic prediction accuracy to decay (Muir 2007) without consistent retraining (Sonesson & Meuwissen 2009). Wolc *et al.* (2011) reported substantial accuracy retained five generations post-training using both GBLUP and Bayesian models. This was also shown by Pszczola *et al.* (2012), who simulated a TS of 2,000 dairy cows phenotyped for traits of moderate (0.30), low (0.05), and extremely low (0.01) heritability and selected the structure of the training population to vary the relationship with the target population from 0.0487 to 0.0946 on average based on pedigree estimates of additive genetic relationship. Genomic prediction reliability (squared accuracy) increased with increasing squared genetic relationship and heritability and decreasing generations between the TS and target populations; given the same average squared relationship, a randomly chosen TS achieved the highest average reliability, possibly because the animals within the TS had the lowest average relationship to each other. This is consistent with Calus (2010), who suggested that selecting animals to represent the widest range of possible genotypes may increase DGV reliability.

Genomic selection model

Another factor affecting genomic prediction accuracy is the choice of model, which is dependent on the true distribution of QTL effects for a trait, which is unknown. Therefore, there is a wide variety of methods that may be used to implement genomic selection, and the optimal model may depend on the trait and population being analyzed. Broadly, genomic selection models may

be divided into parametric and non-parametric approaches, and within parametric approaches, either penalized or Bayesian methods. This review will focus on parametric methods, which assume the data derives from a type of probability distribution. Within this category, methods differ in their assumptions about the distribution of QTL. Ridge regression assumes that markers are normally distributed with mean zero and a common variance, such that all marker effects are equally shrunk toward zero (Meuwissen *et al.* 2001), consistent with an infinitesimal model for QTL effects. Other models allow marker variance to be heterogeneous. Meuwissen *et al.* (2001) defined two Bayesian models, termed Bayes A and Bayes B. In Bayes A, it is assumed that QTL are normally distributed with mean zero and locus-specific variance, and Bayes B extends this model by the further assumption that a fixed proportion of loci (π) have zero effect and the remaining proportion ($1-\pi$) distributed as in Bayes A. In either, the locus-specific variance has a scaled inverse-chi square prior distribution with fixed values for the degrees of freedom and scale parameters. Another alternative is Bayes C π (proposed by Habier *et al.* 2011), in which the locus-specific variance in Bayes A is replaced with a single variance for all loci, also distributed with a scaled inverse-chi square prior, and the proportion of zero effect loci is unknown with its own prior distribution, as well as Bayes D π in which the scale parameter is also treated as an unknown. Bayes C π is an extension of stochastic search variable selection (SSVS; Meuwissen & Goddard 2004, Verbyla *et al.* 2009) as suggested by George and McCulloch (1993).

For use in cattle, the importance of the choice of model has varied. Using the 13th QTL-MAS simulated data set for which the distribution of QTL effects was unknown, the choice of method between ridge regression, Bayes A, Bayes A/B hybrid (Verbyla *et al.* 2010a), and SSVS were found to have little effect on genomic prediction accuracy (Verbyla *et al.*, 2010a). This is consistent with results reported in dairy cattle (VanRaden *et al.* 2009, Hayes *et al.* 2009a), where the assumption that all markers are informative with equal variance is effective for most traits, and the additional benefit of Bayesian approaches was minimal. In comparison, variable selection methods which assume heterogeneous marker variance have been reported to result in reduced accuracy (Cole *et al.* 2009, Su *et al.* 2010), despite outperforming non-Bayesian methods in simulation (Meuwissen *et al.* 2001, Habier *et al.* 2007, VanRaden 2008). Wolc *et al.* (2011) found that the additional benefit of using Bayesian methods in layer chickens depended on the veracity of the assumption of heterogeneous marker variance, as there was a positive correlation between estimates of π and improvement in accuracy. This is consistent with Daetwyler *et al.* (2010), who found that relative accuracy was dependent on M_e . Given these

varied findings, it is likely that the optimum model will depend on the trait and population, so it may be important to perform comparative tests of different genomic prediction models when approaching a new genomic prediction study.

One consideration for methods which explicitly estimate marker or haplotypic effects is whether to include an additional random polygenic term to account for residual genetic variance (Haley & Visscher 1998). Including a polygenic term has been associated with several benefits including: reduced bias in the estimation of marker or haplotype variance (Calus & Veerkamp 2007, Rius-Vilarrasa *et al.* 2012), increased the persistence of accuracy across generations (Solberg *et al.* 2009), and reduced the sensitivity to the prior distribution of marker effects (Rius-Vilarrasa *et al.* 2012). The inclusion of a polygenic term may be especially useful for low heritability traits, as it was reported to explain a greater proportion of the genetic variance of a low heritability (0.1) trait than a high heritability (0.5) trait (56-82% vs. 50%) (Calus and Veerkamp 2007). Goddard (2009) suggested that models including a polygenic term could account for variance contributed by rare alleles that were not in consistent LD with the common variants found in dense genotyping arrays.

An alternative to explicitly estimating marker effects is to incorporate marker data into animal evaluation by replacing the numerator relationship matrix (**A** matrix), estimated from the average relationship between individuals based on pedigree, with a genomic relationship matrix (**G** matrix), estimated from dense marker data (Nejati-Javaremi *et al.* 1997, Garrick 2007, VanRaden 2007, Zhang *et al.* 2007, VanRaden 2008), in an approach termed GBLUP. A benefit of this approach is that individual animal reliabilities can be calculated by inverting mixed model equations including these genomic relationships (VanRaden 2008). Unbiased evaluation can be achieved by scaling the G matrix to be compatible with the A matrix and avoiding excessively high MAF SNP exclusion thresholds which, while minimally affecting the accuracy of prediction, could bias upward accuracy calculated by inversion (Chen *et al.* 2011). These accuracies are more useful than those derived from cross-validation, as accuracies derived from GBLUP can be adjusted for any intensity of selection whereas those derived from cross-validation are limited to a single breeding scheme, resulting in underestimation of the benefit to accuracy of including genomic information when selection differs between the sexes (Bijma 2012). GBLUP has been reported to outperform Bayesian mixture models in a combined population of Swedish Red Breed and Finnish Ayrshire cattle, both in GEBV accuracy and the extent to which GEBV captured the Mendelian sampling term (Rius-Vilarrasa *et al.* 2012). Clark

et al. (2012) compared GBLUP accuracy to that derived using shallow (1-generation) or deep (10-generation) pedigree BLUP methods, and found that, while accuracies of pedigree BLUP and GBLUP were similar when individuals in the TS and validation populations were closely related, GBLUP could derive a baseline accuracy that was greater than zero for distantly related or “unrelated” (within 10-generations) individuals, in contrast to pedigree methods for which EBV for unrelated animals are zero. The authors suggest that this baseline accuracy could be optimized by obtaining a TS that covers the genetic diversity of the population or breed, in agreement with Calus (2010).

As an extension of the GBLUP method, phenotypic and pedigree data from animals that have not been genotyped can be incorporated into genomic evaluation by creating a joint relationship matrix including pedigree and genomic relationships (Misztal *et al.* 2009, Legarra *et al.* 2009, Christensen and Lund 2010). Aguilar *et al.* (2010) reported the first single-step genetic evaluation including pedigree, phenotypic, and genotypic information for final score of U.S. Holsteins, which was completed in only slightly more time than a traditional pedigree-based analysis and with comparable accuracy to a multiple-step procedure using a combination of pedigree BLUP and GBLUP to incorporate the same information.

A last consideration in terms of genomic prediction methodology is the choice of phenotype to be used in training. Given the structure of dairy and beef cattle populations, in which breeding bulls sire many progeny and are of great economic value, which can offset the cost of high density genotyping, TS have typically been composed of bulls. However, the optimum phenotype to use has varied between research groups. As of 2009, genomic evaluations conducted by Interbull members were performed using daughter yield deviations (DYD) weighted by effective daughter contributions, deregressed proofs (DRP) weighted by their (deregressed) reliabilities, unweighted estimated breeding values (EBV), or unweighted raw phenotypic records (Loberg & Durr 2009). DRP, derived from EBV (Jairath *et al.* 1998), are essentially pseudo-phenotypes which account for all the information present in an individual’s EBV, with a heritability equal to the reliability of the EBV. For animals with high accuracy EBV, training on DRP may effectively increase the heritability of the trait, and thus improve the accuracy of the resulting genomic prediction.

When the original phenotypic data is not available for genomic evaluation, DRP are an alternative to training on unweighted EBV. Garrick *et al.* (2009) advocated for the use of

weighted DRP instead of EBV in order to avoid both the shrinkage present in EBV and the correlation between TBV and EBV prediction error, to account for differing EBV accuracy between individuals in the TS using appropriate weighting, and to adjust DRP to account for parental contribution, such that DRP encompassed only the information of the individual and its descendants in order to avoid double counting animals that are members and ancestors of the TS. However, Su *et al.* (2010) commented that EBV contain less random error, thus reducing prediction error variance. The results of comparative studies have varied. Several studies have found genomic prediction to be inflated when DRP were used as the response variable (Aguilar *et al.* 2010, Lund *et al.* 2010). Gredler *et al.* (2010) reported that training with EBV outperformed DRP and DYD for protein yield and inter-insemination interval in Fleckvieh dual purpose cattle using GBLUP and Bayesian methods. In a simulated dairy population, Guo *et al.* (2010) found that training on EBV resulted in equal or somewhat higher accuracies relative to training on DYD, with starker differences when heritability or average EBV or DYD reliability was low. This is expected as the correlation between EBV and DYD decreases with reliability. In contrast, Ostersen *et al.* (2011) reported higher accuracies using DRP as the response variable for the evaluation of daily gain and feed conversion ratio in Danish Duroc pigs, in which the average EBV reliability (0.62 ± 0.18 and 0.36 ± 0.12 in 1,375 reference animals) was lower than is common in many dairy evaluations. DRP were also used as the response variable in the evaluation of 16 traits in Angus cattle conducted by Saatchi *et al.* (2011), in which an average accuracy of 0.441 calculated by K-means clustering was reported given TS for each trait ranging from 698-3,231 DRP records with average reliability 0.40 to 0.79.

For expensive-to-measure traits recorded on females or terminal animals, it is worth considering whether training on individual phenotypes may be a better approach to condensing the performance of many individuals into a single record attributed to a common sire. Verbyla *et al.* (2010b) estimated genomic prediction accuracy for energy balance using a TS of 527 Dutch Holstein-Friesian heifers to be 0.29, which would be expected to increase with increasing TS size. Using simulated TS of phenotyped cows, Buch *et al.* (2011) estimated that DGV accuracy for a low heritability (0.05) trait increased from ~ 0.15 in year 1 to ~ 0.35 in year 10 with 2,000 cows phenotyped per year, exceeding DGV accuracy using sires alone as the TS during the same interval. Wall *et al.* (2011) used four experimental dairy populations from three countries to create a pooled reference population of 1,630 cows phenotyped for both commonly recorded traits (e.g. milk, fat, and protein yield) but more importantly, expensive-to-measure traits (e.g. dry matter intake, energy intake, and energy balance), and found the genetic correlation

between herds for the same trait consistently high (≥ 0.85). If high density genotyping were implemented in such pooled reference populations, this would constitute a valuable TS for genomic selection.

Genomic prediction in multiple populations or breeds

Goddard and Hayes (2009) proposed that multiple breed TS could be used to improve the accuracy of DGV if there was sufficient linkage disequilibrium between markers and QTL. Ibáñez-Escriche *et al.* (2009) agreed and further concluded that accurate multi-breed evaluations would work only if the breeds were closely related due to variability in linkage disequilibrium between breeds. Though the current application of GS has favored single breed application, Brøndum *et al.* (2011) reported increased genomic prediction accuracy using a multi-breed TS incorporating Swedish Red Breed (SRB) and Finnish Ayrshire (FAY), two populations with strong genetic links corroborated by the G matrix reported in that study. Using the same populations, Rius-Vilarrasa *et al.* (2012) compared GBLUP with Bayesian models assuming a range of proportions for the lowly informative loci. GEBV accuracy increased with increasing proportion of informative markers in mixture models, but was generally surpassed by GBLUP accuracy. This study also revealed a condition under which differences between genomic selection methods is significant. It was proposed that, in contrast to the finding of Hayes *et al.* (2009a), *DGAT1* does not contribute as strongly to the genetic variance of fat yield in SRB and FAY, as flanking markers are nearly at fixation (0.93 allele frequency), as opposed to the case in Holstein cattle, for which the allele frequency of the K variant of *DGAT1* can range from 0.35 to 0.70 between populations (Grisart *et al.* 2001, Spelman *et al.* 2002, Winter *et al.* 2002, Thaller *et al.* 2003). In contrast, the choice of priors and model were found to have minimal impact on genomic prediction accuracy in a multi-line study in chickens (Andreescu *et al.* 2010), but population structure was critical. Using 10 breeding lines, the authors showed that correlations between DGV and progeny means were low when training and validation sets were divided along breeding lines (train in 9 lines, predict 10th line) rather than including all lines in both training and validation sets (correlation with progeny means: 0.09 vs 0.51 on average), reiterating the importance of genetic relationship between TS and validation populations to genomic prediction accuracy.

Similar findings were reported in Angus cattle (Saatchi *et al.* 2011), in which using K-means clustering to minimize the relationship between animals in the TS and validation populations reduced accuracy relative to using random clustering or dividing the TS and validation

populations by year of birth. Considering the case of admixed and crossbred cattle, Toosi *et al.* (2010) reported that, in a simulation using a TS of 1,000 animals genotyped with marker density of 5 SNP per cM and phenotyped for a moderate heritability trait, admixed or crossbred populations could be used to develop GS prediction equations that would be effective in both the mixed breed and the constituent purebred populations, but would be of reduced accuracy in breeds not included in the TS due to reduced relationship between TS and validation populations. However, in that study, the average distance between pair of markers with LD $r^2 \geq 0.7$ was 3x larger in purebred than in admixed or crossbred populations, suggesting that greater marker density would be required to obtain markers in consistent linkage disequilibrium across breeds, emphasizing the importance of utilizing high density genotyping arrays. In terms of methodology, there may be some improvement in accuracy derived from fitting breed proportion in GBLUP, as Makgahlela *et al.* (2012) reported 2-3% improvement in the reliability for genomic prediction of milk and protein indices in Nordic Red cattle.

Conclusions and Implications to Genetic Improvement of Beef Cattle

Significant progress has been made in the development of genomic prediction in cattle. Moderate to highly accurate single breed prediction has been reported using the Bovine SNP50 genotyping assay, and it is expected that high density assays such as the BovineHD and BOS1 will improve the accuracy of multi-breed prediction. Preliminary findings in Holstein and Jersey populations suggest that marker density after quality control may provide sufficient levels of LD to achieve high accuracy genomic predictions derived in simulation studies. However, linkage disequilibrium is only one of several critical factors which determine genomic prediction accuracy. Others include TS size and characteristics, the heritability of trait, the distribution of QTL effects, and the suitability of the genomic prediction model. High accuracies have been obtained with reduced computational demand using GBLUP and single-step methodology, but when the true number of QTL affecting a trait is low, Bayesian approaches that allow heterogeneous marker variance can be more effective relative to other parametric approaches. Based on studies in dairy cattle, there is potential to use pooled reference populations of phenotyped females to obtain more accurate genomic predictions for reproductive or other expensive or difficult to measure traits rather than focusing only on influential bulls. With higher density genotyping assays available, it is envisaged that data may be pooled across breeds to obtain accurate genomic predictions for economically-relevant traits that are not currently included in national beef cattle evaluations.

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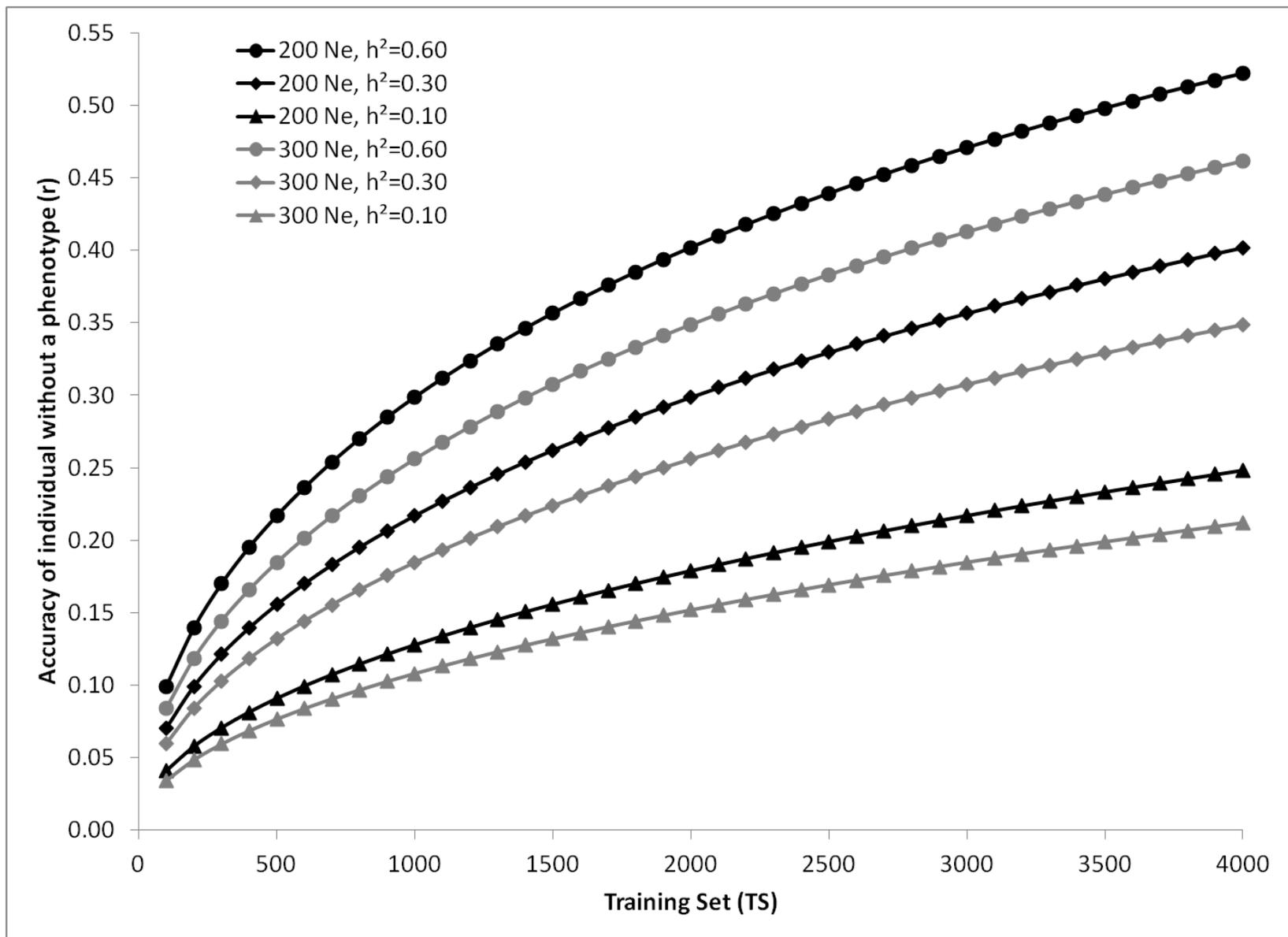
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Figure 1



2012 SEEDSTOCK PRODUCER AWARD NOMINEES

Bianchi Ranches

Owners/Managers: Robert, Chris and Erica Bianchi
Gilroy, California

The Bianchi Ranches operation is located in the foothills east of Gilroy in Santa Clara County. They have run cattle at this location for over 20 years. Purebred cows are wintered in the hills along with their commercial herd. In the summer the spring calving cows are run on 60 acres of permanent pasture and the rest are run on dry land hayfields.

The operation consists of 120 Charolais cows, 40 Hereford cows, 15 Red Angus cows and 50 Pinzgauer cows. They also run 300 commercial cows. They calve in the spring and fall, because they have a variety of bull buyers that purchase bulls to use at different times of the year. Typically buyers from California turn out bulls in the fall, and buyers from Oregon and Nevada turn their bulls out in the spring, and they like to be able to meet their needs. Charolais bulls are used on the mature cows while Red Angus bulls are used on their first calf heifers. They are constantly trying to produce bulls for their buyers that will meet all of their needs. They use the bulls they produce on their own commercial cows as well. If they would not use the bulls on their own herd, they will not sell them to anyone else to use.

Bianchi Ranches is proudly nominated by the California Beef Cattle Improvement Association.

EJ Shepherd Charolais

Owners/Managers: Everett and Julie Shepherd
Stuart, Iowa

The EJ Shepherd Charolais herd is located on their farm at 1308 Quebec Avenue, Stuart, IA. They have been in the cattle business for 46 years and have been producing Charolais cattle for 36 years. They started with a registered Angus herd, then crossed them with black white face Simmental for 10 years, then gradually eliminated them and went to purebred Charolais. They have decreased their cowherd from 200 head down to 65 head. Their calving season is from January 15th to March 30th and from August 15th to October 15th.

They started with hogs, cattle, corn, beans, hay and permanent pasture. They eliminated the hogs about 20 years ago. They utilize the rough ground for hay and pasture and bring their cows home to graze on cornstalks after harvest.

The American International Charolais Association is proud to nominate EJ Shepherd Charolais.

HeartBrand Beef

Owners: Ronald and Joan Beeman
Managers: JoJo and Kaci Carrales & Jacob Tipp
Harwood, Texas

HeartBrand Beef, Inc. is a very diverse operation located southeast of Austin, Texas, in Caldwell County. HeartBrand has been raising Akaushi Cattle for their Branded Beef Program since 1995. Although the headquarters is southeast of Austin, HeartBrand raises over 1600 Akaushi cows from Idaho to Texas. Due to the fact of different climates and keeping a constant supply of fresh beef,

HeartBrand is split into dual calving seasons. The concept of source verifying 100% of their beef product requires staff effort from multiple sectors of production.

HeartBrand raises and sells fullblood Akaushi genetics through private treaty to commercial cattlemen throughout the United States that will source the Akaushi sired calves back to the HeartBrand Beef Program. This program is the first of its kind to require breed designation through DNA parentage. Customers that purchase Akaushi bulls not only become members of the American Akaushi Association, but are provided with a premium buy back guarantee.

HeartBrand raises 100% of its replacement females and on average keeps the top 60% of the female calf crop. The heifers are developed after weaning at HeartBrand's grower operation and are artificially inseminated to calve at 24 months.

Besides following these strict guidelines that go into HeartBrand's Beef program like no added growth promoters and no antibiotics in the final feeding phase, HeartBrand is also USDA verified as NHTC (Non Hormone Treated Cattle) and Sourced and Aged.

HeartBrand Beef is proudly nominated by the American Akaushi Association.

Hounshell Farms

***Owners/Managers: W.C. "Buster" Hounshell and Clayton Hounshell
Wytheville, Virginia***

Located in the western portion of Wythe County, Virginia, Hounshell Farms qualifies as a Centurion farm dating back to the late 1700's. Current owners Clayton & Buster Hounshell (father & son), created a partnership in the mid 1970's that continues today. Buster's two sons, Greg & Jason and their children, make-up the 7th and 8th generations to work this farm of 650+ acres owned and leased.

From the time Buster graduated from Virginia Tech in 1969, his appreciation for the Simmental breed resulted in changing the Hereford based cattle operation into the first purebred registered black Simmental herd in Southwest Virginia.

Artificial insemination was a priority in developing their herd. Currently there are 185 head of black Simmental females, approximately 110 Sim-Angus with the balance being purebred black Simmentals. Using a fall and spring calving program, HSF calves 135 fall cows, and approximately 50 spring cows.

Performance evaluation data began through recording data with the American Simmental Association and the Virginia BCIA. Since 1980, females have been recorded with ASA. The first bulls were tested in 1987 through the Virginia Beef Cattle Improvement Association program.

In an effort to improve herd performance and enhance data, HSF began participating in Virginia's Retained Ownership Program in 1997. Since 2000, all calves (except those used for bull development or female replacement) have been shipped to Circle Five Beef Incorporated in Henderson, Nebraska. Data is received on these cattle and serves as one of the criteria for bull and female replacement selection. The retained ownership program also allows Hounshell Farms to receive premiums from age and source verification and extra value created by known genetics.

The Virginia Beef Cattle Improvement Association is proud to nominate Hounshell Farms.

Liberty Ranch

Owner: Roger Comeau

Manager: Mike Smith

Plainville, Kansas

Liberty Ranch (LR) was founded in 1976 in the Post Rock country of the Saline River valley in western North Central Kansas. LR's cow herd has ranged from 1000-1500 females made up of primarily Limousin, Red Angus, and Angus cows. LR was intensely involved in commercial cow-calf production in the early years, but has placed more emphasis in the last 30 years on seedstock production. LR females are a predominately spring cow herd with 10-20% of LR cattle calving in the fall. Post-weaning, the calves are back-grounded on site in the Liberty Ranch feeding facilities.

Over the years LR has placed emphasis on purchasing LR sired calves through their customers programs to bring home and background prior to being sent to commercial feedlots. LR has participated in numerous value-added beef programs such as Laura's Lean, US Premium Beef, Decatur County, Tyson, and numerous other beef grids in the early years. Selection pressures over the years have always been to raise a better cow for our environment and management philosophy, while maintaining feed efficiency, performance, and balanced carcass traits in LR fed cattle. Over time, LR has emphasized educational and informative events accessible by our customers and neighbors. Events have ranged from commercially maximizing Limousin and Ranching for Profit to Liberty Ranch & Pfizer Animal Health's Low Stress Livestock Handling Symposium. LR is in constant pursuit of being better stewards of the land, focusing on low stress livestock handling, and prioritizing superior animal health protocols. Customer satisfaction is always our number one priority.

The North American Limousin Foundation is proud to nominate the Liberty Ranch.

McCurry Brothers Angus

Founding Partners: Dale, O'Dell and Cecil McCurry

Managing Partners: Greg, Brad, Geoff and Barry McCurry

Sedgwick, Kansas

McCurry Brothers Angus is a family-owned and managed operation located in Sedgwick and Harvey counties near Sedgwick, Kansas. The cowherd originated when Walter McCurry purchased two Angus heifers from his brother-in-law, Johnson Workman, in 1928. Many bloodlines today can be traced back to Workman's herd, which descended from the very first Angus cattle imported to the U.S., specifically Victoria, KS, by George Grant. In 1958, Walter's five sons, A.J., Dale, O'Dell, Bob and Cecil, formed McCurry Brothers Angus. Dale, O'Dell and Cecil McCurry still are involved in the business. The day-to-day operations are run by managing partners, Greg, Brad, Geoff and Barry McCurry, who represent the third generation on the ranch and bring a lifetime of experience to the business.

Today, McCurry Brothers Angus consists of about 550 registered Angus cows, of which two-thirds calve in the spring and one-third in the fall, and an irrigated and dryland farming business. About 150 bulls are sold yearly through private treaty. With 85% of their customers being commercial cattlemen, they strive to produce functional, trouble-free cattle that excel on pasture, in the feedyard and on the rail. Proven carcass genetics are used in the herd. At the same time, they acknowledge there are traits EPDs cannot measure, and work to keep the herd structurally correct and sound. Artificial insemination, embryo transfer, EPDs and ultrasound are used to produce consistent cattle with superior genetics.

The Kansas Livestock Association is proud to nominate McCurry Brothers Angus.

Perks Ranch

Owner: Doug Perks

Managers: Tom and Tammy Boatman

Rockford, Illinois

Perks Ranch was founded as a working horse and cattle ranch in 1961. Owned by Doug Perks and operated by Tom and Tammy Boatman, the ranch is located in Rockford, Illinois. Averaging 36 inches of rain annually, the ranch includes rolling grasslands, cropland, and protected forest. The Perks Ranch program has been built on Hereford genetics and even included Red Angus cattle from 1999-2010. Home to approximately 120 registered Herefords and 75 commercial cows, they are currently rebuilding their herd with a goal of reaching 150 Herefords and 100 commercial females.

A dual calving season is utilized to diversify risk and take advantage of different marketing opportunities throughout the seasonal cattle cycles. Spring calving is within a strict 90 day window ranging from February 1st until April 30th. Fall calving's 30 day season spans from September 1st until September 30th. Females are marketed through an annual fall production sale at the ranch and in spring they are sold through a partner's sale in Oklahoma. Bulls are sold off the ranch by private treaty, as well as their Oklahoma cooperators location.

Perks Ranch is in the beef business because they enjoy what they do. Helping producers stay profitable through genetic improvements within their own herd ensures consumer satisfaction and keeps them going and striving to improve on a daily basis.

Perks Ranch is proudly nominated by the University of Illinois Extension and the Illinois Beef Association.

Schuler Red Angus

Owners: The Darrell Schuler Family

Manager: Butch Schuler

Bridgeport, Nebraska

Located in the panhandle of western Nebraska, Schuler-Olsen Ranches was started by Darrell and Mary Lou Schuler in 1959 with commercial Hereford cattle. A crossbreeding program was implemented in the 1970s after witnessing the benefits of heterosis and breed complementarity first-hand, a registered Red Angus herd was started in 1976 to develop genetics for use on the ranch's commercial cattle and to sell to neighboring ranchers.

The seedstock herd expanded in the 1980s and was improved through artificial insemination, utilization of EPDs and a complete performance-testing program. Recognizing the need for identifiable carcass traits, in 1991 Schuler Red Angus began finishing its commercial progeny and collecting carcass data. This program soon grew into a structured carcass progeny test, including customer cattle sired by Schuler Red Angus bulls. Today, over 25% of the Red Angus breed's high-accuracy carcass trait sires have been proven by Schuler Red Angus.

A composite seedstock herd called "Schuler Reds" was started in 1992 which included Red Angus, Hereford, Gelbvieh, and Simmental genetics giving Schuler Red Angus customers the opportunity to add heterosis and breed complements via a simple crossbreeding system.

The current ranching operation encompasses 17,000 acres including 2,000 acres of private pasture leases and 1,250 acres of irrigated farm ground. Butch and Susan Schuler with their children Stephanie and David manage the operation today with approximately 1,000 head of spring-calving females. The Schuler's hosted their 30th production sale this spring selling 150 registered Red Angus and Schuler Red composite bulls.

The Red Angus Association of America along with the Nebraska Cattlemen are proud to nominate Schuler Red Angus.

Springfield Angus
Owner: Phil Goodson
Manager: Brett Flach
Louisburg, North Carolina

Springfield Angus, located near Louisburg, NC, is a progressive seedstock operation owned by Phil Goodson. Farm manager is Brett Flach.

Goodson, reared on a diversified farm that included commercial beef cattle, showed beef animals in 4-H and was determined to own a purebred Angus herd. He earned an MD degree, served as US Air Force flight surgeon, and then had a distinguished career as a surgeon in Raleigh.

In 1976, he purchased a farm and four bred Angus heifers to begin fulfilling his dream. He established the goal of developing a profitable, sustainable farm producing genetically superior seedstock for commercial producers.

With expanding customer demand, Goodson purchased the present 400-acre farm in 1983, with an additional leased 120 acres. Springfield is calving 250 females and 150 recipis.

The breeding program represents a balance of low to moderate birth weights with strong maternal, growth, and carcass genetics utilizing elite sires. Goals are to provide producers breeding stock that excels in all areas and to assist customers in marketing. Top performing bulls completing Springfield's on-farm bull tests and passing rigorous reproductive soundness exams, are marketed private treaty. Females are marketed through private treaty and production sales.

Goodson seeks advice from university and industry experts in developing breeding, health, nutrition, forage, and management programs. An early adopter of technologies that help further his goals, he has continuously incorporated an embryo program since 1982, produced the first recorded cloned Angus bull, and more recently incorporated ultrasound and genomic profiling into breeding and selection. Goodson currently has two bulls in AI studs, including Rito 9M25, the top \$Beef Angus bull.

Goodson is a leader in the NC Angus Association, NC Cattlemen's Association, NC Cattlemen's Beef Council, and the NC Cattlemen's Foundation.

The North Carolina Beef Cattle Improvement Program is proud to nominate Springfield Angus.

Tanner Farms
Owners: Gary and Lorrie Tanner
Manager: Tim Hardy
Ellisville, Mississippi

Gary and Lorrie Tanner were both raised on family farms, high school sweethearts, and married during their college years. They returned home to begin a business, teach school, raise a family, and manage the herd that is Tanner Farms today.

Tanner Farms is a grass roots, registered and commercial Angus operation which originated in Jones County in 1977 and expanded to Noxubee County in 2000. There are approximately 600 registered cows and 800 commercial cows with both a spring and fall calving season. The goal is to produce functional and profitable Angus cattle, not only for their own operation, but also for those of their customers. They continually strive to improve on the strong genetic base that has served as the foundation of their program.

Tanner Farms is proudly nominated by the Mississippi Beef Cattle Improvement Association.

V8 Ranch

Owners: Sloan and Mollie Williams

Managers: Jim and Luann Williams; Brandon and Rachel Cutrer
Boling, TX

V8 Ranch is a registered Brahman and Shorthorn cattle operation that was established in 1944. In 1971, the ranch was purchased by Sloan & Mollie Williams who have served as owners for 41 years. As a hands on, working family ranch, they are very proud of the fact that V8 Ranch has been worked and managed by their immediate family each and every day of the year. They are also proud that today, there are three-generations of their family working together daily for their combined goals of success.

The ranch operates in a four-county area on approximately 5,000 acres of land both owned and leased along the Texas gulf coast. The purebred Brahman herd consists of 300 breeding age females with a large emphasis on embryo transfer. Their Brahman herd is primarily a closed herd, with focus on linebreeding exceptional cow families since 1944. The purebred Shorthorn herd includes 30 breeding age females. In addition to these herds, they currently own and manage a commercial herd of 1,400 females which are part of their Brahman F-1 program. These Brahman influence females are used in a three-breed rotation mated to Angus and Hereford bulls to create Brahman F1s. The resulting offspring are then bred to Charolais and Angus bulls for terminal crosses. While they are known for their purebred herds, they feel their experience as a commercial producer gives them an advantage as a seedstock producer since they also have more than 50 years of making a living in the commercial business. Their commercial herd is also used as a tool to show their commercial bull buyers a practical example of how to use their Brahman cattle in a crossbreeding program.

V8 Ranch is proudly nominated by the American Brahman Breeders Association.

Williams Angus Farm

Owners/Managers: Joe and Faye Williams
Newton, Alabama

Williams Angus Farm is located in the southeast corner of Alabama in Dale County. Angus cattle were first purchased 49 years ago and farm operations began at the current location in 1964. Today, Williams Angus Farm has an Angus seedstock operation with a cowherd of approximately 150 head. A 90 day fall calving season is planned to capitalize on high quality, cool season grazing and to meet marketing goals. In addition to Angus seedstock production, the farm is comprised of several agricultural enterprises, such as commercial beef cattle, peanuts, cotton, small grains, grain sorghum, hay and corn silage. While complimentary, these enterprises were selected to diversify the farm for flexible, sustainable production.

The prime directive of the Williams Angus Farm's seedstock operation is to produce high quality seedstock, which are functional, practical and performance oriented for commercial beef production in the Southeast. The ultimate goal is to produce high quality, high value herd sires that will sire feeder cattle that excel in all beef industry segments and demand premium market prices. The breeding program of the seedstock operation, emphasizing economically important traits, is designed to complement and fill the needs of their commercial customers, as well as, their own commercial operation.

Eighteen years ago, Williams Angus Farm came together with like minded cattle producers to establish the Southeast Alabama Feeder Cattle Marketing Association. The education gained through interaction with the feeder cattle buyers, stocker producers and feedlot operators has provided a deeper perspective of the beef industry and refocused the prime directive for the Angus seedstock enterprise toward producing high quality beef.

Williams Angus Farm is proudly nominated by the Alabama Beef Cattle Improvement Association.

2012 COMMERCIAL PRODUCER AWARD NOMINEES

Carswell-Nichols Herefords

Owners/Managers: Jim & Carol Nichols and Brock & Carolyn Nichols
Alton, Kansas

Carswell-Nichols Hereford Ranch is a livestock and grain operation located in north central Kansas near Alton. Harold Carswell, founder of the ranch, started the cowherd in 1935 with his first 4-H heifer. Since then, the operation has grown to include his grown daughter, Carol Nichols, son-in-law, Jim Nichols, two grandsons, Brock and Ryan, granddaughter-in-law, Carolyn, four great-grandchildren and 300 head of Hereford and Angus cattle.

Hereford cattle are the heart of the operation and remain the true passion of their family. Their philosophy is that Hereford cattle continue to be the benchmark against which other breeds are measured as cattlemen continue to seek optimum traits inherent in Herefords. Those traits, critical to survival in the cattle business, are exactly the same traits Carswell-Nichols Herefords offers their customers in today's industry: fertility, reproductive performance, feed efficiency, optimum size and growth and documented feedlot and carcass superiority. They believe in combining superior genetics, progressive management and industry partnerships to provide consumers a quality beef product and reputable breeding stock.

Today, the Carswell-Nichols cowherd consists of one-third registered cows and two-thirds commercial. The family raises 1,750 acres of wheat and 2,000 acres of fall crops that consist of corn, milo, soybeans, silage feed and cane hay. Cows run on 3,000 acres of native grass pasture.

Joining Jim and Carol at the ranch is son Brock, his wife, Carolyn, and their four children. Their son Ryan is a banker in Wichita, working in agri-finance, and is a huge influence in their marketing and keeping up-to-date on resources. Ryan also helps in the advertisement and marketing of the registered and commercial herds.

The headquarters of their operation have been at the current location, the home of Jim and Carol and previously home to Harold and Pat, since 1950.

The Kansas Livestock Association is proud to nominate Carswell-Nichols Herefords.

Five Dot Ranch

Owners: Todd and Loretta Swickard
Standish, California

The Swickard family has been ranching in California since 1852. Originally from San Jose, Jack and Midge Swickard moved to Lassen County with 200 registered Herefords where they started Five Dot Land & Cattle Company in 1959. The herd size of their western range operation grew tremendously and shifted to a primarily Angus herd.

In 1994, Todd Swickard took over the daily management of the ranch, changing the operation to an all-natural program with a stronger focus on environmental stewardship. These changes allowed Todd and his wife Loretta to start their all-natural, locally grown branded beef business in 2006. The goal of their newly developed program was to produce and market a specialized beef product directly to the consumer, while maintaining the functionality of the ranch in the changing economy.

On the cattle side they employ AI, and embryo transfer along with traditional range bulls to breed cattle that fit their environment and marketing needs. They take extensive measures to evaluate their progress. Equally important is improving the lands they graze which are scattered over 6 counties from the Sierra Nevada Mountains to the grazing lands near the San Francisco Bay area. In California,

threatened and endangered species are not the exception but the norm on all of the lands they raise beef cattle. With the seventh generation now being integrated into the company, Five Dot Ranch has the room and potential to grow.

The California Beef Cattle Improvement Association is proud to nominate Five Dot Ranch.

Glenmary Farm

Owners/Managers: Tom and Kim Nixon
Rapidan, Virginia

Tom and Kim Nixon of Rapidan, Virginia own and operate Glenmary Farm, LLC, a 3,500 acre cattle operation along the Rapidan River. Glenmary Farm is a diverse operation which is centered on 750 commercial fall and spring calving beef cows, along with custom cattle feeding facilities which is home to the Virginia BCIA Culpeper Bull Test. Supporting the operation is 1,800 acres of cropland and 2,500 acres of pasture and hay land.

A rotational crossbreeding system is implemented for the cow herd utilizing Angus, Charolais, SimAngus, and Gelbvieh Balancer genetics. Proven, high accuracy bulls are utilized through artificial insemination and high quality natural service sires are acquired through the state bull test program. The calf crop is marketed in several ways, with the majority sold as weaned, value added feeder cattle in load lots in conjunction with other progressive producers in the region. Glenmary Farm calves have established a strong quality reputation among cattle feeders in the eastern Corn Belt as well as Midwest. Additionally, both fall and spring calving commercial bred heifers are developed and sold. The confinement cattle finishing facility provides further flexibility in the marketing of calves, with capacity of finishing 1,600 home-grown and custom cattle annually. The Nixons utilize extensive production and financial records to guide short and long-term business decisions which impact the livelihood of the family operation and their five full-time employees.

Numerous awards have been presented to the Nixons over the years. Tom and Kim have been recognized by Virginia Farm Bureau as Young Farmer of the Year and the Culpeper Soil and Water Conservation District recognized them as Conservation Farm of the Year. They also received the 2005 BCIA Superior Service Award.

Tom is very active in the local Central Virginia Cattlemen's Association, serving as a founding board member and three years as president. Additionally, Tom has been a director for the Virginia Cattlemen Association and for Orange County Farm Bureau. Kim has served as an associate director for the Culpeper Soil and Water Conservation District and is a volunteer leader for 4-H. Tom and Kim have a daughter, Elizabeth age 17, and son Robert, age 15. Both are actively involved in 4-H livestock projects, judging programs, FFA activities, and the farming operation.

Glenmary Farm is proudly nominated by the Virginia Beef Cattle Improvement Association.

H&T Bies Cattle Company

Owners: Harold and Judy Bies, Travis and Deanna Bies,
Donna and Dean Klapperich
Rapid City, South Dakota

Nestled near the Black Hills of western South Dakota, the operation's 1,100 head of Limousin-Angus cross cows graze on both deeded land and Forest Service land. H&T is a true Bies family operation. The partnership consists of Harold and wife Judy, son Travis and wife Deanna, as well as Harold and Judy's daughter, Donna and husband Dean Klapperich.

Consistent proven genetics from top Limousin herds have allowed H&T to pursue the all-natural niche market. Through careful genetic selection for high maternal and growth EPDs, H&T is still able to

wean a heavy calf in late September without the use of growth implants. By following the strict all-natural protocol, this provides them access to specific, value-added markets. Cows are calved in open pastures and they retain their own replacements so an emphasis is put on maternal characteristics and calving ease.

H&T understands the value of information at marketing time as they rigorously document their cowherd's genetic and health records. They also age and source verify their calves each year using IMI Global's verification system. In addition, H&T is certified for the non-hormone treated market (NHTC), qualifying their cattle to sell into the European Union. Selling their calves with this verified information has enabled them to receive premiums. They also participate in the Global Animal Partnership (GAP) program. H&T's commitment to information and an extensive individual identification system have allowed them to assess their cowherd in a more intensive manner.

The North American Limousin Foundation is proud to nominate the H&T Bies Cattle Company.

Jones Brothers Farm

Owners/Managers: Crawford and Cooper Jones
Prattville, Alabama

Jones Brothers Farm, owned and operated by Crawford and Cooper Jones, is located in Autauga County, Alabama. The operation includes beef cattle, cotton, small grains, and hay production and consists of approximately 3,500 acres of both owned and leased land, presently leasing Twin Valley Farms from Dr. Ron Henderson. Jones Brothers Farm began in 2000, with the purchase of 11 open replacement heifers from the Chilton County BCIA Heifer Sale, and has currently grown to 300 breeding females, with a goal of aggressive growth to 400 females by 2014. The cow herd consists of a 3 way cross of Simmental, Chiangus and Brangus cattle. A 75 day fall calving season from October 1 to December 15 is planned to capture market advantage for feeder cattle in a cooperative tele-auction each August. In 2010, 72% of the calf crop was born in the first 30 days of the calving season, and the herd has been honored for ranking in the top 3 herds within the Alabama BCIA large herd division for the past 3 years and has produced Alabama BCIA Gold Star Dams for the past 6 years.

Performance-minded cattle production is in the genomics of the Jones Brothers. Their grandfather, Ed Wadsworth, was a charter member and served as the first president of Alabama BCIA in 1964, and further supported by their mother, Carol Wadsworth Pearson, who gave them their first pastureland to begin their cowherd from the original Wadsworth Brothers Farm. Expressing their performance genetics and applying 21st century savvy business skills, these young cattlemen are building toward the future.

The Alabama Beef Cattle Improvement Association of America is proud to nominate Jones Brothers Farm.

Kempfer Cattle Company

Owners: Billy & Reed Kempfer Families
Saint Cloud, Florida

Kempfer Cattle Company (KCC) is a 25,000 acre family owned and operated ranch located in Deer Park, Florida. They have been in business there since 1898; the 6th generation is now starting to help work the ranch. KCC is a commercial cow/calf and seed stock operation. The commercial operation consists of a 3 way cross of Brahman, Angus, and traditional Shorthorns. Charolais bulls are used for a terminal cross on less productive Angus and Shorthorn sired cows.

Their calving season is November through January, with 85-90 percent being born in the first 60 days. The majority of calves born in the last 30 days are from second-calf heifers. They run 2,500

momma cows and 750 replacement heifers. Their business has made a shift over the past five years to raising and selling quality replacement heifers. High fertility and fleshing ability, along with balanced growth and carcass traits has brought great demand in recent years.

They started their seed stock business in 1978 raising purebred Brahmans. Their primary goal has always been to raise bulls for their commercial herd, but demand has enabled them to market bulls to other registered and commercial breeders throughout the Southern U.S. They have participated in a number of sire evaluation projects over the past 20 years. Most are done in cooperation with feedlots, primarily Decatur County, Kansas, University of Florida, and the American Brahman Breeders Association (ABBA). This, combined with retaining ownership on many of their commercial calves, is a great tool in helping them move their herd in the right direction.

Kempfer Cattle Company is proudly nominated by the American Brahman Breeders Association.

Maddux Cattle Company

Owners: Jack and John Maddux

Wauneta, Nebraska

Maddux Cattle Company is a cow/calf, yearling cattle operation located in southwest Nebraska. Taylor and Clara Maddux homesteaded the ranch in 1886, 11 miles north of Wauneta on the Stinking Water Creek. The ranch has grown today to encompass 40,000 acres of owned and leased land that sustains 2,500 mother cows and 5,000 yearlings. Native range consists of sandhills and hard land canyons that are part of the watersheds of three creeks that run through the ranch. The operation has approximately 1,800 irrigated and 600 dry land farming acres, the balance being native grass, some of which is sub-irrigated meadows. Jack and John Maddux, the third and fourth generation owner/operators of the ranch, manage the operation.

Replacement heifers and cows are bred to calve in April and May. Cow/calf pairs summer on native range, calves are weaned in the early fall, and wintered in backgrounding facilities or winter grazed with supplementation of wet distillers grains. All calves, with the exception of home raised replacement heifers and bulls, then go to leased grass in the spring. Steers and heifers are marketed off grass each August as 900-pound yearlings.

After weaning, cows are winter grazed on leased cornstalks from November through mid-March. Cows are then driven back home to native range roughly one month before calving. In this system, the Maddux cowherd has a full 12-month grazing system with no hay or supplement fed to the mature cowherd. Some strategic protein supplementation is used for first-calf heifers precalving and pre-breeding.

The cowherd is a maternal composite of five breeds: Red Angus, Tarentaise, Red Poll, South Devon, and Devon. Cows are British in body type and production levels; with breed selection aligned with year-round grazing and the low input system of the ranch.

Maddux Cattle Company is proudly nominated by the Nebraska Cattlemen.

Matador Cattle Company

Owner: Koch Agriculture Company, a subsidiary of Koch Industries, Inc.

Manager: Randy Lair

Wichita, Kansas

The Matador Cattle Company, a division of Koch Agriculture Company, operates three ranches: Beaverhead in Montana, Spring Creek in Kansas, and Matador in Texas. Originally acquired by Fred

C. Koch in the 1940s and 1950s, the ranches encompass 425,000 acres, including about 240,000 deeded acres.

The company employs a market-based approach to management, ensuring the ranch's ability to create real long-term value for customers and society. As a result, an intensely challenged decision-making framework is employed to ensure an optimal balance between livestock, wildlife and natural resources.

The ranch is 100 percent owned by The Matador Cattle Company, an indirect subsidiary of Koch Industries, Inc. The ranch's primary income is from the marketing of cattle, hunts and horses.

The ranches annually wean about 10,000 calves and support more than 15,000 head of mostly Hereford and Angus commercial cattle. In 2010 and 2011, the company began to shift its sire base to Akaushi bulls. The Texas ranch raises Quarter horses for ranch use and external markets. As the demand for high-end hunting and outdoor recreation has grown, Matador Ranch also has expanded its wildlife program. The ranch markets trophy deer hunts, along with turkey, quail, dove and predator hunts.

The Matador Cattle Company is proudly nominated by the American Akaushi Association.

Slykhuis Farms

Owners: Charles and Todd Slykhuis

Manager: Todd Slykhuis

Raleigh, Illinois

Slykhuis Farms of Raleigh, Illinois was the recipient of the Illinois Beef Association Commercial Producer of the Year Award at the 2010 IBA Annual Meeting. The Slykhuis Farms is owned and operated by Charles and Virginia Slykhuis and Todd Slykhuis of Raleigh, Illinois. This award is presented to progressive, performance oriented commercial cow-calf producers that utilize the latest in breeding, management, and forage production to optimize production and profitability of their operation.

Slykhuis Farms was founded by Charles in 1972 with the purchase of 392 acres. Since then the farm has expanded to over 1,000 acres comprised of cash crops of 140 acres corn, 285 acres of soybeans and 40 acres of wheat. Besides these cash crops there are 100 acres of hay and 450 acres of pasture.

The cattle operation was started in 1972 with 100 cows with the farm. The cattle operation was moved to a spring and fall calving herd through the early 1980s. Also, the number of brood cows was reduced in the late 1980's; however more rapid expansion in the number of brood cows up to 270 in 2010 with plans to continue to expand up to 400 brood cows in the future. Besides these brood cows there is usually 75 to 100 head of replacement heifers being developed and bred.

Not only has the number of cows increased, but the performance and quality of the herd sires has made dramatic improvement. In recent years an aggressive artificial insemination (AI) program has been implemented with close to 400 brood cows and heifers bred via AI in 2010.

The University of Illinois Extension and the Illinois Beef Association is proud to nominate Slykhuis Farms.