

Today's Beef Cattle Genetics Research and Education Engine: Ready and Primed for the Industry's Future?

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Introduction

Genetic improvement in livestock has a truly amazing history, with the beef industry having been blessed with many of the major scientific innovations that have occurred along the way. In recent years, it has been nearly impossible to miss seemingly daily news reports about exciting discoveries in the new field of molecular genetics and genomics. While most of these reports have focused on the unraveling of the human genome and its implications for human health, there has been significant spillover in to plant and animal agriculture as well. At times over the past 15 years, it has seemed that this new and exciting field would hold all of the immediate answers to breeding better beef cattle. Today we have an initial DNA sequence assembly of the cow genome completed and made publicly available along with a host of rapidly developing diagnostic tools. Along with a number of major societal shifts that are predicted to result in changes of epic proportions for the beef industry and its producers, the question is being posed as to whether existing U.S. programs and infrastructure in beef cattle genetics research and education are “in tune” and adequate to address future needs. The objectives of this presentation are to: 1) provide a historical context for how we have arrived at where we are in 2007; 2) discuss the major societal issues that are predicted to change the landscape of the beef industry and beef cattle genetic improvement in the near term; and 3) discuss the current and future challenges of the beef genetics research and education community in

being properly primed and ready to serve the current and future needs of the industry.

A Brief History of Beef Cattle Genetic Improvement

It is believed that cattle were domesticated over 5,000 years ago. Only in the last few hundred years has the human race applied systematic animal breeding programs to these amazing animals to mold them in to more specific roles – i.e. meat, milk, or draft. Today the number of distinct cattle breeds numbers in the hundreds across the world.

In the U.S., our cattle industry quickly developed as segregated in to dairy and beef sectors. By the dawn of the 20th century, the beef part of this industry had essentially become made up of three breed populations – Aberdeen Angus, Hereford, and Shorthorn. It is unlikely that our ancestors engaged in the beef business at that time – for most of us our grand- or great-grandparents - would have been able to predict the dramatic changes that would take place in the next 100 years.

The first half of the 20th century was an immensely prolific time in agricultural science. Arguably, the most dramatic discoveries were actually in the fields of genetics and statistics. During the 1920s and 1930s, the field of population genetics came of age – primarily as a means of quantifying and describing Darwin’s writings from the late 1800s. The emerging leaders of this field helped to describe the concepts of genes, gene loci, chromosomes, and cellular reproduction. They also were

instrumental in establishing the field of biometrics – statistics as applied to biological phenomena. These early statisticians developed much of the underlying theory used broadly in science today. What most people do not know is that they originally were geneticists trying to describe how populations of animals change over generations! Also, at the same time there were pioneering scientists who had the foresight to develop populations of beef cattle upon which they began to practice long-term selection and inbreeding – ones like the Miles City Hereford lines that gave us the Line 1 of today.

Scientists also made what seemed to be an unrelated, but extremely valuable, discovery in plant genetics during this same time period. Scientists observed that when two unrelated lines of germplasm were crossed – or “hybridized” – the resulting crossbred progeny had better performance than the expected average of the parents. The concept of heterosis between lines was born – and with it the seed industry and crop agriculture was revolutionized. At the time, livestock breeders did not see any great benefit from this phenomenon – but as we now know, that would dramatically change later.

The post-WWII era was a particularly exciting time for livestock genetic improvement, as it was in many fields. The 1940s saw some of the greatest minds to ever grace the study of livestock genetic improvement at their prime. Jay Lush, who many refer to as the modern day father of animal breeding, was busy defining with co-workers Lanoy Hazel and Gordon Dickerson the concept of the “selection index” and “breeding value”. The field of biometrics had matured to the point where it was now possible to determine from experimental populations that performance for traits affecting production could be measured – and that many of these traits appeared to be heritable.

In 1953, James Watson and Francis Crick presented for the first time in the scientific

literature the molecular structure of the genetic code – i.e. DNA. Combined with the theories of genes and heritable variation of traits, it was now possible to visualize how these genetic differences at the gene level might one day be exploited for genetic improvement.

Also, in the 1950s, two significant events occurred which would permanently change the nature of cattle breeding. The first was that artificial insemination techniques matured to an adoptable level for cattle breeders – especially dairy producers. Coupled with the institution of the Dairy Herd Improvement programs of USDA a bit earlier, volumes of data began to accumulate matching pedigrees to milk production records. At the same time, computing technology was beginning to surface as a usable tool – even though it was rudimentary to what we now have today. Dairy cattle breeders had enough foresight, however, to understand the power of coupling quantitative genetics theory to artificial insemination and as a result genetic evaluation as an applied science was born. Now, through all of the technological and computing improvements of the last 45 years, we have seen that this works – to the tune of almost 100% improvement in milk yield per cow!

Thankfully, the plans of the dairy industry did not go unnoticed by beef cattle breeders. The American Angus Association and the American Hereford Association quickly established performance recording programs for their breeders – focusing initially on 205 day weaning weights within herds. In the late 1960s, some visionary cattle breeders, including Sally Forbes, Frank Baker, Jim Brinks, Bob deBaca and others, formed an organization called the Beef Improvement Federation. This organization was instituted to take on the task of developing uniform guidelines for performance recording programs, the same task that it still performs 40 years later. One of the initial visions of this group was that it would soon be able to develop methodology to compare

animals across herds – making the standardization of performance recording critical.

The late 1960s and early 1970s was the next time of great change in beef cattle breeding. Two things occurred somewhat simultaneously – the importation of semen from a number of continental European breeds of cattle and the next generation of computing technology coming of age. As a result of their higher growth rates, size, and muscularity, a number of these breeds quickly took a strong foothold in the beef cattle seedstock industry – especially Simmental, Limousin, and Charolais. As the American Simmental Association took its first steps, it carefully studied the performance recording movement and was quick to the chase to be the first group to recommend that they should attempt to take advantage of the improvements in genetic prediction methodology, artificial insemination and computing technology to compute and make publicly available the first “across herd” comparisons. They did so, using what was called a “sire model” developed at Iowa State University by Richard Willham in 1972. This allowed the prediction of “estimated breeding values” (EBVs) for the growth traits by tying herds together through a reference sire network. The era of true beef cattle evaluation was now born. Shortly thereafter, maternal grandsires were added to the evaluation framework – allowing “maternal” weaning weight EBVs to be added.

At the same time, it was clear that much more information was needed for beef producers to effectively sort out the widening levels of genetic variation available to them for commercial production. Additionally, producers discovered that hybrid vigor was indeed possible – and very economically beneficial – when many of the new breeds were bred to the available Hereford and Angus cows. Crossbreeding and hybrid vigor seemed to have a place at the table. Fortunately, USDA’s

Agricultural Research Service saw the need for scientific data in this area. As a result, the US Meat Animal Research Center at Clay Center, NE was born and within a short time initiated two monumental projects – the Germ Plasm Evaluation (GPE) program led by Larry Cundiff and the Germ Plasm Utilization (GPU) program led by Keith Gregory. At the same time the Fort Robinson station was being closed, and the selection lines of cattle there were relocated to MARC – becoming the third piece of the puzzle led by Bob Koch. Over the next 30 years, this collective effort produced the fundamental body of knowledge now used world-wide to understand genetic variation, and how to effectively use it in beef cattle production.

The 1980s was a true time of transition for beef cattle breeding. Computing technology had now matured to the level where statistical methodology developed by a dairy geneticist named Charles Henderson in the 1950s could be applied to beef and dairy performance data – so called BLUP (Best Linear Unbiased Prediction) methodology. Scientists worked out the kinks and were successful in using these methods to compute for the first time what we now know as EPDs – *Expected Progeny Differences* within breeds. These new genetic evaluation tools were significantly more powerful and accurate to allow breeders to sort not only bulls – but also cows -- than the previously used EBVs from the sire/maternal grandsire model approach. Over the ensuing 20+ years we have become the beneficiaries of continual refinement in genetic prediction methodology, including more accurate predictions as well as a plethora of new traits added to the evaluation pipeline. We would even see the US MARC GPE populations serve another useful role, when in the early 1990s, data from the breeds evaluated in the GPE project coupled with breed genetic evaluation data, were used to develop an “across-breed” adjustment process allowing commercial producers for the first time to compare bulls across not only herds, but also across breeds.

The other monumental event in the 1980s was the unleashing of a new field of science referred to as “genomics”. This term was first used in 1986 to collectively describe the scientific discipline of mapping, sequencing, and analyzing genomic level DNA information. A technology called “polymerase chain reaction”, developed in 1987 by Kary Mullis in California, literally unleashed the forces of research into the genetic code of plants and animals. It had only taken 34 years to go from understanding the structure of DNA to being able to start the process of deciphering the code!

As molecular genetics tools became available to lab scientists in the late 1980s, researchers began the arduous process of genetic mapping. Because they were unable at that time to know the base sequence of the DNA code, they had to use a somewhat “black-box” approach to identify locations on the chromosomes that might contain genes affecting these traits. This process, called linkage mapping, took advantage of DNA polymorphisms called microsatellite markers, a type of variation found readily throughout the genome. In 1994, the first genetic linkage maps of cattle detailing a few hundred markers were published by USDA-ARS scientists from US MARC and Australian CSIRO scientists. Today, these linkage maps, combined with what are known as radiation hybrid and bacterial artificial chromosome maps, are much better defined with a total of over 21,000 individual markers identified and localized to chromosomes in the recent “composite bovine map” spearheaded by US MARC’s Warren Snelling (<http://genomes.tamu.edu/cgi-bin/gbrowse/bosmap2/>).

The availability of the first linkage maps allowed researchers to begin the search for regions of the genome harboring genes containing polymorphisms causing differences in performance for economically important traits – what have become known in the jargon as quantitative trait loci (QTL). This research,

conducted at several locations in the US, Australia, New Zealand, and Canada first required the establishment of cattle resource populations that would have a high probability of having different copies of the genes on an individual animal’s maternal versus paternal chromosome. A number of these resource populations were formed at the US Meat Animal Research Center and subsequently utilized to identify over 25 QTL affecting a wide variety of traits on 11 different chromosomes. Other research groups also identified a number of QTL, principally the Angleton population at Texas A&M funded primarily by the beef checkoff and the CRC/MRC projects in Australia. The results of these projects were exciting and stimulated a considerable amount of attention in the beef industry in the mid to late 1990s. Unfortunately, as is too often the case, in the rush to find the silver bullet, the immediate promise of genomics was clearly oversold, as it has since become clear that the identification of QTL was only the first “baby step” in the process to bringing these results to a practicable technology.

Fortunately for the cattle genomics community, the US government had placed a high priority through its human medical research arm – the National Institutes of Health (NIH) – on deciphering the human genetic code. The idea was very similar to what has been described in this paper for cattle – except that in this case the target was to develop new ways to combat human disease / improve human health. Initially, many of the same approaches of linkage mapping were used in human genomics, with the additional twist that model organisms were intensely studied as proxies for man – principally the laboratory mouse and rat. This was possible because as we began to be able to see small regions of DNA code, the similarities between species were remarkably high – usually at the 90% or higher level. Scientists also observed that while the arrangement of the pieces of the genetic puzzle was not the same

across species, large regions of the genome had been conserved throughout evolution. This now allowed the opportunity to take information from species being studied with very large research budgets in comparison to cattle to infer what might be the case in cattle using “comparative mapping”. While this approach did yield results, including the identification of the myostatin gene causing double-muscling in cattle, only a handful of genes have been mapped in cattle to date through the “QTL-search followed by comparative mapping / fine mapping” approach.

The human genetics community quickly recognized that if progress in building new tools through genomics for human health applications was to occur expeditiously, infrastructure needed to be built right up front. Linkage maps, QTL searches, comparative mapping and some fine mapping were useful, but extremely inefficient, timely, and high in cost. Thus, in the last half of the 1990s, the National Institutes of Health, through its National Human Genome Research Institute (NHGRI), built a plan for sequencing the human genome, along with the highly used lab species of the mouse and rat (<http://www.genome.gov/10001691>). The project became broadly known as the “Human Genome Project” and involved a network of “sequencing centers” contracted to do high-throughput sequencing (i.e. determination of the DNA base code) of the human genome. An initial rough draft of the human genome sequence was completed in 2001, followed by a complete, finished sequence in April of 2003, fifty years after Watson and Crick’s initial elucidation of the double-stranded helical nature of DNA! The Human Genome Project was not cheap (in the billions rather than millions of dollars), but is widely believed by many to be the most important scientific project in the history of mankind to date.

The cattle, poultry, and swine industries, however, were placed in a position to reap huge rewards from the infrastructure built by NHGRI

to sequence the human genome. In order to build the most comprehensive infrastructure to capitalize on the human genome for discoveries in human health, NHGRI launched down a path in 2002 of supporting the sequencing of a number of other genomes (<http://64.225.252.6/nstc/html/IWGGAD2004.pdf>). These were chosen to most highly leverage the investment in human genomics, as based on comparative mapping and medical model species use. Fortunately, the cow has been widely used as a model species in a number of areas for human medicine, especially in the area of reproductive physiology. As a result, the agricultural community developed a “partnership” approach in 2003 with NHGRI to move forward the sequencing of livestock genomes, including the bovine which was launched in December of 2003 at the Baylor College of Medicine in Houston, TX (<http://www.hgsc.bcm.tmc.edu/projects/bovine>).

The bovine genome sequencing project was a first in cattle genetics in many ways. The first was that it required \$53M in funding which came from an international consortium including NHGRI (\$25M), USDA (\$11M), the state of Texas (\$10M), Genome Canada (\$5M), Australia and New Zealand (\$1M each) and the national, Texas, and South Dakota beef councils (\$1.2M). This followed an initial investment of over \$4M to develop the scaffolding, called a bacterial artificial chromosome (“BAC”) map, invested by an international consortium of ten laboratories in seven countries, led by USDA-ARS. The animal providing the DNA for the sequencing project was a Line 1 Hereford female from the USDA-ARS long-term linebreeding and selection project at the Fort Keogh Livestock and Range Research Lab at Miles City, MT. All sequence information from the project was immediately deposited in the public domain, through the NIH’s National Center for Biotechnology Information (NCBI, <http://www.ncbi.nlm.nih.gov/>), allowing all researchers around the globe to have access to spurn forward developments.

In September 2006, the assembly (7.2-fold sequence coverage) of the bovine genome was announced by the project team. Additionally, light sequencing of animals representing the Holstein, Jersey, Angus, Limousin, Brahman, and Norwegian Red breeds allowed detection of over 2M new single nucleotide polymorphisms (SNPs) and the process of validating a set of 39,000 of these SNPs has been carried out on a panel of 19 breeds to evaluate genetic diversity of the world cattle population and to develop a haplotype map of the bovine genome. Additionally, the Hereford female used for the sequencing project and one of her progeny supplied a wide array of tissues to the project team to allow development of 10,000 full-length cDNAs for the study of gene expression. Currently the genome sequence is being annotated by a group of researchers around the globe to provide a full picture of the “gene atlas” of the species. The availability of the genome sequence is expected to speed gene discovery by a factor of 100 fold!

As the bovine genome sequence was being completed over the past few years, the development and release of commercial DNA tests began to escalate. With several companies now in the market space for this group of technologies, most with quite different business models, a variety of tests and platforms have come of age. Beginning with the initial release of the GeneSTAR Marbling test based on a polymorphism associated with the thyroglobulin gene to now several GeneSTAR and other tests for calpastatin and u-calpain, leptin, DGAT, and others – the field of DNA diagnostics is rapidly growing. The recent release of multiple marker platforms by Merial, Igenity, and MMI Genomics has moved this technology fully on to the radar screen of the industry and has many wondering whether the DNA age has truly arrived. Exciting times do appear to be upon us – including the potential for whole genome selection using haplotype maps developed from dense SNP maps.

As the genome is mined over the coming years, what can beef cattle producers expect to see as a result? Will DNA selection tools essentially replace breed genetic evaluation programs / EPDs as we know them today? Will we no longer need to worry about collecting expensive performance data? Will we essentially be able to know the genetic value of a calf in utero? Will we be able to predict the perfect range cow for a given production environment, sort that cow out with genomics, and then mass clone her?

As genomics technology matures in the coming decade, we will undoubtedly see an explosion of genes that are identified for various traits. It is easy to predict that as we identify many of the genes underlying variation in performance for traits, we will identify more questions than we do answers. Some of those are likely to be:

- 1) **What is the function of these genes in the physiology of the animal and how is this function altered by changes in the production environment?** We are now routinely talking about the next big opportunity area of livestock genetics research being in “*functional genomics*” using “*systems biology*” to develop “*precision mating*” followed by “*precision management systems*”.
- 2) **How do the various genes impacting economically important traits interact with one another at the genome, proteome, and metabolome levels?**
- 3) How many animals within a population (i.e. a herd or a breed) need to be “DNA profiled” in order to get *enough* information?
- 4) Will “*whole genome selection*” using large panels of SNP with linkage disequilibrium work – will this approach replace progeny testing and performance data?
- 5) **Can we combine phenotypic performance information with gene level DNA information to come up with**

“DNA-enhanced EPDs”? WHO IS GOING TO DO IT – and who is going to be the service provider to the breeders?

- 6) How will the free enterprise system embrace this technology – i.e. what is the best business model to capitalize on these advances? DNA testing companies, AI / genetics companies / supply chain alliances / feeding companies / big pharma / breed associations / something yet to be defined????
- 7) How will the cost of this technology be borne by the industry? One cannot expect the genetics or commercial sectors of the beef industry to pay several hundred dollars to profile a narrow set of characteristics to identify the top sires as has been proposed in the initial ventures of gene testing in to the public marketplace. The value capture of this technology is likely to require a new type of business model unlike anything we have seen previously in cattle genetics.

This somewhat exhaustive and comprehensive history lesson has been presented here to intentionally bring light to the fact that the process of getting to today’s state of the art beef cattle breeding has not been easy, or achieved quickly. One could argue that 100 years in the bigger picture of 5,000+ years of domesticated livestock production is a drop in the bucket. However, most of us would still argue that those 100 years have been a monumental and unprecedented effort. As we enter the era of “genome-enabled” genetic improvement – we must be careful to remember the big picture, and that while these new tools are fascinating and almost unbelievable to many of us, they are simply the next pieces of the puzzle in a long process of continual refinement and improvement as beef cattle breeders.

Is Society Re-Drawing the Landscape of the Beef Industry?

One might argue that the past five years have revealed the beginning of major shifts in our society that are changing the “look” and activities of the beef industry and its producers. From the impact of the first few (and only) cases of BSE in the American cattle population on world beef trade dynamics to various issues associated with food safety and biosecurity to dissension within the industry in terms of: 1) trade policy; 2) national animal identification; 3) country-of-origin labeling; 4) increasing integration / consolidation and impacts on market structure and price discovery; and 5) research and promotion through the producer beef checkoff program; the past few years have undoubtedly been volatile. Add the recent impact and ripples being felt throughout the industry from increased fuel prices, and now competition for feedstuffs (i.e. code language for cheap corn) from biofuel production, and we are seeing industry leaders now talk about the biggest paradigm shifts in the industry’s history in North America. The following are societal and industry shifts and changes that are occurring around us as we speak that are certainly requiring us to think differently about the next generation than many of us might have anticipated:

- 1) An increased call from the general public for decreasing the environmental footprint of livestock and poultry production, including range, water, and air quality.
- 2) Competition for energy sources and feedstuffs for alternative energy production, heightening the emphasis on improved energy utilization and animal adaptability to production environments.
- 3) Increased attention to animal well-being and welfare, pointing out the need for robust scientific criteria to actually assess animal well-being in our production systems.

- 4) Increased “brand” / process / historical identity of products being called for in the marketplace by retailers and their consumers.
- 5) Increased interest and purchasing power, whether deserved or not, of consumers for organic / natural / grass-fed beef products.
- 6) Recognition that we are concerned about the narrowing of the gene pool – while also recognizing the need to increase product uniformity and consistency. Considerable debate and disagreement in the industry regarding the value and usefulness of heterosis in the commercial sector exists.
- 7) The need for information continues to accelerate – with the cry for emphasis on Economically Relevant Traits to the commercial industry – yet we have done little to put in to place evaluation for animal health, functionality, and adaptability traits (i.e. still heavy on outputs with not much to work with on the input side of the profit equation).
- 8) We have lived in a “breed” world through the history described above, yet the commercial cattle producer of today need’s BEEF CATTLE gene pool-wide evaluation more than they need breed-specific tools.
- 9) Mining the genome in the post-genome sequence world is here to stay, yet we are woefully inadequate in being set up to handle all of the information that is upon us in a practically meaningful way.

Some will argue the long-term relevance and impact of this list of concerns. Yet, there is no doubt that they all deserve our rather immediate attention if we are to provide the leadership needed to guarantee a successful and sustainable beef industry in the future.

Are We Ready and Poised for These Challenges?

One does not have to be a rocket scientist to quickly come to the conclusion that we are far from done in the field of beef cattle breeding and genetics. One might, in fact, argue that we are entering a “Renaissance” period for the field. The issues above, coupled with the fact that we are now fully headed in to the age where we have more data than we know how to effectively handle in an era where technology is outpacing our abilities to utilize it, lead me to the conclusion that we need to significantly “re-engage” the troops. No longer can the industry be passive in championing the need for a re-building of our infrastructure in this area.

While the ushering in of the genomics era has been immensely exciting scientifically, it has not come without significant and tangible costs. This research is expensive to conduct, requires large project teams, is lab intensive, and brings the new elephant to the table of intellectual property rights. As research and education programs around the U.S. geared up to make inroads in to this arena, other programs were often sacrificed to chase molecular dreams. As a result, the vast majority of traditional beef cattle breeding positions and research herds in the land grant university system were eliminated, or re-directed, into genomics and molecular biology, over the past 20 years.

A noticeable outcome of the “re-direction” of quantitative genetics programs in to genomics and molecular biology was the need for the few remaining beef cattle quantitative genetics programs involved with national cattle evaluation research, discovery and tech transfer to band together in to the National Beef Cattle Evaluation Consortium (NBCEC). Over the past decade, these four universities have been able to attract federal earmark funding within USDA’s Cooperative State Research, Education, and Extension Service (CSREES) to provide infrastructure for this important area.

This only happened, however, due to the foresight of a small group of geneticists and producers who recognized that unless something was done to support this area of research and education, the critical mass of beef cattle breeding and genetics expertise would have continued to dwindle to non-existent levels. The NBCEC is now fighting for its life in the funding arena with an attempt being made to provide a permanent structure for funding this effort in the future. This must be done to address the long laundry list above, and it needs to be done at a level that will add significant critical mass to the effort – including extension and outreach.

The following are questions that the U.S. Beef Improvement Federation and its constituencies need to carefully consider to ensure future success in the industry:

- 1) Where are the scientists with practical knowledge of the needs of the industry going to come from who can navigate these waters? We are churning out some very highly skilled molecular biologists, but the vast majority of them do not know one end of a cow from the other?
- 2) We are facing a huge deficit of quantitatively skilled people to be able to make sense of all of these data. Do we need to re-open the textbook on quantitative beef cattle genetics?
- 3) Who is going to educate the public? Just as we needed a major public outreach effort to educate the industry on EPDs and associated tools, we now have the same need on “genome-enabled selection”, precision mating and management systems with phenotypes and genomic tools. Where has extension gone and what have we replaced it with?
- 4) What is going to be the role of breed associations in the future? Is there a new service sector set to emerge or will the genetics industry adapt? This is eerily reminiscent of the discussion that circled

in the industry throughout the past 15 years on what should the role be of the Livestock Marketing Association and its sale barn members in the new era of “value-based marketing”. There are opportunities out there, but who is going to “seize the day”?

- 5) We may not be looking hard enough at some of our international competitors – careful study of what is happening in Australia, Brazil, New Zealand, as well as competing protein industries, is a very good idea.
- 6) Is it possible that animal agriculture in the U.S. could eventually be shipped off-shore? There are certainly factions at work in the public who cleverly have this as a goal cloaked underneath other agendas (animal welfare, environmental protection, vegetarianism, humanitarianism). I recall telling students in my Beef Production course in 1989 that they should be prepared for the day when grain became too expensive to feed to cattle. They looked at me like I was from Mars, just as the reader might feel after reading this concern – but in 2007 we actually find that prediction to now be coming true?
- 7) Is there adequate funding available in today’s research and higher education and outreach system to address these challenges? Assuming that the answer is a resounding NO, what should be done about it, and, who is willing to champion the cause?

The last point is certainly multi-faceted. It is worth noting that the trend in publicly funded research and higher education over the past couple of decades has been to shy away from production-oriented “traditional” agricultural research in favor of “sexier” areas such as animal health, food safety, human nutrition (with the current buzz being obesity), and environmental management and protection. While there is no doubt that these areas are

important and deserve attention, it is extremely short-sighted to say that we are done addressing the challenges of how to produce more with less. The recent turn of events that led to \$4 corn this past year should be a wake-up call to this industry to be vigilant in supporting production research as well, and, the critical need to convince the policy and legislative arenas to do likewise.

Our family had the pleasure of seeing our oldest child, Justin Lucas Green, matriculate from the secondary school system and head off in to the world of higher education this past month. Watching him and his three siblings mature over the past several years has given my wife Jane and I pause to think about the future and what will be required for these young people to accrue the same benefits we have enjoyed in our lives. This generation of young people is impressive, bright, aggressive, and bold. They are capable of accepting challenges and they seem to understand that much will be required of them. They have been compared in many ways to the generation that responded to Hitler

and World War II, only they are the ones who saw the WTC towers collapse as opposed to Pearl Harbor being bombed.

I would argue that we need to regain some of their 18-year old idealism and “wide-eyed vision” in order to provide the leadership so direly needed to address the questions facing the beef genetics sector. I have no doubt that the leadership and passion to do so exists within the ranks of those who have lived our lives serving and producing in this industry. It does seem, however, that we need a jump start, and it is my hope that this presentation and discussion will provide such a charge. We all must be vigilant in thinking through the solutions to these questions. Can we in 2007 think and act big enough to ensure that the history of beef cattle improvement can be looked back on in 2047 with thanks and gratitude? Sal Forbes, Frank Baker, Bob DeBaca, Howard Stonaker, Jim Brinks, and their colleagues did in the late 1960’s. I do think we can do so as well in the late 2000’s. Q.E.D.

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