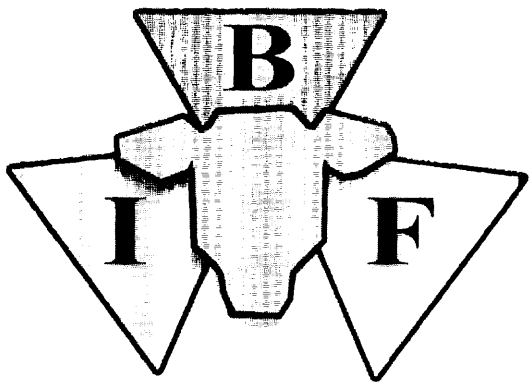
Proceedings

Beef Improvement Federation 36th Annual Research Symposium and Annual Meeting



May 25-28, 2004
Sioux Falls Convention Center
Sioux Falls, South Dakota

Hosted By

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South Dakota Cattlemen's Association

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Beef Improvement Federation

36th Annual Research Symposium and Annual Meeting
Sioux Falls Convention Center
Sioux Falls, South Dakota
May 25-28, 2004

Tuesday, May 25

5:00 pm South Dakota Welcome Reception

7:00 pm Application of Developing Technologies in Animal Agriculture. *Moderator: Don Boggs, South Dakota State University*

Reproductive Technologies. *David Faber, Trans Ova Genetics*

Application of Transgenic Technology in Animal Agriculture. *James M. Robl, Hematech, LLC*

DNA Testing and Marker Assisted Selection. *R. Mark Thallman, U.S. Meat Animal Research Center, ARS-USDA*

Wednesday, May 26

8:00 am Welcome

8:15 am New Technologies – Increased Cost or Increased Profit. *Moderator: Jerry Lipsey, American Simmental Association*

Multiple-Trait Selection in a Single Gene World. *Dave Notter, Virginia Polytechnic Institute and State University*

Panel Discussion. *Dave Notter, Virginia Polytechnic Institute and State University; Dick Quaas, Cornell University; Craig Huffhines, American Hereford Association; and Robert Williams, American International Charolais Association.*

9:45 am Break

10:15 am The Pricetag of Innovation. *Barry Dunn, King Ranch Institute for Ranch Management, Texas A&M - Kingsville*

12:00 pm BIF Recognition Luncheon

2:00 pm Roundtable Discussions

Genetic Prediction. *Chair, Larry Cundiff, U.S. Meat Animal Research Center, ARS-USDA*

Producer Application. *Chair, Sally Northcutt, American Angus Association*

Live Animal, Carcass, and Endpoint. *Chair, Robert Williams, American International Charolais Association*

6:00 pm Evening Out. *Washington Pavillion*

Thursday, May 27

8:00 am Meeting Demands. Moderator: Daryl Strohbehn, Iowa State University

Expectations of End Users – Restaurant and Retail Perspective. *Speakers to be Announced*

The Cost of Meeting Consumer Demand. *John Lawrence, Iowa State University*

10:00 am Break

10:30 am Final Report: NCBA Tenderness Project. *Dan Moser, Kansas State University*

11:30 am Annual Meeting and Director Elections

12:00 pm BIF Awards Luncheon

2:00 pm Roundtable Discussions

Cowherd Efficiency. *Chair, Mark Enns, Colorado State University*

Emerging Technologies. *Chair, Craig Huffhines, American Hereford Association*

Selection Decisions. *Chair, Darrh Bullock, University of Kentucky*

Night on the Town - *Dinner on Your Own*

Table of Contents

Advancements in Reproductive Technology in Cattle

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Abstract

Animal Biotechnology represents an expanding collection of rapidly developing disciplines in science and information technologies. The bovine provides many opportunities to utilize these disciplines and evolving competencies.

Commercialization of biotechnology in cattle is presently taking two pathways. The first application involves the use of animals for biomedical purposes. Very few companies have developed all of the core competencies and intellectual properties to complete the bridge from lab bench to product. The second pathway of application is for the production of animals used for food and fiber.

Artificial insemination, embryo transfer, *in vitro* fertilization, cloning, transgenics, and genomics all are components of the tool box for present and future applications. Individually, these are powerful tools capable of providing significant improvements in productivity. Combinations of these technologies coupled with information systems and data analysis, will provide even more significant changes in the next decade.

Any strategies for the commercial application of animal biotechnology must include a careful review of regulatory and social concerns. Careful review of industry infrastructure is also important. Our colleagues in plant biotechnology have helped highlight some of these pitfalls and provide us with a retrospective review.

In summary, today we have core competencies which provide a wealth of opportunities for the members of society, commercial companies, and cattle producers. Successful commercialization will benefit all of the above stakeholders, and provide a safe and efficient supply of food and pharmaceuticals.

Introduction

Reproductive technology on cattle has made significant strides over the past fifty years. This is a continuum which began with artificial insemination. The utilization of AI was greatly enhanced with cryopreservation of semen and the ability to synchronize estrus by utilizing prostaglandins. The beef and dairy industry has focused on developing elite sires and selection through pregnancy testing.

Genetic progress was further enhanced via embryo transfer technology. Non-surgical collection and transfer, cryopreservation of embryos, improved synchronization methods, and "direct transfer" embryos have improved efficiency, decreased costs, and increased the utilization of embryo transfer by both beef and dairy producers.

The continuum of reproductive technology continues with techniques such as *in vitro* fertilization, separated semen, and nuclear transfer or cloning. Each of these areas will be discussed in greater depth in this paper.

In Vitro Fertilization

By the middle of the 1990's, several commercial IVF laboratories were developed in the United States, Canada and Europe (mainly in Germany, Italy, France and Holland). Years later, they were accompanied by other laboratories in South America (i.e. Brazil and Argentina) and Oceania (i.e. Australia and New Zealand). The adoption of the transvaginal ovum pick-up guided by ultrasonography (OPU), facilitated IVF use in live females (11). The initial purpose of commercial IVF was to obtain viable embryos from females that may not be able to produce progeny through conventional techniques. At present, IVF is a complement to an ET program. Its application could be for females that will not respond to superstimulatory treatments, fail to produce transferable embryos, or possess abnormalities in their reproductive tracts (i.e. ovarian adhesions or blocked fallopian tubes). IVF is also used for females that are terminal (age, accident, disease, etc.), or that are pregnant heifers and cows during the first trimester of gestation, and for heifers and cows with and without calf during the first one, two or three months after calving (post-partum period). It also has applications for normal cyclic heifers and cows, and pre-puberal calves.

IVF allows an improvement in efficiency of utilization of sperm. While Intracytoplasmic Sperm Injection (ICSI) has not been widely implemented in commercial bovine IVF programs, IVF still provides opportunities to use relatively low numbers of sperm to produce viable embryos. This allows for the utilization of high value semen and may provide significant opportunities when coupled with gender separated semen.

Commercial and research centers have used OPU-IVF in diverse categories of females (pre-puberal calves, heifers, cows), age (pre-puberal, post-puberal, aged cows), breeds, reproductive status (cyclic, pregnant, post-partum), aspiration frequency (once weekly, twice weekly, twice per month), use of hormones (FSH, rBST) and IVF protocols (co-culture BRL cells, chemically defined media, serum) with different degree of success (4, 5, 6, 16, 23, 26, 30, 31, 33, 42, 43, 53, 67, 74, 77). Overall results with problem cows are presented in Table 1. A summary of results with and without

superstimulation is presented in Table 2. Oocyte quality aspirated is presented in Table 3, and breed performance is presented in Table 4. Data was compared by "T" Student and Chi-square analysis. During the period from 1992 to 2000, a TCM-199 and then Menezo B2 with BRL cells co-culture system (with 10% FCS) was used to produce embryos. At the beginning of 2001, the culture system was changed to SOF citrate semi-defined culture media with 5% FCS (36) to avoid or diminish the risk of large syndrome calves. In the SOF system, the petri dish is not observed until day 6.5 of culture and the incubator atmosphere condition is 5% O_2, 6% CO_2 and 89% N_2 with high humidity.

All of these embryos were transferred fresh due to the poor results obtained with frozen *in vitro* embryos. This higher sensibility (48, 59, 66, 71) would be due to the culture conditions or fertilization protocol and would produce modifications in the *in vitro* embryo (13, 25, 29, 37, 38, 52, 57, 68, 70, 76, 82, 85, 86, 88, 102).

Table 1. Overall OPU-IVF results with problem cows.

Years	No. Donors	FSH Treatment	OPU Sessions	Oocytes	Oocytes/ Session	Embryos/ Session	Embryos (%)	Pregnancy Rates (%)
1992	47	-	331	1769	5.34	0.98	323 (18.3)	117 (36.2)
	4	+	4	22	5.50	1.75	7 (31.8)	3 (42.9)
1993	152	-	795	5775	7.26	1.20	952 (16.5)	414 (43.5)
	48	+	75	738	9.84	1.53	115 (15.8)	56 (48.7)
1994	153	-	846	7238	8.56	1.37	1162 (16.0)	591 (50.9)
	89	+	155	2185	14.10	2.01	312 (14.3)	182 (58.3)
1995	160	-	853	5769	6.76	0.70	595 (10.3)	326 (54.8)
	173	+	569	7544	13.26	1.27	721 (9.6)	390 (54.1)
1996	107	-	595	4010	6.74	1.01	603 (15.0)	294 (48.8)
	111	+	315	3599	11.43	1.45	457 (12.7)	249 (54.5)
1997	72	-	375	2189	5.84	1.15	430 (19.6)	175 (40.7)
	48	+	80	773	9.66	2.83	226 (29.2)	105 (46.5)
1998	52	-	344	1869	5.43	0.98	338 (18.1)	139 (41.1)
	40	+	65	678	10.43	2.46	160 (23.6)	80 (50.0)
1999	62	-	376	1704	4.53	0.86	322 (18.9)	157 (48.8)
	43	+	68	615	9.04	2.12	144 (23.4)	77 (53.5)
2000	45	-	222	881	3.97	0.65	144 (16.3)	65 (45.1)
	51	+	103	878	8.52	2.11	217 (24.7)	111 (51.1)
2001	37	-	187	829	4.43	0.65	121 (14.6)	49 (40.5)
	37	+	69	509	7.38	1.55	107 (21.0)	40 (37.4)
2002	36	-	151	699	4.63	0.99	150 (21.5)	44 (29.3)
	17	+	28	156	5.57	1.50	42 (27.0)	16 (38.1)
Total	1584		6606	50429	7.63	1.16	7648 (15.2)	3680 (48.1)

Table 2. Summary OPU-IVF results with problem cows with and without superstimulation.

Treatment	No. Donors	OPU Sessions	Oocytes	Oocytes/ Session	Embryos/ Session	Embryos (%)	Pregnancy Rates (%)
No-FSH	923	5075	32732	6.4	1.0	5140 (15.7)[a]	2371 (46.1)[a]
FSH	661	1531	17697	11.6	1.6	2508 (14.2)[b]	1309 (52.2)[b]

[a,b]Values with different superscripts in the same column differ ($P < 0.05$).

Table 3. Oocyte quality in OPU-IVF problem cows.

Treatment	Oocyte quality. No. (%)				
	A	B	C	D	E
No-FSH	295 (7.75)[a]	643 (17.0)[a]	1947 (51.1)[a]	601 (15.8)[a]	322 (8.4)[a]
FSH	360 (17.0)[b]	495 (23.3)[b]	885 (41.7)[b]	254 (12.0)[b]	128 (6.0)[b]

Grade A: many layers of cumulus cells, B: 3 to 4 layers of cumulus, C: 1 to 2 layers of cumulus, D: denuded, E: expanded cumulus.

[a,b]Values with different superscripts in the same column differ ($P < 0.05$).

Many factors influence the efficiency of IVF technology, but the main factors could be the status of the donor, oocyte quality and the technique used to culture the embryos from the zygote to blastocyst stage. Although there has been enormous progress in IVF since the beginning of its implementation in animal breeding, particular areas need to improve. These include improving the freezability of oocytes and embryos, minimizing the culture effect on calf size, improving oocyte quality, successful use of sexed semen, ICSI and preantral follicle culture.

Commercial Semen, Embryo and Fetus Sexing

The possibility of sex pre-selection always had sparked great interest among livestock producers and the cattle industry. Sexed semen could contribute to increasing the profitability desired by the dairy and beef industries through desired sex offspring production, thus taking advantage of specific marketing or commercial production demands (like herd replacement, herd expansion, or increasing the male sales to slaughter). The clearest examples could be the production of females for dairy or replacement and males for meat production. Other applications would be for cattle breeders and AI semen companies to test elite bulls on a small number of females (35). Several methods have been used to reach this objective which is presented in Table 4.The result and accuracy of most of these techniques are satisfactory, and according to the established objective, it is convenient to opt for a pre-selection (sexing semen or embryo) as opposed to post-selection (fetus) methods of sex. In the case of sexing embryos, the only method used routinely on a commercial scale is to biopsy embryos and amplify Y-chromosome-specific DNA using polymerase chain reaction. This method is effective for more than 90% of embryos and is > 95% accurate (81).

Table 4. Different methods of sexing.

Sexing	Method	References
Semen	DNA content	(3, 34, 40, 62, 79, 87)
Embryo	Biopsy and PCR, fluorescence in situ hybridization,	(9, 51, 78)
Fetus	Ultrasonography at 60-90 days of gestation	(14)

However, determination of embryo sex by PCR is inefficient. All embryos are biopsied, tested, and then approximately 50% of the undesired sex are discarded. Costs of donor board, superovulation and collection have to be carried by a small number of embryos. The determination of fetal gender can be identified at 55 – 90 days of gestation. While this provides management opportunities, it fails to alter the sex ratio unless one elects to terminate unwanted pregnancies. Such methods of altering the resulting sex ratio are both cumbersome and expensive.

A commercial embryo sexing program was initiated at Trans Ova Genetics with AB Technology methodology (Pullman, WA). The procedure takes 5 minutes to perform each embryo biopsy and 2 hours for the PCR process. With some embryos, primers Ampli-Y (Finnzymes, Finland) were used. The results between the years 1994 and 2002 are presented in Table 5.

Table 5. Trans Ova Genetics results of sexed embryos using embryo biopsy and PCR technique.

		Fresh	Frozen
No. biopsies		716	144
No. indeterminate tubes following PCR (%)	AB Technology primers	57/665 (8.6)	4 (2.8)
	Finnzymes primers	14/51 (27.4)	
No. transfers		389	67
Pregnancy rates (%)		184 (47.3)[a]	20 (29.8)[b]
Sex confirmations by ultrasound - Accuracy (%)	AB Technology primers	30/33 (91)	
	Finnzymes primers	10/15 (66.6)	

[a,b]Values with different superscripts in the same row differ ($P < 0.05$).

At present, one company (XY, Inc., Fort Collins, Colorado) has technology that has been documented to be successful in the separation of X and Y bearing spermatozoa. The sex pre-selection is based on identifying differences in DNA content between X- and Y-bearing sperm. The X chromosome contains about 4% more DNA in cattle and horses than the Y chromosome. The high-speed cell sorting machine employed can separate 6 million X or Y sperm per hour with 90% purity (40).

Sexed semen appears to be an interesting tool that can be implemented in AI, ET, and IVF programs. The results published currently indicate that AI of heifers results in a similar pregnancy rate (around 50%) between low (1-1.5 $x10^6$ sperm) and high dose (3 $x10^6$ sperm) units of frozen sexed semen deposited in the uterine body (79). Similar results were obtained by Goyaike in Argentina (10). In IVF, it is feasible to reach 18% - 26% of embryo development with frozen sexed semen (54, 56).

The commercial application for Artificial Insemination will depend on separation efficiency (cost), and resulting pregnancy rates. This application has the potential to revolutionize cattle breeding strategies in both beef and dairy. Presently, the efficiencies obtained with separated semen are on the verge of commercial application. At first glance, application of sexed semen technology would appear to fit well when coupled with embryo transfer programs. However, super-stimulated beef and dairy donors may fail to transport sperm efficiently to the site of fertilization in the oviduct. (76) This may delay the widespread application of sexed semen in commercial embryo transfer programs.

The commercial application of separated semen coupled with IVF appears to provide the most logical and first commercial application for separated semen. The inherent cost of separated sperm fits well into commercial IVF schemes, where small quantities of sperm are needed to achieve fertilization. The potential to separate frozen-thawed sperm would provide additional advantages to applications with IVF production of embryos.

Trans Ova Genetics is currently harvesting ovaries from Holstein cows. Oocytes are recovered and fertilized with X bearing, or female, sperm. The resulting embryos are then implanted into dairy cows. Improved conception rates, sustainable cross breeding, and approximately 90% heifer progeny are all potential value propositions.

Somatic Cell Cloning

Cloning is the colloquial term used to describe the process of somatic cell nuclear transfer (SCNT), and falls on a continuum of assisted reproductive technologies (ARTs) currently used in agriculture.

The most acclaimed example of animal cloning is, of course, the report by Wilmut et al. in 1997 (97), the first to demonstrate that cloning of adult mammals was possible. While animal cloning by nuclear transplantation is inefficient, the fact that cloned animals representing various species have not been produced by a number of different laboratory groups has spawned great interest in reproducing (cloning) specific genotypes (1, 12, 84, 94). Economics and genetic improvement are not always the sole purpose of cloning. Cattle may be cloned for show purposes, "insurance" purposes, and sentimental value.

Presently cloning applications are limited to high value bio-medical or seedstock production. In the future, cloning technology could play an important role in commercial beef and dairy production. Cloning could speed the dissemination of genetic progress generated in the nucleus population(s) to the commercial populations. Embryo cloning could have a large impact in dairy cattle. Instead of inseminating commercial cows with high-merit semen, embryos of the best available clone in the nucleus population could be used. Having been selected as the best of the clones being produced in the nucleus, the genetic merit will be greater than the average merit of the commercial population (14, 16, 17, 64, 100). Clones enable widespread exploitation of non-additive genetic effects, dominance and epistasis, both within and between breeds.

Using cloning in commercial farms to produce replacement animals reduces the percentage of cows that are required to produce replacement heifers. This advantage could also be captured by the use of sexed semen or embryos. The use of sexed semen or embryos also offers an opportunity for the farmer to reduce calving difficulties and thereby improve animal welfare. The remainder could be used for the production of animals for beef production or to gestate nucleus herd embryos (99).

The efficiency of cloning cattle by nuclear transplantation is extremely variable (94). The sources of variation which likely affect the outcome of nuclear transplantation include not only genotype, but the type of nuclei donor cell utilized, treatment of donor cells prior to nuclear transfer, and source of recipient ova. Dermal fibroblasts are the most common source for donor cells. These cells are easily harvested from either sex and cultured using standard tissue culture conditions.

In our facility, we have worked with various laboratories. In addition, cloning attempts have been made from unmodified fetal cells, genetically manipulated cells, second generation clonal lines, and unmodified adult cells. Attempts have also been made with endangered species where donor cells are fused with bovine cytoplasts.

Significant percentages of calves die within one week of birth due to various health problems. In our facility, 24% of cloned calves born failed to survive the first week. The leading causes of mortality include respiratory distress, birth defects, non-viable calves, and enteritis (Clostridium sp)

The commercial application of cloning in cattle is dependent on societal and regulatory acceptance, coupled with favorable cost vs. return economics.

Economics can be evaluated with the following parameters:

a. Cost of implementation
b. Genetic gain / Improved productivity
c. Uniformity of clones
d. Cost of cloning.

Certainly the primary driver in all assisted reproductive technology is economic return versus cost. With the extreme variability and relative inefficiency reported with cloning, its primary application was for bio-medical applications and for the elite agricultural animals. Bovine cloning holds great promise to be used in wide scale applications. This stems from the fact that cloned embryos can be made efficiently, and acceptable pregnancy rates are already being achieved. Pregnancy maintenance and calf livability are the major hurdles to widespread application of the technology (2, 27, 98).

Potential reduction of the cost in producing cloned animals can be divided into three primary areas: embryo production, gestation, and improved calf survival.

Cloned embryo production has essentially three cost drivers: output of volume produced, embryo development efficiency, and the number or percentage of embryos transferred.

Cloning Laboratories are expensive to equip and operate. Calculated cost can range from $100 to $200 per blastocyst. Production must forecast a conservative rate of development to assure an adequate number of embryos are available to implant into available recipients. This means that excess embryos are often created and wasted from days or cell lines where development rates are high.

The best way to reduce embryo cost per pregnancy would be to transfer one embryo per recipient. This would result in a 50% reduction in embryo cost, assuming comparable calving rates. The second best way to reduce costs would be to have consistent development so that output per fixed cost could be maximized. This could also result in a 50% reduction in cost. The third would be to improve blastocyst development rates. This potential would represent only a 5 to 10% reduction in cost.

Maintenance of large open recipient populations, embryo transfer, gestation, and calving contribute the majority of cost in producing cloned cattle. The majority of clones are presently harvested by caesarian section due to calf value and LOS.

While input costs will vary widely depending on geography, and resources, the basic physiology of estrus synchronization and gestation are relatively consistent around the world (Table 6). Table 7 is included to reveal calving rate as the primary driver in reducing the cost of producing cloned animals. Improved neonatal survival represents the second largest opportunity. Reduction in the cost of cloned embryo(s) that are implanted into recipients is also important.

Combinations of the above could significantly reduce the cost of clones, and allow for significant market penetration (Fig. 1).

Table 6. Cloning cost inputs.

Recipient Needs	
Pre Implant days	45
Implant to Preg. Check, days	45
Post Implant/calving, days	45
Total Head Days	135
Recipient Head Day Cost/day	$3.25
Gestation cost/day	$3.25
Total Head Day Cost	$438.75
Embryo Implant Cost	$50.00
Health Tests & Vaccines	$50.00
Synchronization	$14.00
Recipient Interest & Depreciation	$75.00
	$627.75
Cloned Embryo Cost	$102.58
C-Section cost % Recipient cow depreciation	$400.00

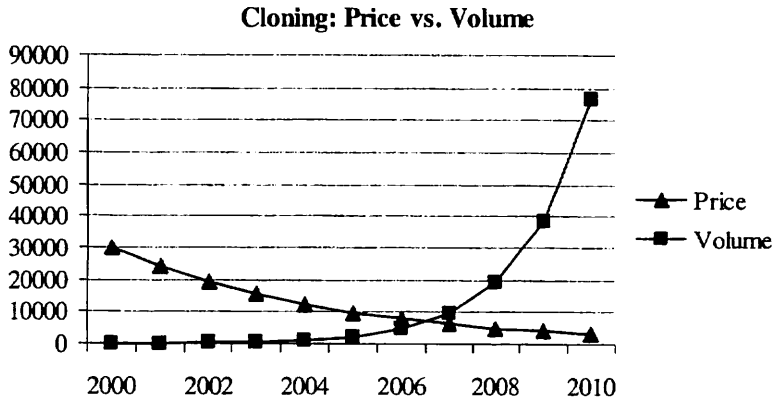

FIG. 1. Cost and marketing estimates of cloned cattle. (Trans Ova Genetics, 2002).

Table 7. Cost of producing a cloned calf.

Assumptions								
# embryos implanted/recipient	2							
40 days pregnancy rate		30%	35%	40%	45%	50%	55%	60%
% of 40 day pregnancies carried to term		25%	30%	35%	40%	45%	50%	55%
% calving rate		7.5%	10.5%	14%	18%	22.5%	27.5%	33%
% survival rate		50%	55%	60%	65%	70%	75%	80%
% live calves		3.75%	5.78%	8.4%	11.7%	15.75%	20.63%	24.6%
Cost per calf produced								
Recipient costs	$628	$16,740	$10,870	$7,473	$5,365	$3,986	$3,044	$2,378
Cloned embryo cost (2 embryos)	$205	$5,471	$3,552	$2,442	$1,753	$1,303	$995	$777
Gestation cost of pregnancy loss	$390	$1,560	$1,300	$1,114	$975	$867	$780	$709
Gestation cost of live born calves	$780	$1,560	$1,418	$1,300	$1,200	$1,114	$1,040	$975
C-section cost & recipient cow depreciation	$400	$800	$727	$667	$615	$571	$533	$500
Total Cost Cloned Calf		$26,131	$17,868	$12,996	$9,909	$7,841	$6,392	$5,339

Genetic Gain /Improved Productivity

Breed improvement is accomplished through two objectives. The first is the generation of genetic improvement by selecting animals based on their estimated breeding value (EBV). In most livestock improvement schemes, selection is based on breeding values that are estimated using "best linear unbiased prediction" (BLUP). BLUP utilizes the phenotypic information on all traits and relatives to predict the EBV.

Secondly, genetic superiority must be distributed from the nucleus to the commercial population. The nucleus animals usually represent a small fraction of the population. In pigs and poultry, closed nucleus schemes are generally used in which nucleus animals are kept on a small number of farms and only animals from these nucleus farms contribute to genetic improvement of the nucleus population. In beef and dairy cattle, nucleus animals are identified from open seed stock and commercial herds. These animals are used for artificial insemination and MOET programs for both current commercial production and generation of the next nucleus animals.

By the creation of large numbers of identical individuals, embryo cloning has the potential to greatly increase accuracy of selection. Each clonal line can be evaluated on the average phenotypic performance of many copies of itself. Cloning offers the opportunity to test candidates under different environments, to subject them to a disease challenge that would not ordinarily be applied in other breeding schemes, or to measure carcass and meat quality traits directly on selection candidates. Testing clones instead of half-sibs or full-sibs provides more information in these cases because the clones share Mendelian sampling (dominance and epistasis) with the selection candidate. Clones can be tested under various conditions. Conversely, modern agricultural producers would have the opportunity to manage, refine, and optimize the environment for specific clonal lines. This may allow for more uniformity than predicted by heritability of a particular trait (90). The use of crossbred clones in dairy cattle offers a unique opportunity to protect the breeding stock of individual companies, while producing the opportunity for a sustainable crossbred dairy cow strategy.

A key element in the dissemination of genetic material is the genetic lag, i.e. the difference in genetic merit between the nucleus and the commercial populations. Cloning can be used to improve the dissemination of genetic gain generated in the nucleus population to the commercial population. Van Vleck (90) and Villanueva and Simm (91) described that cloning could lead to the removal of one or two tiers in the pig breeding pyramid. van Arendonk and Bijma (88), for example, concluded that the main advantage of cloning is faster dissemination of superior genetics to commercial farmers using cloned embryos from desirable genotypes. In beef and dairy cattle, elite seedstock genetics could be rapidly distributed resulting in a short term genetic gain. Since beef and dairy cattle breeding has been an open system where genetics are sampled and selected from an open population, this "quick" gain could also improve the availability and accuracy of future selection candidates.

Uniformity of clones

Ideally, cloning individuals with outstanding performance would guarantee that all mates of the clone are genetically superior to other animals and that the clones would be uniform and predictable.

The usual, but perhaps incorrect, perception would be that an animal with a high record or other desirable attributes could be safely selected to be the origin of a family of clone mates. There is no sure way to identify superior animals except by testing many clone mates or by testing multiple progeny of a bull. The situation would also change when molecular information is available to assist in prediction of the phenotype.

Phenotype (P) equals Genotype (G) plus Environment (E). $P = G + E$.

For most traits, additive genetic variance accounts for 10 – 50% of total variance, a fraction denoted as heritability (h^2). (Table 8 and 9) Only if heritability is 100% will clone mates have complete uniformity. For example, with h^2 of .50, which is larger than for most traits, this measure of uniformity is only 30% better than for unrelated animals. If heritability is 25%, then the standard deviation among clones would be 87% of that of uncloned animals (90).

Table 8. Heritability estimates for Holsteins from the USDA-AIPL website (www.aipl.arsusda.gov).

Trait	*Heritability %*	*Trait*	*Heritability %*
Milk Yield	30	Feet & Legs	15
Productive Life	8.5	Daughter Pregnancy Rate	4
Somatic Cell Score	10	Direct Calving Ease	9
Size	40	Maternal Calving Ease	6
Udder	27		

Table 9. Heritability estimates for Angus cattle from the American Angus Association website (www.angus.org).

Trait	*Heritability %*	*Trait*	*Heritability %*
Birth weight	33	Scanning weight	57
Weaning direct	20	Intra muscular fat	31
Weaning (milk)	14	Rib eye Area	38
Post weaning gain	20	12-13th Rib Fat Thickness	39
Yearling height	50	Retail Product	39
Yearling weight	37	Scrotal circumference	43
Mature Height	87	Mature Weight	53
Carcass weight	30	% Retail product	25
Rib eye area	28	Marbling Score	36
Fat Thickness	25		

Currently, most cloned embryos are gestated by non-lactating beef cows. Low conception and calving rates coupled with dystocia associated with Large Offspring Syndrome (LOS), prohibit the use of lactating dairy cows as recipients (2).

However, cloning a genetically superior animal also could capture optimum dominance and epistatic genetic effects that are otherwise difficult to select for. Capturing this effect could allow producers to manage the environment to maximize agro-economic traits of the clones.

Societal Values and Regulatory Impact on Commercialization

Historically, most technology introductions have been met with some skepticism. The birth of Dolly has tended to polarize public opinion on the application of biotechnology in agriculture. In agriculture, Artificial Insemination was greeted with questions and concerns about the normality of the resulting calves. The birth of the first human baby by IVF created a lot of public debate on the morality and ethics of technology. Over twenty years have passed and 100,000 assisted reproductive technology babies have now been born.

Regarding agriculture, the ultimate test for most consumers is the level of assurance that can be credibly provided that the application of these technologies does not inversely impact food safety. These risks may be real or perceived. Our fellow researchers in transgenic plants have helped illustrate the consumer concerns.

Society is placing animal welfare as an increasingly important part of food production. The public and regulatory officials are increasingly seeking assurances and demands to

ensure that advances in biotechnology will not result in an increase in animal suffering (22, Table 8).

Environmental concerns included numbers or population density of specific genotypes, and the lack of genetic diversity. In addition, some species such as transgenic salmon must provide assurances that the escape of transgenic salmon will not upset indigenous feral populations and ecosystems. Livestock have an advantage in containment and trace ability when compared to plants and species such as fish. However, in many countries inadequate systems for cattle identification and traceability are in place to provide for conception to consumer tracking of product.

In the United States, the FDA commissioned the National Academy of Sciences (NAS) to identify and prioritize any safety concerns that bioengineered and cloned animals might present to food, animals and the environment.

After consulting with pioneers in the field of cloning and holding a public workshop, the NAS published its report entitled "Animal Biotechnology: Science-Based Concerns" in August 2002. According to the report, "there is no current evidence that food products derived from adult somatic cell clones or their progeny present a food safety concern." The report recommends collecting additional information about food composition to confirm that these food products are, in fact, safe. The NAS's job was to identify the potential risks of cloning. Now the FDA is studying those risks to determine how to manage them. The FDA is developing risk assessments describing the potential risks, if any, of consuming food products from animal clones and their offspring, and describing health risks to animal clones and their offspring. The FDA will use these assessments to develop an appropriate science-based regulatory approach, in the form of policy or guidance for industry, to manage any food and animal health risks.

Summary

Commercialization of bovine reproductive technology for food and bio-medical applications represents significant opportunities. Artificial insemination, embryo transfer, *in vitro* fertilization, cloning, transgenics, and genomics all are components of the tool box for present and future applications. Individually, these are powerful tools capable of providing significant improvements. However the greatest gain will come from the application of combinations of these technologies.

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Application of Transgenic Technology in Animal Agriculture

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Abstract

Significant advancements have been made in bovine transgenic technology in the past 20 years. Currently, it is possible to target genetic sequences into predetermined sites in the host DNA, to transfer independent microchromosomes with the capacity to carry hundreds of genes into the bovine genome and to sequentially introduce multiple genetic modifications into a single genome. The most likely first genetically modified cattle to be commercialized will likely produce human therapeutic proteins.

Development of Transgenic Technology for Cattle

Over 20 years ago transgenic mice were produced carrying extra genes for growth hormone. The work was published in Nature (Palmiter et al., 1982) and the cover of the magazine showed a comparison of the transgenic mice and their non transgenic litter mates. The transgenic mice were huge; twice the size of their litter mates. This image stimulated the imaginations of both the public and scientists and created a tremendous amount of speculation about the potential impact of transgenic technologies for agricultural animals. It was surmised that by inserting a single growth regulating gene into an animal of agricultural value that growth rate and feed efficiency could be greatly increased and fat deposition reduced; transforming the entire meat animal industry. Furthermore, many other applications; including, enhanced milk production, production of milk with novel properties, enhanced disease and parasite resistance and increased wool production were imagined. Since then there has been a slow, but relatively steady, effort to apply transgenic technologies to agricultural species.

Initially, technical limitations, cost and a lack of understanding about genes and their regulation severely limited progress, particularly in species such as the cow. Up until 1998, transgenic animals were made by microinjection of a few thousand copies of a genetic sequence into one of the pronuclei in a newly fertilized zygote. And in the early 1980's, when transgenic technologies were first developed in the mouse, the only source of newly fertilized bovine zygotes was a superovulated cow. Zygotes had either to be recovered surgically or after slaughter from hormone treated animals. The donor cow could only be used once and yield of useable embryos was low (2 to 4 per cow) because of the precise timing required to obtain the optimal stage of embryo for microinjection. Development of microinjected pronuclear embryos was generally low, so transfer directly back into recipient cows was considered impractical. Also, in vitro culture systems were not well refined; consequently, embryos were transferred into the oviduct of surrogate sheep for development to the blastocyst stage at day 7, then recovered and transferred, non surgically, into recipient cows. Production of a single transgenic calf required microinjection of over 1,000 embryos, supplied by 300 to 500 donor cows, and transfer of embryos into 150 recipients. Finally, when the offspring were born most would not be transgenic and those that did carry a copy of the exogenous gene often didn't express the gene or didn't pass it on to its offspring (reviewed by Pinkert and Murray, 1999). As one would expect, progress in making transgenic cows was minimal with these significant limitations.

By the late 1980's, oocyte in vitro maturation and fertilization systems were sufficiently well developed so that embryos could be obtained by fertilizing oocytes recovered from ovaries of random slaughtered cows. Furthermore, in vitro culture systems could finally be used to grow embryos for the 7 days necessary to produce blastocysts that could be transferred, non surgically, into recipient cows and develop at a reasonable rate into calves. In many laboratories around the world, in vitro produced embryos support calving rates well above 50%. These breakthroughs enabled researchers to produce, microinject and culture thousands of embryos at very low cost. Even with the damage caused by microinjection, transgenic calves can now be made with relative ease and at moderate expense. One study reports the microinjection of over 36,000 in vitro produced zygotes (Eyestone, 1999).

In spite of progress in technologies for making large numbers of inexpensive cow embryos the DNA microinjection system had several significant limitations. Integration of the transgene into the host DNA is random with microinjection and can result in detrimental mutations and variations in gene expression levels. Only a small percentage of calves born will actually be transgenic. Of those that are transgenic, the transgene may not be in the germ cells and, therefore, not transmitted to offspring. Finally, no two founder transgenic animals have the gene inserted into the same place, consequently, animals, homozygous for the transgene, can only be made by crossing offspring from a single founder animal. For the cow, production of a homozygous line from a single founder would require about 5 years.

The next breakthrough in bovine transgenic technology occurred with the discovery that somatic cell nuclei could support full term development of cloned calves (Cibelli et

al., 1998). The process of somatic cell cloning involves replacing the DNA in an unfertilized oocyte with DNA from a somatic (body) cell. The oocyte has the ability to reprogram the somatic cell DNA so that the unfertilized oocyte can develop as an embryo and, in some cases, give rise to healthy calves which have DNA that is entirely from the somatic cell. Because it is possible to obtain an unlimited number of genetically identical somatic cells from an animal, cloning is a technology that can be used for producing genetically identical calves. However, the somatic cell can also be genetically manipulated prior to being introduced into the oocyte, so cloning is also a convenient method of making transgenic cattle. Using cloning technologies, only about 10 to 15 recipients are needed to make transgenic calves, consequently, the cost of making transgenic cattle is substantially reduced.

A recent advancement in cattle transgenic technology is gene targeting. In all transgenic work with agricultural species that has been done up until the past couple of years, genes were inserted randomly into the host DNA by pronuclear microinjection. In the last couple of years a robust method for gene targeting in cattle, using somatic cell cloning technology, has been developed. Gene targeting is the insertion of a transgene, or any exogenous DNA sequence, into a specific, targeted site in the host DNA. The technique is more complex than random gene insertion but gene targeting is a much more powerful technology because it can be used to inactivate genes, insert new genes into predetermined sites or replace one variation of a gene with another variation. It overcomes many of the limitations of random gene insertion by microinjection. Because the insertion site is predetermined, a series of transgenic founder animals can be made, including both males and females, which can be mated to make homozygous offspring. An even simpler approach to making homozygous transgenic animals is to sequentially insert a copy of the transgene into one member of a pair of chromosomes and then insert a second copy into the other chromosome without germ line transmission of the transgene. To accomplish sequential gene targeting we have developed a rejuvenation system for bovine fibroblast cells. The system involves making a genetic modification in a fibroblast cell line established from a bovine fetus. Because the cells only grow for a limited number of cell divisions in culture only one genetic modification can be made before the cells become senescent and stop dividing. The cells are then used in a cloning procedure to produce cloned fetuses. Young healthy cell lines can then be made from the fetuses and used for a second round of genetic modification. When the genetic modifications are complete then the final fetal cell line can be used for making calves. Sequential gene targeting has been accomplished in our laboratory recently and homozygous transgenic calves have been produced (unpublished observations).

A second advancement in cattle transgenics, which has been accomplished recently, is microchromosome transfer (Kuroiwa et al., 2002). A microchromosome is different from a typical transgene in a couple of characteristics. First, a typical transgene consists of a couple of gene sequences and may be up to 25,000 DNA bases long; whereas, a microchromosome typically consists of millions of DNA bases and can contain either very long genes or potentially hundreds of genes. Second, a typical transgene must integrate into the host DNA, either randomly or targeted to a specific sequence, to be carried along through cell division. Microchromosomes do not integrate but replicate on their own and are carried along during cell division as independent chromosomes. We have been successful in inserting a human-derived microchromosome into cattle. A microchromosome was needed because our objective was to transfer the human antibody genes into cows. Antibody genes are very complex and are up to several million DNA bases long; well beyond the capacity of a typical transgenic vector. The microchromosome is stable in cattle and appears to have no harmful effects on the animals.

In the 20 years since production of the first transgenic mice, work in cattle has focused primarily on technology development. At this time, many technical hurdles for application of transgenic technology to cattle have been overcome. In fact, transgenic technologies for the cow are now comparable to that of the mouse. The question now is, what are the challenges facing us in the next 20 years and will transgenic technologies be moved into commercial application? Two kinds of applications for transgenic technology in cattle are being pursued. One involves genetic modifications that are aimed at improving the efficiency of food (meat or milk) production. The second is for the production of novel products; such as pharmaceutical proteins for human health care.

Transgenic Cattle for Food Production

Of the few research reports describing the use of transgenic technologies in cattle only one is directed towards a food production application. Brophy et al., (2003) introduced additional copies of bovine beta or kappa casein into dairy cattle and evaluated the effect on milk production and composition. Transgenic offspring had an 8 to 20% increase in beta casein and a two-fold increase in kappa casein. In swine several attempts have been made at improving growth and composition by the addition of transgenes. In one study expression of an exogenous insulin-like growth factor gene in the muscle of pigs resulted in significant reduction in fat and an increase in lean muscle in gilts but not boars (Pursel et al., 1999). In another study, a widely expressed exogenous growth hormone gene tended to increase live weight gain, improve feed efficiency and reduce back fat thickness (Nottle et al. 1999). Although these studies demonstrate the feasibility of improving food production efficiency with transgenics, no attempts have been made to commercialize any transgenic food producing animals.

In addition to technology, there are several factors that will impact the use of transgenic cattle for food production. The first involves regulatory approval of meat or milk from genetically modified cattle. The federal agencies regulating genetically modified animals must address three factors; 1.) safety of the food product for human consumption, 2.) environmental impact of the genetically modified animals and 3.) welfare of the animals. Conceptually, many of the modifications that might be considered to enhance production efficiency would not have any impact on the safety or quality of the food product. Since there are no wild bovine species, the transmission of modified genes into wild species is not a concern with cattle as it is with genetically modified plants, therefore, it is unlikely that genetically modified cattle would have a significant impact on the environment. The welfare of the animal could be a concern with some genetic modifications but could be easily evaluated. Overall, the factors that are of concern to the federal regulatory agencies regarding genetically modified cattle could be scientifically addressed. However, obtaining approval for the first genetically modified animal food product is not likely to be straightforward due to the controversial nature of genetically modified food products.

The second factor to consider is the type of business model that would result in a financially successful commercialization effort for the modified genetics. A general lack of integration of the production chain in the beef industry would limit the kinds of genetic modifications that would be commercially viable. It is unlikely that a trait that might benefit the retailer would be adopted by the cow calf producer if the trait is not easily identified or if the financial benefit derived by the retailer is not shared with all components of the beef production chain. The most likely trait to be adopted would be one that produces an easily observed benefit for the cow calf producer since it is the cow calf producer that would make the decision about adopt the improved genetics.

The business model would also have to take into account whether the trait is dominant, additive or recessive. The value of a dominant trait would be observed in heterozygous offspring and therefore, could be passed on to all calves by a homozygous bull mated to non transgenic cows. A recessive trait, however, would require both parents to have homozygous genetic modifications for the trait to be observed in the offspring. The value of an additive trait would also depend on the zygosity of the parents.

The genetics of transgenes can be complex, particularly if the transgene is randomly integrated into the host DNA. To determine if the transgene disrupted any endogenous genes would require breeding a line to homozygosity and evaluating the animals in detail for a possible deleterious effect of the mutation. Breeding from a single animal is not ideal because of the inevitable inbreeding that would result. Furthermore, breeding a population from a single animal would reduce selection progress for other traits. A better strategy would be to use gene targeting to ensure that the transgene does not cause a deleterious mutation. Gene targeting could be used to make homozygous animals without breeding and additional animals could be made with the same genetic modification at any time to add to the population.

Transgenic Cattle for Human Therapeutic Production

A second application for genetically modified cattle is the production of human therapeutic proteins. Human proteins that have been expressed in milk include human lactoferrin (van Berkel et al., 2002), human alpha lactalbumin (Eyestone, 1999), human serum albumin (Behoodi et al., 2001) and human bile salt stimulated lipase (Chen et al., 2002). The mammary gland in dairy cows is an excellent protein production factory. Large quantities of very complex proteins can be produced and collected at very low cost.

In our laboratory we are using microchromosome transfer and gene targeting technologies to develop a line of genetically modified cows that produce human polyclonal antibodies. A microchromosome transfer system is used to introduce the human antibody genes into cows. A microchromosome system is necessary because the human antibody genes are very large (millions of DNA bases) and very complex and two different gene products are needed to make an antibody molecule. To get rid of contaminating bovine antibody the bovine antibody genes are targeted with a knock out sequence to prevent expression.

Antibodies are currently used for many different human clinical applications; including treatment of infectious disease, cancer, transplanted organ rejection, autoimmune diseases and for use as antitoxins. To make a human antibody product the genetically modified cows are immunized with a vaccine containing the disease agent. For example, a product could be made for treatment of Staphlococcus aureus infections acquired following hospitalization by immunizing the genetically modified cow with the Staphlococcus aureus bacterium. Following immunization the cows builds up an antibody response to the bacterium. To harvest the antibodies from the cows blood plasma is collected using a procedure that is similar to collecting plasma from human donors. The plasma is then processed to remove all contaminating bovine components so the final product is a human antibody that reacts to Staphlococcus aureus which can be injected into hospital patients to help them fight an infection.

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DNA Testing and Marker Assisted Selection

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Introduction

Beef cattle breeders have heard for years that DNA testing is coming and that it will change the way they breed cattle. At long last, the time is here when DNA testing for economic traits is available, albeit in a very immature form. Breeders must decide whether to use the technology, and if so, how to use it. Breed associations must decide what role they will play in the adoption of this technology.

DNA testing has a number of potential applications in cattle breeding, including parentage testing, tests for genetic diseases or defects, and tests for qualitatively inherited traits such as color or horns. However, most economically important production and end-product traits are influenced by several or many genes. The individual genes that influence such traits are known as quantitative trait loci (QTL). The identity of these genes may be known, but in many cases only the general location of the QTL on a chromosome is known. This presentation will focus on tests for quantitative traits.

Benefits of DNA Testing

DNA testing can make evaluations available shortly after birth, or even at the embryo stage. This is an important advantage for traits that can only be measured after the age at which selection decisions are normally made (or postmortem).

It should provide greater information from each phenotype that is measured. This is especially important for traits that are expensive to measure or sex-limited.

It should provide greater opportunity to select for traits with antagonistic genetic relationships (e.g., birth weight and growth rate).

Current Status of DNA Testing in Beef Cattle

As recently as four years ago, there were no commercial DNA tests for quantitative traits in beef cattle, but today there are at least seven companies performing or marketing such tests. The tests currently available include at least the following:

- GeneStar Marbling (thyroglobulin) – Genetic Solutions/Bovigen
- GeneStar Tenderness 2 (calpastatin and 1 SNP in μ-calpain) – Genetic Solutions/Bovigen
- TenderGENE (2 SNP in μ-calpain) – Frontier Beef Systems/GeneSeek
- IGENITY L (leptin) – Merial/Quantum Genetics
- MMIG Mu-Calpain Tender (2 SNP in μ-calpain) – MMI Genomics

The names of the genes upon which these tests are based are listed in parentheses, followed by the name of the company that markets and(or) performs the test. Single nucleotide polymorphisms (SNP) are locations in the genome at which differences in sequence occur. Mention of trade names or commercial products in this article is solely for the purpose of providing specific information and does not imply recommendation or endorsement by the U.S. Department of Agriculture. A description of most of the above tests (by the company marketing each of them) is provided in the proceedings of the Genetic Prediction Workshop held in December, 2003. Those proceedings are available online at:
http://www.beefimprovement.org/gp_proceedings.pdf.
Hopefully, the list of commercial DNA tests will continue to grow rapidly. A list of available tests is maintained by Alison Van Eenennaam (University of California, Davis) at http://animalscience.ucdavis.edu/animalbiotech/Biotechnology/MAS/index.htm.

Most of the current DNA tests are offered by only one testing company. It is anticipated that a greater number of non-proprietary tests will be offered by multiple companies in the future. Nonetheless, breeders that wish to evaluate their cattle as thoroughly as possible must currently send samples to several DNA service labs and this situation is expected to continue. Other breeders will seek to use one company that offers the best (albeit not complete) suite of tests relative to price. In any case, breeders need independent information with which to make decisions about their use of DNA tests.

Independent Characterization of DNA Tests

Considerable information about a DNA test is required in order to decide whether to use it or not. Some of the required information may seem technical, but breeders are becoming more familiar with it as they gain experience using DNA tests.

Some of the information required to decide whether or not to use a DNA test could only be provided by the company that is providing the testing service. However, other information can be provided by an independent institution using standard resource populations with phenotypes for the desired traits in cooperation with the testing company. This is currently being done through the

National Beef Cattle Evaluation Consortium (NBCEC). The NBCEC provides DNA to the testing company, which runs the test on the DNA and sends the test results back to the NBCEC. The NBCEC then analyzes the data and reports the results publicly.

Ideally, the reports will include not only information on the individual test, but also its interactions with other DNA tests. This is important both for selecting tests and for inclusion of the results in National Cattle Evaluation (NCE).

Independent characterization of commercialized DNA tests provides better information from which to decide which tests to include in NCE. Furthermore, it should enable DNA testing companies to market tests more effectively and with greater confidence. The process also generates information (such as the effect of the test) that is needed in order for DNA testing data to be included in NCE.

Successful implementation of independent characterization requires the cooperation of a number of groups. Breed associations, independent ranching operations, and/or research institutions need to provide DNA and phenotypes on appropriate groups of animals. The DNA testing companies need to provide the testing services. A research institution needs to conduct the data analysis. Finally, none of this is likely to happen regularly unless the breeders provide motivation and encouragement for it. Breeders should recognize that it is important for this information (even the more technical aspects of it) to be available, because much of it will be necessary in order to include DNA test data in NCE.

Guidelines for Use of DNA Testing

It would help if the information provided by the independent characterization process was presented in a standard format so that comparable information was available for each DNA test. The format for this "label" could be included in the BIF Guidelines.

A subcommittee of the Emerging Technologies committee has been formed to write a section of the BIF Guidelines dealing with DNA testing. The guidelines are likely to cover a wide range of topics including terminology, independent characterization, which animals should be tested, collection/storage of tissues, reporting of results, the role of breed associations in the process, inclusion of the results in NCE, and most importantly, use of the information by breeders.

Traits Emphasized in DNA Testing

All of the DNA tests listed above are associated primarily with meat quality traits. There are undoubtedly tests related to carcass composition in the development pipeline. For good reason, most interest in DNA testing is focused on traits that are difficult or expensive to measure; EPDs are very effective for traits that are routinely measured prior to selection.

Considerable efforts are underway to develop tests related to feed efficiency, reproductive efficiency, and disease resistance. Such tests are challenging to develop, for exactly the same reasons that they are difficult to improve using conventional means. DNA testing is probably our best hope for improving such traits, but it should not be expected to happen immediately.

We are all learning together about the application of DNA testing to cattle breeding. One of the big challenges is that phenotypes are scarce for the primary traits influenced by currently available tests. This makes it impractical to do large-scale evaluations from field data of the performance of the tests or to address questions such as whether the tests perform the same in all breeds or whether some tests need to be enhanced in order to describe genetic variation that exists in certain lines of cattle.

A potential benefit of DNA testing, which has perhaps received too little emphasis, is selection for sets of traits that have antagonistic genetic relationships. Perhaps we should put some emphasis on developing and using DNA tests for genes that influence growth rate without changing birth weight. Those phenotypes are readily available and that is an important, but somewhat challenging objective of current breeding programs. We would almost certainly learn a great deal about fundamental aspects of DNA testing in beef cattle that could be applied to DNA tests for traits with fewer phenotypes.

It is unfortunate that DNA tests tend to be labeled as influencing one particular trait. This reinforces the common misconception that there is a one-to-one relationship between genes and traits. Quantitative traits (which include most economically important traits in cattle) are, by definition, influenced by at least several genes and most genes influence a variety of traits. The later is a cause of genetic correlations and large volumes of data supporting the existence of these have been amassed.

How Should Breeders Use Information from DNA Testing?

The availability of DNA testing will bring, along with all of the advantages, misuse of information, especially in the early years when only a few DNA tests are available. We have heard much discussion of the evils of "Single-Trait Selection." Breeders must now face the temptation of "Single-Gene Selection," which may have far greater consequences.

For example, a bull with one of the top EPDs in his breed for a trait, had the least desirable, but most common, genotype (test result) for a DNA test for one of the genes affecting the trait. Semen sales on this bull dropped off sharply following the release of the test result. Apparently, breeders decided that they could not use bulls with the less

favorable allele (form) of this gene, a prime example of "single-gene selection." This is understandable, but is not good use of DNA test information for several reasons:

- Applying this much selection pressure to one gene, greatly reduces the selection intensity that can be applied to the other genes that affect this trait and others, especially when the frequency of the desirable allele is low. Selection is more efficient when applied to all genes simultaneously, in proportion to the size of effects of the genes and the relative economic importance of the traits.
- Few animals have two copies of the desired allele. Restricting the choice of herd sires to only those with the desired genotype of the "single gene" would put the breed through a bottleneck that would reduce the effective population size and increase inbreeding. When tests for more genes become available, very few animals will have the desired genotype at each of ten, or perhaps even 100, genes that we might test for.
- Given that the bull's EPD is very high in accuracy (presumably due to numerous progeny with phenotypes), a DNA test result should not greatly influence our estimate of his overall genetic merit for the trait. This may sound counterintuitive, but it is an important point. His EPD estimates his total genetic merit at all genes that influence the trait. The DNA test predicts his genetic merit at one of those genes. Therefore, an unfavorable DNA test result should be interpreted to mean that he is probably even better at the other genes affecting the trait than we would have guessed without the DNA test. Consequently, our estimate of the high accuracy bull's breeding value is not influenced much by his DNA test. The DNA test does suggest that we might want to breed the bull's daughters to sires with the desired genotype. DNA testing is most useful for individuals that would otherwise have low accuracy genetic evaluations. There is little opportunity for change in the evaluation of an animal with a high accuracy EPD.

In summary, DNA tests should not be used as all-or-none selection criteria, but rather should be used as one of several sources of information upon which selection is based.

Use of DNA Test Results in National Cattle Evaluation

For the foreseeable future, DNA tests will only account for some of the genetics of any trait; we will still need EPDs. One vision of the future is illustrated in Figure 1, where phenotypes and DNA tests on the individual and its relatives are combined, through NCE, to produce marker-adjusted EPDs, upon which selection decisions can be made. The methods used in NCE will have to be enhanced to accommodate DNA testing.

At recent BIF meetings, there has been considerable discussion of the optimum allocation of selection pressure to the various traits that are evaluated. The problem can be partitioned into a biological component and an economic component. The economic component involves determining the relative economic value of each economically relevant trait (ERT), which is usually done by modeling the relationships between the ERT and some measure of profit for a particular set of circumstances. The biological

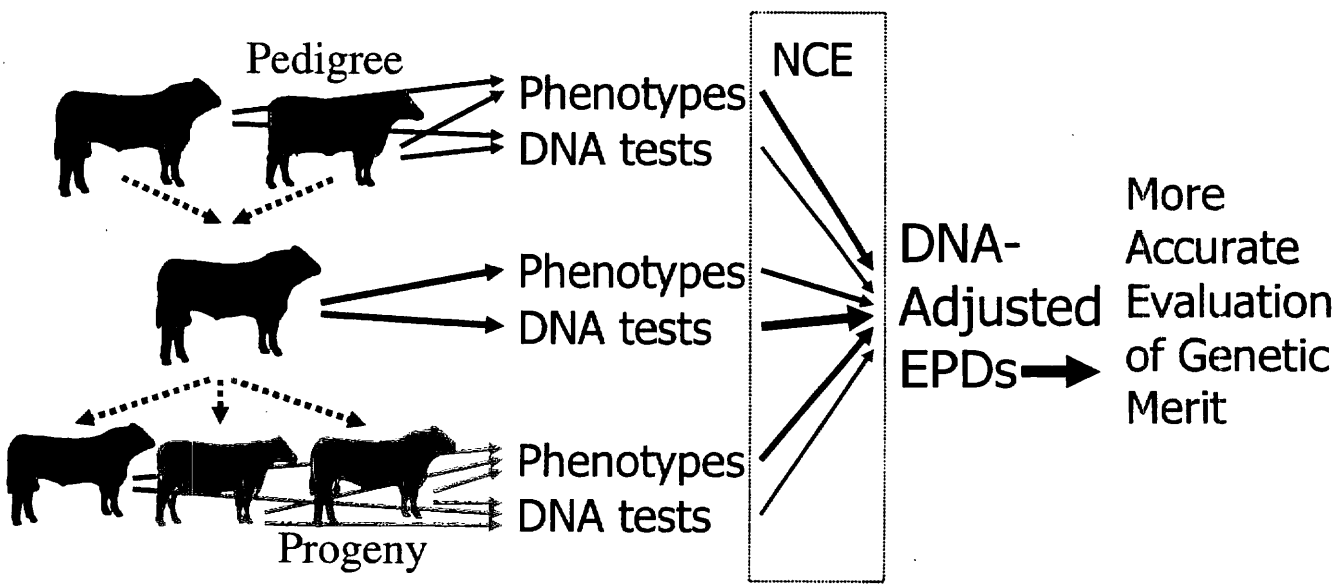

Figure 1. A Vision of NCE in the Future

component involves estimating the genetic relationships between the indicator traits (those that are actually measured) and the ERT (the traits we would ideally measure, if it were practical to do so).

If DNA testing technology is successful, there will be too many tests available for breeders to make breeding decisions based on raw test results. The relative emphasis on each gene will need to be weighted by its effect and the relative importance of the trait(s). Most DNA tests will be related to several traits. This adds a new dimension to the problem of allocating selection pressure. The biological component of the allocation problem is expanded to include relationships among DNA test results, as well as, indicator traits and ERT. Fortunately, the DNA test results do not need to enter into the economic component, which is sufficiently complicated without them. Therefore, inclusion of DNA test results in the NCE process should be an effective means to put the appropriate degree of emphasis on each DNA test.

It has been suggested that EPDs could be externally adjusted for DNA tests by simply adding or subtracting fixed amounts to or from the EPDs, depending on the DNA test results. This approach, referred to as the "myth of additivity," is illustrated in Figure 2. However, DNA test results affect low accuracy EPDs much more than they do high accuracy EPDs; therefore, the adjustment factors would have to be "shrunk" by an amount depending on the accuracy of the EPD to be adjusted. Furthermore, DNA test results affect the evaluation of progeny of heterozygous (have two different forms of a gene) parents more than they do the progeny of homozygous (have two identical copies of a gene) parents. Therefore, any "adjustment factors" that might be developed for DNA tests would not be generally applicable and would make the process of using DNA test results unnecessarily complicated. Simultaneous analysis of DNA test results and phenotypes, resulting in "DNA-adjusted EPDs" as illustrated in Figure 1, will be the most effective means to include DNA test results in the NCE process. This will not happen overnight, but it is an objective of the National Beef Cattle Evaluation Consortium.

Which Animals Should be Tested?

When a breeder or breed association decides to begin using a DNA test, the next logical question is "which animals?" A good place to start is usually the influential sires in the herd or breed. This will allow the frequencies of the various test alleles in the population to be estimated and also provides the most information about which untested animals are most likely to have the desired allele. For sires that have either no EPDs or low accuracy EPDs for the traits associated with the DNA test, the test will provide some information about the genetic merit of sires for those traits. For sires that have high accuracy EPDs for the traits associated with the test, the test results should have little influence on the evaluation of genetic merit of the sires, but could be used to validate or estimate the effect of the test within the breed of interest.

The next set of animals to consider testing would be herd sire and donor prospects. Selection among these candidates has a large effect on genetic progress, but they typically have lower accuracy EPDs, especially for traits that require progeny testing or that are measured later in life. Therefore, the improved accuracy of evaluation that DNA testing could provide could be very beneficial. However, it is important that the DNA test results be used only to influence decisions among animals that would otherwise be

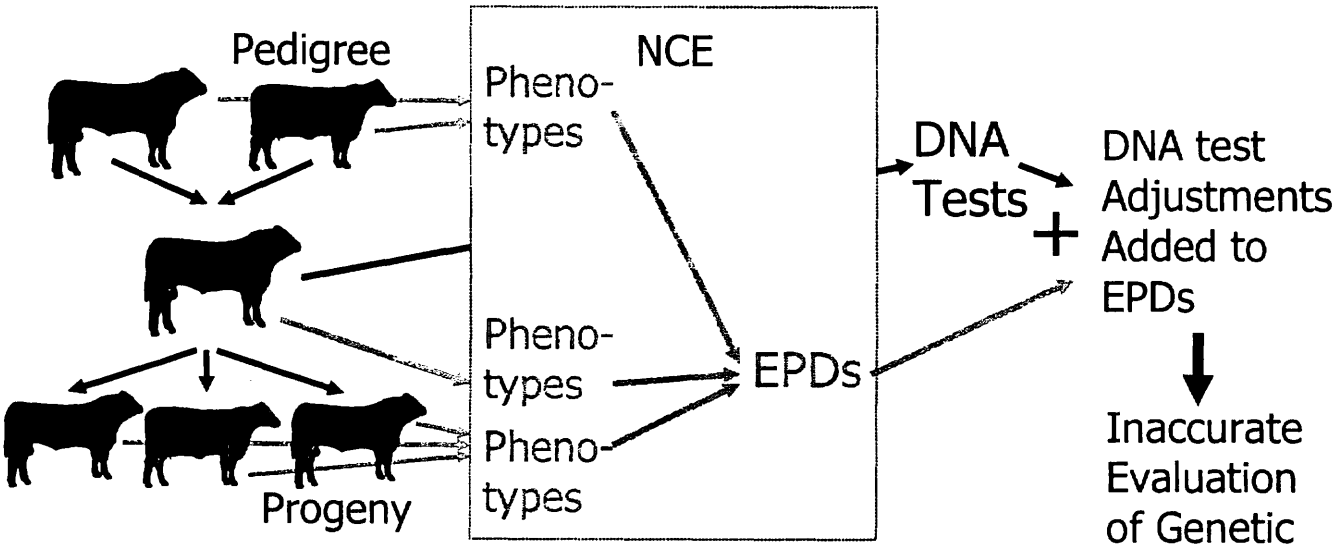

Figure 2. The Myth of Additivity

candidates for selection. The DNA test results should not be used as any kind of "litmus test" that animals must pass before being considered further.

A natural extension to testing herd sire and donor prospects could be testing all candidates to become replacement females, but this would involve testing considerably more animals. In some situations, it might be beneficial to test some or all of the bulls offered for sale. The ideal situation is that it would become cost-effective to test all of the calves produced. How far down this priority list breeders can afford to go will depend on the cost of testing. The cost of testing should decrease as the number of animals tested goes up, but the number tested may not increase sufficiently until the cost goes down. It is likely to require a coordinated effort from testing laboratories, breeders, and breed associations to move beyond this impasse.

Strategies for selecting animals to test also depend of the frequency of the favorable allele. Tests with a high frequency of the favorable allele have the desirable property that breeders will like the results that they get most of the time. However, tests with a low frequency of the favorable allele actually offer greater opportunity for genetic improvement. Breeders must test more animals to find one with the result they are looking for, but the very fact that they are rare can add considerable value to those animals that do have two copies of the desired allele.

For tests with a low frequency of the favorable allele, a reasonable testing strategy may be to first screen influential sires, and then to test descendants of those sires that have at least one copy of the desired allele.

What Should the Role of Breed Associations Be?

Breed associations can play an important role in encouraging the flow of DNA testing information into NCE and reporting the resulting DNA-adjusted EPDs back to the breeders. They will need to provide education on how to use this technology effectively and on how not to misuse it.

Selective reporting of DNA test data is likely to be a much greater problem for NCE than selective reporting of phenotypes is. Therefore, it would help greatly if the breed associations required that all DNA test data be submitted directly to them for use in NCE. However, this would require the cooperation of the DNA testing companies and it might decrease the submission of test data to NCE. As testing companies begin to offer "panels" of tests, breed associations should consider policies that, if one test in a panel is reported, all tests in the panel must be reported.

Breed associations may also participate in negotiating contracts for DNA testing and storage to protect the interests of their members. For example, who owns DNA or tissue that is left over after a DNA test is performed? What happens to stored tissue samples if the testing and(or) storage company goes out of business?

It is inevitable that breed associations will have to deal with contradictory results (sometimes referred to as "non-Mendelian inheritances") of DNA tests between close relatives. Some simple examples are when a parent and offspring do not share an allele in common (e.g., parent is GG and offspring is CC) or when an offspring has an allele that neither of its parents have (both parents are GG and offspring is CG). These situations could be due to pedigree errors, errors in the genetic test results, sample labeling errors, or mutations. If there are only one or a few markers in common between the individuals, it will be difficult or impossible to distinguish between these alternatives.

When contradictory DNA test results occur, the best solution is to run a parentage panel on the individuals involved to determine whether the pedigree is correct. If the pedigree is correct, then it may be appropriate to retest (from new tissue samples) one or more of the animals involved in the non-Mendelian inheritance and/or relatives of those animals.

Sample misidentification is a problem that breed associations will have to deal with. Some cases will be detected through non-Mendelian inheritances and some will be detected through samples for the same animal being submitted to multiple testing companies that run some tests in common. Some cases will be detected as a result of multiple entities submitting samples for the same animal. It is possible that semen samples may be submitted for testing by entities that have no ownership in the bull.

Some breed associations have programs in which animals are randomly sampled for parentage verification. Such programs could be expanded to include tests for quantitative traits. Random re-sampling of animals for which DNA test results had previously been submitted could also be contemplated. Statistical methods to identify likely errors in pedigree (beyond exclusions) and in DNA test results are available. Sampling programs could involve testing of individuals (or their relatives) that are most likely to be in error (either pedigree or sample identity).

It should be possible to develop methods to identify instances in which selective reporting of DNA tests is likely to have occurred. Semi-random testing in such instances could be an effective means of mitigating the impact of selective reporting on NCE.

Increased use of DNA testing will provide increased opportunities for breed associations to be proactive in protecting the integrity of the data they record, but a number of new issues will need to be considered.

The data processing requirements for DNA testing data are likely to be substantial enough that it may not be practical for each association to expand its data processing software to handle such data. Instead, it may be more efficient for the breeds to work together to jointly contract out the data processing to one, or at most a few, organizations.

It may be beneficial for breed associations to collect sets of DNA on the most influential sires in the breed and fund DNA testing on those sires.

Breed associations should also ensure that DNA is collected and stored from animals in future progeny testing projects so that they can serve as resources to tie DNA test data to phenotypes so that DNA tests can be characterized within individual breeds and test effects can be estimated directly in NCE. The National Cattlemen's Beef Association Carcass Merit Project is a great start, but to be most effective, it should be followed up periodically with more current sires.

Expectations for the Future of DNA Testing

In the short run, DNA testing should not be expected to simplify cattle breeding. Selection decisions will be based on more pieces and types of information and breeders will have to decide which tests to run and which animals to test.

There is a common misperception that DNA tests will eliminate the need for phenotypes, especially for traits like tenderness that are expensive to measure. However, phenotypes will continue to be important. Although DNA testing can increase the amount of information that each phenotype contributes and thus reduce the number of phenotypes needed, DNA testing can not completely replace phenotypic data.

New tests will continue to be developed for the foreseeable future. DNA tests should not be considered absolute or unchangeable. They should be expected to improve over time, just as EPDs have improved over time and will continue to improve.

We should assume that the cost per test will decrease over time due to improvements in technology and to greatly increased volume of DNA testing. Eventually, it should not cost much more to run a battery of many tests per animal than to run only one test per animal.

Conclusions

It will be a challenge for the beef industry to develop systems through which DNA testing data are shared sufficiently to allow their inclusion in NCE so that they can be used appropriately in selection decisions. This will require a direct benefit to whoever has to pay for the testing. However, it seems unlikely that the beef industry will be able to maintain market share over the long term without fully utilizing the information that can be provided by DNA testing. There are more challenges in using DNA testing effectively in beef cattle than in some other food species. Nonetheless, cattle breeders are making strides in implementing DNA testing and are making changes in traits, such as tenderness, that have been difficult to select for in the past. Undoubtedly, the way in which DNA testing is used by the beef industry will change over time, but the early adopters of the technology are likely to be in a better position to capitalize on that change.

Multiple-Trait Selection in a Single-Gene World

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Introduction

Sequencing of the bovine genome and the ongoing process of discovery of associations between observable DNA sequence variants and animal performance will be one of the great endeavors of 21st Century cattle breeding. Despite our knowledge, hopes, and dreams, the specific path this developmental effort will take remains largely terra incognita. However, we can make a few informed predictions about some things that probably will occur:

- We will find (and indeed have found) DNA sequence variants that influence, and occasionally control, traits of economic importance;
- We will continue to record performance data and calculate EPDs much as we do today. Performance recording to identify outstanding candidates for selection, and progeny testing of sires, will continue;
- In the future, EPDs will be derived from a combination of performance records and DNA sequence information to provide better genetic predictions, although the precise nature of the predictors and the relative importance of DNA markers are not yet clear.
- The capacity to screen large numbers of animals for substantial numbers of genes (e.g., 10 to 100) in a single assay will emerge, but issues of cost and potential impact remain.

The challenge we face is how to begin to utilize genetic markers with a minimum of wasted effort, without losing useful genetic resources along the way, and in a way that permits the industry and its customers to all reap appropriate benefits. Mature technologies, like BLUP, that we have come to rely on will require a make-over, and the BIF guidelines are going to start getting thicker again. There will be arguments, lies, damn lies, and statistics. It's going to be a great time to be in the cattle business!

Genetic Markers—What Are the Options?

This is hardly a crystal ball. In fact, it is more like a future seen through a glass darkly. However, some types of DNA markers do seem to be emerging as potentially more useful than others for the beef industry. At any rate, we need to become comfortable with the different sorts of markers and be able to recognize their pros and cons. We also need to acknowledge the present and likely future structure of the industry and of National Cattle Evaluation (NCE), involving, as it does, large numbers of individual producers in federation with one another and reliant on others for much of the genetic information generated in the system.

The categories of genetic markers available for use in marker-assisted selection were ably reviewed by Garrick and Johnson in the 2003 Genetic Prediction Workshop. I will use those categories for this presentation.

Gene-assisted selection (GAS).

In this situation, a known quantitative trait locus (QTL) presents two or more alternative DNA sequences and the different sequences have been shown to be associated in a causal way with variation in economically important traits. The different DNA sequences commonly (though not inevitably) differ by a single base substitution and commonly result in both a change in the gene product and a change in the functionality of that gene product. The result is a change in animal performance. Changes such as these are often referred to as functional mutations (changes in DNA sequence that produce changes in gene function), though I prefer to call them functional sequence variants, since the term "mutation" has connotations involving evolutionary history (which is often not known) and often implies an unwarranted distinction between the "normal" and the "abnormal".

The knowledge that a gene affects an economically important trait does not tell us anything about the size of the effect or the importance of the gene in a particular breed or breeding system. Effects may be large or small and must be determined. In a few cases, animal characteristics are exclusively defined by a single gene. Examples include red versus black color, horned versus polled, and various genetic disorders that are often the result of recessive gene action.

One example of a gene that takes several different forms and has a very large effect on a quantitative trait is the myostatin gene. In this case, the common ("functional") form of the gene results in regulation of muscle growth to produce a "typical" muscling pattern. However, several different sequence variants are known to exist in this gene, all resulting in a loss of regulatory function and, when homozygous, in expression of double-muscling, with an associated increase in carcass lean percentage and decrease in marbling score.

Markers in linkage disequilibrium with favorable QTL sequences (LD-MAS).

In this situation, DNA sequence variants have been identified and one or more of the variants has been shown to be reliably associated with differences in animal

performance. The presumption is that these markers are extremely close to an associated functional sequence variant in a QTL and that the favorable marker sequence can be reliably (though not perfectly) used to predict the presence of the favorable QTL sequence. The presence of a tight association between marker and QTL sequences generally suggests that these associations are reflective of evolutionary history and that the association between a favorable marker and a QTL sequences is likely to be consistent within at least some populations, perhaps only within a breed, but potentially (though not certainly) across cattle as a whole.

Confidence in the value and potential for widespread use of LD-MAS markers increases when these markers are known to exist within a gene of biological importance and when the sequence variants that define the marker are "functional" in their own right; i.e., when the different marker sequences result in changes in a gene product. This is certainly not a necessary condition for LD-MAS: the marker can be any detectable sequence variant, so long as it is very tightly linked to the QTL. However, when a marker is found within a gene of known effect, it adds confidence in the value of the marker and seems to be the situation for many of the markers of current interest in cattle.

In an excellent review of marker-assisted selection for beef palatability characteristics in last year's B.I.F. proceedings, McPeake (2003) noted that several of the markers of interest for palatability traits are themselves functional sequence variants within genes that may be anticipated to affect marbling and tenderness. These include sequence variants in both the thyroglobulin gene (which is the basis for the GeneSTAR marbling test) and the leptin gene (which appears to affect appetite and therefore potentially affects fat deposition).

These marker sequence variants may or may not be the actual cause of the observed differences in performance. Garrick and Johnson (2003) chronicled the process by which a marker in the diacylglycerol acyl transferase gene associated with milk composition and a marker in the growth hormone receptor gene associated with milk production were shown to be the actual causal changes in the QTL. However, the conduct of LD-MAS and GAS are not substantially different so long as the markers in LD-MAS are validated for each population and are very tightly linked to their associated QTL sequence variants. Both these elements are absolutely critical. Confidence will be greater in use of markers in GAS but LD-MAS can still be very effective.

Markers in linkage equilibrium with favorable QTL sequences (LE-MAS).

These markers have an association with a QTL, but the direction of the association can vary among individuals and cannot be predicted for the population as a whole. Thus in some families, the marker may have a positive association with performance while in other families the association is negative. As a result, the nature (or "phase") of the association between the marker and the QTL must be determined for each family, and the marker will be used primarily to discriminate among offspring of individual sires. To date, LE-MAS has been used (or at least discussed) mainly in dairy cattle, where elite proven sires can have the marker-QTL phase determined from estimated breeding values of their progeny-tested sons and used in screening additional progeny and grandprogeny for evaluation. In most cases, LE-MAS can be used in some, but not all, families within a population. For that reason, LE-MAS may be useful for evaluation of offspring of individual sires in individual breeding programs, but, barring discovery of a particularly important or interesting LE marker, seems less likely than the markers used for GAS or LD-MAS to be incorporated into NCE.

Assessing the Potential Importance of Genetic Markers

The potential impact of a genetic marker can be assessed in a reasonably straightforward way as the additive genetic variation in the trait of interest that can be attributed to the marker (σ^2_{A-M}). For a codominant marker with two alternative forms (i.e., when the heterozygote is exactly intermediate to the two homozygotes), this may be assessed as:

$$\sigma^2_{A-M} = 2p(1-p)a^2$$

where a is ½ the difference in mean performance between individuals that are homozygous for different marker sequences and p is the frequency of the marker in the population of interest. Analogous equations exist for dominant or recessive markers or when the marker has more than two alternative forms. The potential impact of a genetic marker thus depends on both its effect and its frequency in the population. We can also express the marker's impact as a marker heritability (h^2_M) by dividing σ^2_{A-M} by the phenotypic variance (σ^2_p):

$$h^2_M = [2p(1-p)a^2]/\sigma^2_p .$$

This h^2_M can be compared to the reported heritability of the trait (h^2) to assess how much of the genetic variation can be accounted for by the marker.

For a given marker, h^2_M will be largest if the frequency of the marker is close to 0.5, and h^2_M will decrease if the marker frequency is either very high or very low. Also, as the frequency of a favorable marker is increased to above

0.5 by selection, its future value for further improvement declines. At this time, it is nearly impossible to make general statements about "expected" values for h^2_M. However, if we exclude sequence variants with obvious visual effects (like those in the myostatin gene), we see a few situations where h^2_M might account for up to 25 to 30% of h^2, representing situations where a marker might contribute to, but not dominate, the selection process. For h^2 = .5 and h^2_M = .25 h^2 at p = 0.5, h^2_M and h^2 would be expected to decline as the frequency of the marker increases as:

P	h^2	h^2_M
0.50	0.50	0.125
0.75	0.48	0.100
0.90	0.46	0.050

In these calculations, changes in h^2 assume that the total additive variance is also reduced as the marker frequency increases; this may or may not actually happen.

The situation shown above, with relatively rapid change in h^2_M, is different from what we expect from performance-based selection, where h^2 seldom changes noticeably over time. We generally believe that h^2 stays about the same because as selection progresses, new genes or gene variants come into play and the contributions of these variants are automatically picked up in the performance records to bolster and maintain heritability. However, when selection is based on a specific marker, fixation of that marker terminates its utility and continued selection response requires discovery of new markers. The discovery of new markers is anticipated to occur, but it will not necessarily happen in a way that maximizes selection response. Thus we will likely continue to keep performance records for a long time, even for traits that may be difficult to measure. We also usually don't expect h^2 to differ much among breeds, but h^2_M certainly can differ, depending on the frequency of the marker. Thus knowledge of p in the population of interest is extremely important.

Hetzel (2003) reports that individuals that are homozygous for alternative markers in the thyroglobulin gene differ by 3.5 to 11% in marbling score. The phenotypic average marbling score in the Angus database for steer carcasses harvested at less than 480 d of age is about 6.0, with a heritability of 0.36 and a phenotypic standard deviation of about 0.75 (A.A.A., 2004). If the average effect of the GeneSTAR marbling marker is taken to be 8%, that would be equivalent to a value of a (= ½ the difference between homozygotes) of about 0.24 in marbling score. At p = 0.5, that gives h^2_M = 0.038. That value seems small, but recognize that a market allows the genotypic value to be directly observed rather than just predicted from phenotypic information. Decisions about the utility of marker information are best made based upon the size of the marker effect and the frequency of the marker in the population of interest. The value of h^2_M, however, gives an idea of the extent to which the marker accounts for σ^2_A. In this example, GeneSTAR would account for only about 11% of the additive variance in marbling score. Put another way, if the total additive variance for marbling score is 0.27, it would require 9 independent genes with effects similar to those of the GeneSTAR marker to explain all the additive variance in marbling score. This result is not surprising given the size of the GeneSTAR marker effect and shows that while the GeneSTAR marker may be a useful tool, lots of other opportunities to improve marbling scores remain.

We can anticipate the discovery of additional genetic markers for various traits over the next few years, and the discovery process will likely expand with sequencing of the bovine genome. Issues of additivity of marker effects will soon arise. The GeneSTAR markers now include three separate sequence variants, leading to 27 possible genotypic classes. If we add a leptin marker, we get to 81 genotypic classes. We cannot assume that effects of multiple markers will be additive, and each will have its own h^2_M, depending on marker frequencies in the population. On the other hand, we should not assume that marker effects will necessarily not be additive, at least on some scale. In sheep, several different genes are known to have major effects on ovulation rate. All of these genes were discovered in different populations, but Davis (2003) reported that when a crossbred ewe was created that carried one copy of each of three of the markers (Booroola, Invermay, and Woodlands), the ewe has ovulation rate of 5 and 8 at 1.5 years of age and 12 at 2.5 years of age. So in this case, these three genes were at least additive in their effects on ovulation rate. But the ewe still only had triplets at her first lambing.

The validation of genetic marker effects in different populations and the assessments of effects of genetic markers on other traits is a critical endeavor. This issue has been addressed in part through the activities of the National Beef Cattle Evaluation Consortium (Quaas, 2003; Pollak, 2004). The validation process is extremely important. We can likely anticipate that as the effect of a genetic marker on a trait of interest increases, the potential for correlated effects on other traits will likewise increase. Thus markers with the largest effects are most easy to use but probably also have the greatest risk of other undesirable effects, whereas markers with smaller effects may be less likely to affect other traits but are harder to incorporate into NCE.

Development of a Scheme for Proactive Incorporation of Genetic Information into NCE

One of the most significant impediments to effective use of genetic markers in NCE relates to the current selective genotyping and reporting of marker information. That situation is likely to get worse before it gets better, but eventually it needs to get better, and we need to start developing a vision of how to make it better. Over the years, the breed associations have become the recognized repository for performance data. In that role, they have provided genetic evaluation services for their members and driven development of new EPDs. If genetic markers are to have a long-term impact on genetic improvement, I believe the breed associations will need to take control of the process in a proactive way that allows them to interact with commercial labs providing DNA testing from a position of strength and with a sustained focus on the needs of their members.

The eventual mix of performance and marker data that will contribute to NCE is still unknown, but it appears likely that the EPD of progeny-tested sires will remain the gold-standard for genetic evaluation for quite a while. Within that context, here are a few suggestions that breeders and their associations might consider.

Identify an array of genes and markers of importance to the breed.

These would include known genes (for GAS) and marker genes with documented associations with performance (for LD-MAS) that are important to a breed. The marker gene arrays might well differ for different breeds. Such an array might also include a set of informative microsatellite markers that could be used for parentage testing and as a way to link newly discovered markers back to older animals. "Several" markers should be identified on each chromosome, with the exact number defined by future technological developments and cost. These microsatellite arrays would probably be breed-specific but might well include a mixture of some markers common to all (or most) breeds and some unique to a specific breed.

Such an array of genes and markers would necessarily have to have the capacity to evolve over time, as new genes or more informative genetic markers are discovered. Inclusion of a set of microsatellite markers would facilitate this evolution by allowing some genotypes for newly discovered genes to be "inferred" from their position and phase relative to the microsatellite markers rather than determined in the laboratory. Techniques for using microsatellite markers to predict probabilities for the various marker genotypes in animals that have not been genotyped have been presented by Thallman et al. (2001) and will continue to develop. Note that identifying the markers of interest does not imply that all animals will necessarily be genotyped for all (or any) of them. It simply means that a target array of potentially useful markers has been identified, providing guidelines for breeders. The decision about how many animals to genotype will likely depend on the development of cost-efficient, chip-based "multiplex" assays that allow genotypes to be determined for many genes in a single assay. The industry has been waiting for this technology to emerge for quite a while, and is still waiting, but its eventual development seems likely.

Develop a DNA collection strategy.

Access to DNA from the influential animals in the breed will be required for widespread use of marker information in genetic improvement, and access to marker information will likewise be required on substantial numbers of their progeny and mates to facilitate marker discovery and validation. Therefore, easy access to DNA from "many" animals in the breed will be required. At the moment, the most promising and economical way to do this seems to be to adsorb several drops of blood onto cards made of fluoroacetate paper. A card might have "several" sections, each containing a few drops of blood that could be cut out and submitted for DNA analysis, thereby allowing repeated analyses of DNA from the same animal when necessary as new markers are discovered. Storage requirements for the cards are very modest, although they do require physical (as opposed to electronic) storage.

Guidelines for which animals to include in this DNA repository will need to be developed. But we should not rule out the possibility that a registration application or a weaning weight record might someday automatically be accompanied by a blood sample. In any case, some sort of breed policy on DNA collection and storage seems warranted.

Develop a genotyping strategy.

If marker information is going to have a widespread impact on NCE, it is important that the breed associations become the repositories for marker information. Effective use of markers will require that certain animals in the breed be regularly genotyped, although we don't yet fully know just who these animals should be. We likewise can anticipate that genotyping will remain selective, although we cannot yet project the numbers of animals that will be genotyped.

We should anticipate that widespread use of a sire would trigger genotyping of that sire for the current marker array and of a sample of his progeny as needed for validation or future gene discovery. Even if a full multiplex DNA analysis costs a few hundred dollars, genotyping of 10 or 20 potential legacy sires each year would be a reasonable endeavor, and when extended to capture the sires and maternal grandsires of many offspring would be a rich source of genetic information. Such a database would also allow rapid predictions of frequencies of newly discovered

sequence variants in different breeds, allowing calculations of h^2_M and assessment of potential contributions of markers to selection response.

Incorporate marker information into NCE.

Incorporation of marker information into NCE will involve a major developmental effort: conceptually straightforward but technically challenging. We have started to scratch the surface, but just barely, and the operational considerations outlined above will greatly influence the probability of success. The objective is to be able to combine performance records with marker data in a way that will both increase accuracy and avoid bias in resulting EPDs. Equally challenging will be the capacity to work with an evolving set of markers; many animals will not have marker information, and those that do will likely often be genotyped for only a few of the available markers. A breed policy of relatively comprehensive genotyping of influential sires (and of their progeny as necessary for marker validation) could improve the situation, but access to comprehensive, consistent marker data across the breed is unlikely to be realized in the short term or necessarily warranted in the long term.

In animals with marker data, a portion of the genetic variation that would normally be incorporated into the EPD can be partitioned off and attributed to the marker genotype. If several markers are available, then several portions of the underlying additive variance can be carved out, but those marker effects will be additive (i.e., the total marker effect will equal the sum of the individual marker effects) only if the markers are independent, both in their location on the chromosomes and in their effects on the trait of interest. For the foreseeable future, the additive variance that exists independently of the markers (i.e., the residual polygenic variance) will remain very important and cannot be overlooked or devalued in NCE. In addition, we must recognize that average marker effect, even when large and clearly significant, will not necessarily be the same for all animals or all sires. Interactions between the marker(s) and the polygenic genetic background should be anticipated and methods to account for variation in expression of marker effects among sires should be considered.

When animals do not have marker data, predictions of EPDs will continue to rely heavily on performance records, but marker data from relatives can provide useful supplemental information. The challenge will be to deal with different subsets of markers among the different ancestors and relatives.

A proactive, breed-centered program to manage and utilize marker data can provide important dividends. Chief among them will be a capacity to focus the gene discovery process in areas that are most important to the breed. As shown above for the GeneSTAR marbling marker, our current markers provide potentially useful but hardly complete indications of genetic merit. The process of gene discovery needs to continue. Even if we were to be successful in finding a marker of very large effect for some trait, fixation of the marker would quickly lead to a need for additional, new markers, or to a return to performance-based selection.

The capacity to monitor and validate marker effects becomes particularly important if a marker should "stop working" or if an outstanding sire emerges that has the "wrong" marker. Even with LD-MAS (and especially with LE-MAS), associations between the marker and the QTL can break down or reverse due to recombination between the two sites. Attention to progeny-test results can allow prompt recognition of such events and trigger a reassessment of marker relationships.

Even with GAS, changes in marker effects can occur. Other, unknown sequence variants, inherited from ungenotyped ancestors, can cause unexpected results. For example, an animal tested for one of the myostatin mutants that causes double-muscling might be shown to not carry that mutation but could still express and transmit double-muscling if it inherited one of the other mutations that are known to exist for that gene.

Conclusions

The purpose of this presentation is not to list things that should be done. Instead, the focus is on things that could be done and should be considered. Selective, comprehensive testing of high-impact sires for available markers seems clearly warranted to provide ready access to frequencies of the different markers within different breeds and to provide the baseline information necessary to properly validate markers in their progeny. Incorporation of marker data into NCE will occur, though the methodology to be used in that incorporation is still emerging.

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Technology: Price Tag and Profit

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Introduction

In a world that includes the robotic exploration of distant planets, cattlemen may choose to rope calves with lariats in order to implant them with hormones or computer identification chips. As the same calves are branded with a hot iron that has been used as identification for centuries, they may be ear tagged with an insecticide tag and vaccinated against one or several diseases. The choices of available technologies for cattlemen are too numerous to mention. Application rates of available technologies vary greatly between and within industry segments. Cost benefit analysis has long been used as the major tool of evaluation and promotion of the economic benefits of technologies for beef cattle improvements.

Unexpected outcomes are common to the application and use of technologies. A classic example is provided by one of the possible scenarios explaining the epidemiology of BSE (Philips, et. al. 2000). Decades ago, in a country an ocean away, decisions were unknowingly made to allow a BSE infected cow into the food system and to feed her rendered meat and bone meal to other ruminants. Approximately thirty years later, a BSE infected dairy cow is discovered in the United States. The December 23, 2003, announcement of that discovery had a dramatic, yet short term negative impact on the cattle market. Its possible long term impact on consumer demand, country of origin labeling, individual animal identification, age at time of slaughter, and the testing of increased numbers of animals is yet to be determined. Cause and effect are indeed distant in time and space.

Technology designed for cattle production systems needs to be evaluated not only with a cost benefit analysis, but also an understanding of the marginal costs of its application, production functions, and an evaluation of possible implications, interactions, and unexpected outcomes. The evaluation needs to look at technologies not only in their present context but in light of the future.

Cost Benefit Analysis and Partial Budgets

Cost benefit analysis can be made with the help of a partial budget. A partial budget is an estimate of the changes in income and expenses that would result from carrying out a proposed change. An example can be found Table 1. This simple procedure quickly establishes an estimated cost of the application of a technology and compares it to the estimated change in income that results from the use or application of the technology. If the difference is a positive change in net income, it is usually recommended that the technology be adapted.

Table 1. Partial Budget (Kay and Edwards, 1999)

Partial Budget	
Technology:	
Additional Costs:	Additional Revenues:
Reduced Revenue:	Reduced Costs
A. Total additional costs and reduced revenue $	B. Total additional revenues and reduced costs $
Net Change in Profit (B-A)	

While this process seems fairly straightforward, what it doesn't measure may be as important as what it does. For example, risk, affect on cash flow, debt, repayment capacity, inter-relationships, variability, repeatability, and quality of life are not measured with partial budgets. While some technologies are simple and straightforward, others are not, and capturing some intrinsic feel or estimate for things like risk is critical. Beyond the things that a partial budget obviously does or does not measure, there are always unexpected outcomes to change. An example would be the European trade embargo on US beef because of the use of growth-promoting hormone implants. The loss of market

share and its impact on total demand for beef due to the European trade embargo can be measured now, but 25 years ago was unforeseen. A simple partial budget for implanting beef cattle in 1979 would not have been sensitive to the future loss of market share due to trade embargos.

Several other limitations should be discussed. A partial budget does not compare alternatives. While one can create several partial budgets and compare the results, the assumptions one makes to do this may be excessive. One basic assumption for this type of multiple analyses is that all other things are equal. They rarely are. Other assumptions made in the comparison of technologies with partial budgets are that either the results are additive or completely independent. Few are either. Another thing that a partial budget does not do is measure the efficiency of how resources are allocated. For example, perhaps Technology 1 may increase net income to level A. But was it an efficient use of limited resources? Perhaps Technology 2 could increase net income to ¾ A, but at a fraction of the investment. Partial budgets do not measure sensitivity or efficiency. If the results of partial budgeting are put into a ratio, a cost/benefit ratio, then comparisons of alternatives may be more appropriate. Care should still be taken.

In summary, their ease of use and understanding has led to the widespread adoption of partial budgets as a determinate in cost benefit analysis. While useful, they have limited value and must be used with caution.

The Importance of Using the Correct Endpoint

A key step in the evaluation of a technology is to measure its impact at the correct endpoint. Many evaluations of technology in the cattle business have been and continue to be based on a per head basis. For example, a treatment, application, or protocol is reported to cost X dollars per head. Or, it netted Y dollars per head. While interesting, it is much more important to know what the cost or return is per unit of weight sold. This is especially true of technologies aimed at cattle reproduction. A technology may increase pregnancy percentage, but the question becomes, does the advantage carry over to weaning and actually increase the number of pounds of calf weaned? It may or may not. At the very least it is important to know the cost of the technology is on a weight basis. When it comes to the application of a technology in the cattle business, a change in weight or in efficiency is the bottom line.

An excellent example of a comprehensive analysis of the impact of technology on an entire production segment can be found in the recent work of Sandy Johnson of Kansas State University (Johnson, 2002). Johnson compared two estrus synchronization protocols at three labor rates, three semen costs, and three pregnancy rates. The results (Table 2) were reported on a cost per cwt of weaned weight basis. This type of reporting allows a decision maker to evaluate technologies on their impact on the bottom line.

Table 2. 500 lb equivalent weaned calf breeding costs per cwt for a herd size of 100 at various labor and semen costs. (Johnson, 2002)

Systems	Preg %	Semen Costs								
		$3/unit			$13/unit			$23/unit		
		Labor Cost ($/hour)								
		5.77	10.77	15.77	5.77	10.77	15.77	5.77	10.77	15.77
CO-Synch	40	7.82	8.31	8.81	10.48	10.97	11.47	13.13	13.63	14.13
CO-Synch	50	5.36	5.85	6.35	8.01	8.51	9.01	10.67	11.17	11.67
CO-Synch	60	4.84	5.34	5.83	7.50	8.00	8.49	10.16	10.65	11.15
Select Sync	40	7.04	7.90	8.76	8.56	9.42	10.28	10.08	10.94	11.80
Select Sync	50	4.71	5.57	6.43	6.61	7.47	8.33	8.51	9.37	10.23
Select Sync	60	4.33	5.19	6.05	6.61	7.47	8.33	8.89	9.75	10.61

The Concept of Marginality

The understanding of the concept of marginality is a critical part of informed decision making. The principle of Marginal Utility is defined as the amount of additional benefits provided by an additional unit of an economic goods or service (Merriam-Webster, 2001). A classic marginal product curve is shown on Figure 1. This concept is not new. Gray (1968) discussed it in detail as part of ranch management decision making. The basic concept is that the level of economic measures, cost or product for example, will be different for varying levels of an input. As a production function reaches its point of diminishing returns, additional units of input do not correspond with increased levels of output. Also, the unit cost of the last units produced soars. One way to think about it in terms of a cattle production system is that once some other constraint has become limiting, no matter how many additional units of an input are added, the cattle cannot gain weight or reproduce at a higher level. A simple example would be bull to cow ratio. A 1:1 bull to cow ratio will not result in more cows bred or more weaned pounds when compared to a reasonable ratio that has been determined by size of pasture, breed, terrain etc. But it will add dramatically to the unit cost of production. The decision rule is that when the marginal value of the product produced exceeds the

marginal cost of production, product should be produced (Kay and Edwards, 1999).

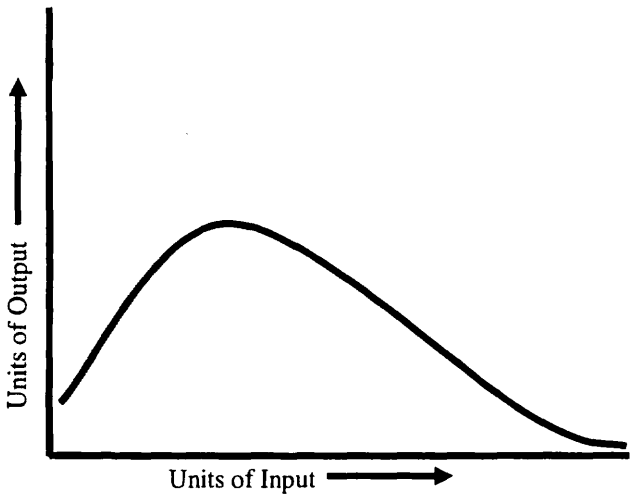

Figure 1. Marginal Product Curve (adopted from Case and Fair, 1996).

There are many excellent examples in beef cattle production. For example: level of nutrients like vitamins or minerals in feed, number of pastures in a rotational grazing system, stocking rate and animal performance on pastures. Other examples where the drop in production is not obvious but there is no increase in production as inputs increase would be dosages of drugs and protein level in feed supplements.

A second important example of the concept of marginality is its affect on costs. Figure 2 shows the impact on cost as levels of input are added beyond the point of diminishing return. The bull/cow ratio, dosage level of a therapeutic drug, and protein level of feed provide excellent examples. While they may be less obvious, all technologies have a Marginal Cost Curve. As one ponders the relatively low level of application of technology in some segments of the beef cattle industry (NAHMS, 1998), the question becomes, is it a matter of cattlemen ignoring potential benefits or an intuitive under stand this fundamental economic principle?

A third area where the concept of marginality applies is on price and revenue. A Marginal Price Curve looks different at the firm versus an industry level (Figures 3 and 4). Because a firm is very small compared to the market place, an increase in production at its level has no impact on price. However, at an industry level with constant demand, the impact on price of increased production can be dramatic. The cattle industry certainly observed these phenomena in the 1980's and 1990's. Beef production rose dramatically in the face of falling consumer demand, and the impact on the real price of beef was negative (Purcel 1998).

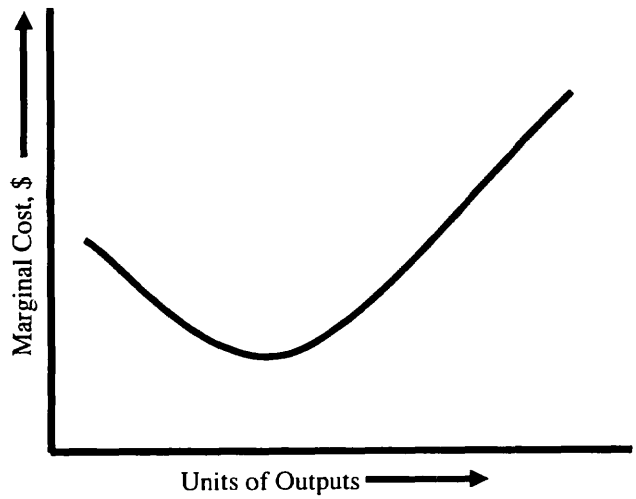

Figure 2. Marginal Cost Curve (adopted from Case and Fair, 1996).

At the ranch, farm, or feedlot level, changes in level of production has no impact on price due to sheer scale of the industry. So, while the adoption of a technology may be presented as having no affect on price, and that each unit of increased production due to the use of a technology will be priced at the same level (Figure 3), at an industry level this may be false. Industry-wide adoption may indeed lower price if demand is constant (Figure 4). This should be considered as an evaluator of technology thinks about the long term application of a technology. Being an early adopter of technology may have different benefits than being a late adopter. It is one thing to observe others to see if the claims about a certain product or protocol are true, it is another to let the benefits be eroded by changes in market dynamics.

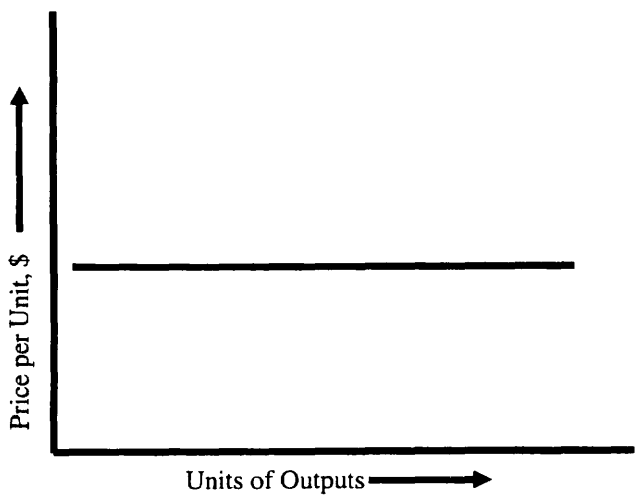

Figure 3. Marginal price curve for a firm (adopted from Case and Fair, 1996).

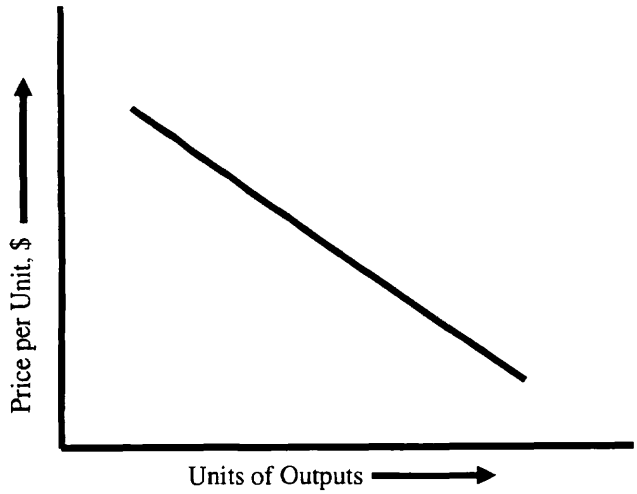

Figure 4. Marginal price curve for an industry at constant demand (adopted from Case and Fair, 1996).

Unexpected Outcomes

One of the characteristics of a complex system is that it exhibits unexpected outcomes to the application of policy or technology (Stermans, 2000). The possible epidemiology of Bovine Spongiform Encephalopathy (BSE) and the affect of growth-promoting hormone implants on beef demand are two of just many examples of unexpected outcomes in cattle production systems following a change in policy or technology. The expression of lethal traits as a result of inbreeding, bacterial resistance to antibiotics due to prolonged low level use, insect resistance to insecticides, negative associative effects in ruminant nutrition, and an increase in calving difficulty with the selection of breeding stock for weaning and post weaning growth are well known examples. Not all unexpected outcomes are negative. Planned crossbreeding systems have provided many positive unexpected results. Early evaluations of crossbreeding recognized the positive impact on growth traits and led to its promotion and adaptation. Later, other benefits of crossbreeding on reproduction, health, and longevity were recognized and measured. Another example of a positive, unexpected outcome of a technology is the feeding of all natural protein supplements to beef cows receiving high roughage diets. The all natural protein supplement not only meets dietary protein requirements but also enhances fiber digestion.

If unexpected outcomes to the application of technology are common, why then are they unexpected? Sterman (2000) suggests that it is because cause and effect are distant in time and space. For example, due to the long generation interval in beef cattle production systems, the result of changes in breeding programs often takes years to express themselves. Another hypothesis may be that under rigid, controlled experimental conditions, the evaluation of technologies is designed to minimize other effects. Even if unexpected outcomes occur, the data collection and analysis system in the evaluation process of an experiment may not be designed to recognize, monitor, or measure them. Also, the length of time that experimental observations occur is often too short to measure other effects that manifest themselves after data collection has ended.

How can possible outcomes of the application of technology be anticipated? A tool called Casual Loop Diagrams is used by many businesses and organizations to analyze the impact of changes in technologies, polices, or procedures (Senge et. al., 1994). This process of diagramming multiple cause and effect relationships helps investigators explore the mental models under which they operate. It might be described as organized pictorial brainstorming. Causal Loop Diagrams can also be used in the development of simulation models (Repenning, 1998). While not a crystal ball, the technique of using Causal Loop Diagrams to build and parameterize simulation models has many success stories dating back over 40 years (Sterman, 1991).

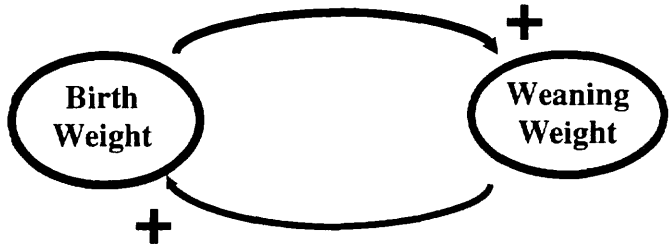

Figure 5. Causal Loop Diagram. Plus sign indicates that change occurs in the same direction.

The Causal Loop Diagram in Figure 5 depicts the genetic correlation between two traits, Birth Weight and Weaning Weight. As selection pressure is placed to increase Weaning Weight, Birth Weight also increases and vice versa. Causal Loop Diagrams can have many variables and depict complex inter-relationships. When information exists concerning the relationship between variables, as it does in this example, simulation models can be parameterized. If on the other hand, the development of a Causal Loop Diagram identifies a relationship that has not been defined, an area of future research needs has been identified.

Measuring the Future Value of a Technology

While many technologies may produce short term financial gains, changing market conditions may erode benefits over time. It is important to measure this phenomenon as accurately as possible. A partial budget measures the profitability of change in a single production cycle. What is the value of a technology years in the future? The process of making that determination is referred to as

calculating the net present value of the benefits. The basic assumption behind the concept is that future earnings will be eroded by the inflationary nature of the economy. The general formula for calculating net present value of future values is (Workman1986).

$$V_n = V_o (1 + i)^n$$

In this formula, V_n is the future value of a present sum at the end of n years, V_o is the present sum, I is the interest rate charged during the period, and n is the number of periods over which Vo is compounded.

Due to the relatively long production cycle of the beef animal and its long generation turnover, the benefits of reporting results of the evaluations of technology in this manner are obvious. It also becomes the responsibility of the evaluator of information to think about benefits in context of their future value. Table 3 (Meek et al., 1999) provides an excellent example of the use of net present values in the evaluation of different aged beef cows. Culling strategies, purchased versus raised replacements, drought management plans, and investment strategies could all be impacted by the different net present values for the two market scenarios. While the rank of the residual values between the two market scenarios in Table 3 is the same, the absolute differences are important to consider. A twelve year old cow in the current market scenario has 70% more residual value than a 12 year old cow in the low point of the cattle cycle. This difference impacts many things on a cattle operation including cash flow, repayment capacity, and the ability or willingness to accept risk. The application of technology may also be different in the managerial response to the example in Table 3. For example, a drop in gross income may incline a manager to wait on the use of products or protocols until the operations cash flow improves.

Table 3. Net present values (NPV) for cattle of ages 1 through 12 yr for two market scenarios. (Meek et al.,1999)

Age of cow, yr	Residual NPV Current cattle market, $	Residual NPV Low point in cattle cycle, $	Remaining life (weighted average), yr
1	783.53	599.69	4
2	1,026.86	794.36	4
3	1,145.81	909.78	5
4	1,210.20	954.46	6
5	1,170.59	936.69	6
6	1,088.04	874.93	5
7	1,068.73	853.35	5
8	1,027.38	797.32	5
9	976.12	714.82	4
10	899.87	612.88	4
11	794.09	480.57	3
12	734.60	431.32	2

One of the difficulties of these types of analyzes is the volatile nature of the commodity beef cattle market. Another difficulty in looking forward in the beef cattle business has been the cyclical, but still unpredictable, nature of the business. Layering estimates of discount rates, the cattle cycle, consumer demand, the price of competing meats, and sensitivity estimates into a decision model is a daunting task. But as the industry moves towards value-based integrated marketing, reporting results of change in discounted future values will be increasingly important.

Summary and Conclusions

The evaluation of the impact of technologies on beef cattle production systems can be enhanced by placing them in their proper context. Suggestions for doing so include:

1. Cost/benefit analysis is a more effective evaluation tool than are simple partial budgets.
2. End weights or market weights should be the denominator of the analysis of economic efficiency rather than per head.
3. Costs and benefits of a technology will change with different levels of production.
4. Technologies may impact individual operations differently than they do the cattle industry as a whole.
5. Unexpected outcomes to the application of technology will be common due to the complicated nature of the business, its long production cycle, and its susceptibility to changes in uncontrollable environmental factors.
6. The future value of technologies needs to be appropriately discounted.

While challenging, it is critical to evaluate technology accurately and appropriately.

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The Cost of Meeting Consumer Demand

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The beef industry has experienced a roller coaster ride on emotions and market prices much of which has been driven by animal disease and resulting trade restrictions. Examples include: discovery of BSE in Japan on September 10, 2001, avian influenza blocking poultry exports to Russia in March 2002, discovery of BSE in Canada in May 2003, and finally, discovery of BSE on US soil in December 2003. Underlying all these shocks were basis supply and demand fundamentals. In late 2001 and 2002, while demand was improved from 1998, the supply of market ready cattle and carcass weights were large and growing. In 2003, inventories and carcass weights were low and declining. The price impacts were quite different in the two years.

This simple analysis is typical of how we economists and the industry in general talk about "the market". We treat it as a commodity and a single beef market. Yet, the market for beef as well as most other food products is changing from a commodity to a fragmented market of differentiated products. While prices for these products will likely be highly correlated because there are many close substitutes, they are not homogenous. The move to more diverse products is to address a changing and more diverse consumer that buys products from a rapidly consolidating but highly competitive retail sector. Consumers, retailers, processors, and society in general are placing more demands on food and people, companies, and industries that produce it. Put another way, the demand *for* beef is increasing, but so are the demands *on* beef. These demands are expressing themselves in both more regulations and requirements on food producers and processors. Part of this stems from the maturing of agriculture. We have traditionally operated on a "trust me" basis but we are now entering a "prove it" world.

I have been asked to discuss the cost of meeting consumer demands which is a tall task since they are evolving daily. I will attempt to address the question of cost in a round-about manner, and in the end hopefully help producers better understand the question and how it may apply in their own operation. We will start with a discussion on the consumer's willingness to pay for specific product attributes. Next, we will look at the changes in the retail sector, increased branded products, and the implications on producers. Then we will discuss process verification and quality management systems as methods to assure the consumer of the traits they want and cover the liabilities of doing so. Finally, we will discuss the cost of not meeting consumer demands.

Consumer Willingness to Pay

The focus of my paper is supposed to be on the cost of meeting consumer demand, but it is important to first define demand and where possible quantify it. More to the point, if consumers really want something, then they should be willing to pay for it. Producers of beef typically think about differentiating beef based on taste and quality. While, Lusk reported that consumers were willing to pay a premium for a "guaranteed tender" steak, most consumers, retailers, and processors, tend to focus more on what have been called "credence" attributes. *These are characteristics that consumers cannot discern even after the consumption of the product.* Examples include content attributes such as affect physical properties of product (nutrient value) and process attributes that doesn't affect product, but refers to how it is produced or processed (organic, free range, country of origin, fair-trade).

Several studies have looked at the consumer's willingness-to-pay for special attributes. These include: non-hormone treated, grass-fed vs. corn-fed, local production vs. unknown source, US produced vs. unknown source, organic vs. conventional and other similar comparisons. For example, Feuz and Umberger found that consumers in Chicago and San Francisco will pay an average of $1.61 per pound more for a domestic grain fed steak compared to an Argentine, grass-fed steak. This result confirms that on average (or if you only have one commodity) US grain fed beef is the right one. However, 23% of the participants preferred the Argentine steak and were willing to pay an average of $1.36 per pound more for their preferences. Thus, with multiple products targeted to the correct consumer there is additional money to be had. In a survey based study regarding mandatory country of origin labeling, Loureiro and Umberger found that the premium for US Certified Steak is 38.3% ($1.53/lb), while the premium for US Certified Hamburger is 58.3% ($0.70/lb).

What is often not known is whether the premium will cover the cost to produce the challenger. Clearly blanket statements or recommendations are not appropriate because the costs differ with the conditions. It is also important to recognize that the cost to produce the live animal with these special traits is only part of the costs. Segregating the product through the supply chain to get to the consumer willing to pay the premium is also costly. The commodity market may have increasing minimum requirements to participate, but it provides for low cost processing and distribution. The more specific the product attributes, and

the more choices consumers have, the more difficult and costly the product will be to market.

Because many of these attributes cannot be detected by a grader, they have to be verified during the process. One of the challenges to differentiating products this way is how to establish market creditability of the product and producers. Thus we are seeing more interest in objective validation of quality claims through third party verification. USDA recently had an open comment period regarding labeling claims and how to define them. There is growing interest in protecting consumers from fraudulent claims, but before USDA or others can verify a claim it must be defined.

Rapid Retail Reorganization

The retail food sector is changing and consolidating rapidly due in large part to the entry of Wal-Mart and European food retailers in the US market. Recent estimates indicate that the ten largest grocery chains have approximately half of the market (Table 1). The consolidation is not limited to the US. Australia has three grocers with a 70% share, the UK has four firms with 70%, and Chile has four firms with 66%. Wal-Mart is the largest food retailer in the US and the World and Sam's Club (owned by Wal-Mart) is currently sixth in the US, and the two combine for over 17% of US grocery sales. Wal-Mart has been successful at least in part because they effectively manage data and information to assure "just-in-time" inventory control and sharing sales information directly with suppliers. Other retailers have followed an adoption of electronic supply chain management between retailers and suppliers that is increasing rapidly and is improving.

Table 1. Estimated Retail Grocery Sales

	Billion $	Share
Wal-Mart	103.2	13%
Kroger	53.6	7%
Costco	41.7	5%
Albertsons	36.2	5%
Safeway	33.6	4%
Sam's Club	33.5	4%
Ahold	26.9	3%
Super Valu	20.3	3%
Publix	16.7	2%
Loblaw	16.2	2%
Other	393.1	51%
Total	775	100%

Source: Supermarket News

It is also important to note that the seventh (Ahold) and eleventh (Delhaize) largest US food retailers are European companies. When you look at the world's 10 largest food retailers two of the top three and four of the top ten are European companies that also operate in the US. The European model of food retailing is clearly different than that of the US and highlights the difference between a commodity market and a product market. In the US, consumers have trusted the government on food safety and food production issues. On these measures all food is alike, a commodity, it is safe and wholesome. For a variety of reasons consumers elsewhere in the world have less faith in their government on these matters and retailers have often filled the void. European retails are referred to as "Chain Captains". They are the Captain of their supply chain and are the ones looking out for the consumer.

The United Kingdom following BSE is probably the clearest example of retailers "protecting" consumers for a profit. Competing retailers or their suppliers would have separate quality assurance schemes that begin beyond where US BQA programs end. The requirements and costs to the producers are significant. The schemes included product use, feed restrictions, animal welfare, and worker health and safety among others. The farms also had to have a third party audit to be in compliance and be eligible to sell. It was not uncommon for a farm to require one audit for crops, a separate one for hogs, and a third one for cattle. If they wanted to sell cattle to two different packers they may require different audits and paper work. Farm organizations were starting to develop their own whole-farm audit system that was more practical and cost effective as an answer to the multiple schemes coming at them from above.

While the on-farm implications of multiple supply chains and audits sounds outlandish, the retail consumer receives variety and has choices on which differentiated product they buy. Five years ago a consumer chose between beef, pork, and poultry, or perhaps they chose on retail store over another because of a reputation of their beef compared to a competing store. In the UK, consumers may have three or more choices of rib eye steaks based on whose quality assurance scheme produced the product.

Our beef industry is beginning to see more branded products where a company is staking their reputation and brand equity on each piece of meat they sell. How long before reputation and liability costs force companies do their due diligence before they put their name on it. These concerns result from moving from an anonymous piece of commodity beef to a branded beef item with the name and customer satisfaction phone number on the label. Thus, if consumers won't pay for the requirements, maybe the retailer will. Or, given the concentration and market power retailers are amassing, it may become a condition of sale.

An issue that is gaining interest particularly in the poultry and pork industries is animal welfare. McDonalds and other restaurant chains have established standards for animal handling in packing and in some cases production. Some of their competitors have similar requirements. The Food Marketing Institute and the National Council of Chain Restaurants in conjunction with industry organizations has

developed guidelines on animal welfare, and have started on farm audits for poultry and swine. Beef may not be far behind. The March issue of *Drovers* identified 54 beef supply chains and vertical coordination programs. Of these 16 were listed as "natural", 23 as preconditioned, and 34 as source verified. With all due respect to each of these programs, do these terms mean the same thing in every case and who provides the oversight?

Quality Management Systems

Thornburgh and Lawrence remind us that traditionally industry organizations or government agencies have established grades or standards to address differing attributes in commodities. They constitute the range of particular attribute a commodity can have and still receive a stated grade; for example, the minimum amount of marbling for a beef carcass to grade Choice, the maximum amount of foreign material for grain to grade No. 1, or how much chicken is necessary for soup to be called chicken soup. While grades and standards have improved commodity markets, a different approach may be needed in value-added non-commodity agriculture. First, grades and standards create commodities by establishing a minimum requirement for a specific grade and then all commodities of that grade are interchangeable. The strategy becomes how to produce a product that is the same as everyone else's at the lowest cost rather than how to differentiate a product that has a higher value. Second, grades and standards rely upon grading of the product and ignore the process. Some attributes cannot be measured by either visual inspection (e.g., natural beef) or by chemical analysis (e.g., BST in milk). Many beef programs to date have relied upon grading and inspection, i.e., CAB has used hide color and USDA grades. No prior information is needed if the determining factor can be observed and evaluated. Of the 40 USDA "certified" beef programs, 22 are Angus and only four are process verified and require more than visual observation. (Programs are listed at http://www.ams.usda.gov/lsg/certprog/speccomp.pdf). While USDA is looking for more detail in the descriptor of a label, producers are also looking for a level of integrity on programs with cattle they are buying, i.e, source verification or validation of vaccination programs. Keep in mind that Lusk's research said consumers would pay for a *guaranteed tender* steak, not an "I think-so" or an "It was tender until you cooked it" steak. Establishing new grades and tolerance levels for traits or relying on testing and inspection to sort into the new grades only establishes a new set of commodities, not a new future for agriculture.

The USDA Process Verified program provides this type of validation that occurs in other industries daily. Quality management systems (QMS) are well established to provide the buyer confidence that the seller is delivering what was promised. These go by different names, but ISO 9000 is the most widely know international standard. Automotive, aerospace, and medical manufactures have further refined the ISO standards for their industry. Agriculture is beginning to move in a similar direction. The process verification program offered by the USDA is built on an ISO frame, but is customized to agriculture and does as the name implies, it verifies the process. Quality management systems are a means of requiring discipline and reproducibility in a production process. Discipline and documentation have not been mainstays of traditionally independent minded agriculture. Quality management systems force operators to document what and how processes are done, then prove through records and audit that the process, however described, is consistent. QMS does not require specific or high quality standards, just that standards are met. QMS are also a convenient framework under which to introduce environmental and/or safety standards.

Another feature of QMS systems in other industries is that firms that adopt them have lower costs and more profits because they improve management. The operations are more efficient, there is less wasted material and motion, and there are fewer accidents, and fewer mistakes or out-of-spec products. Many will argue that agriculture is different since production is a biological process subject to weather and disease or that operations are smaller and tend to have few or if any employees. However, agriculture does deal with tight margins, can't afford mistakes, and it now has higher expectations from buyers and society so the principles of QMS can be beneficial to beef producers. I think that most producers can appreciate practical animal handling guidelines and facilities that are less stressful on the animal and the people working to improve safety and profits. Another example is animal identification for management purposes. Most producers use ID systems within an operation, but pass little information to the previous or next owner. The proposed USAIP will provide the infrastructure to make information transfer practical. There are two studies of quality management systems, one in Europe and the second in Australia and New Zealand reported at www.iowabeefcenter.org.

The Cost of Not Meeting Consumer Demand

It may be futile to talk about the cost of meeting consumer demands if the consumer is willing to switch to a product that does meet his or her demand. Likewise, if a processor or retailer makes one or more of these demands a condition of sale, then they become a market access issue. Simply put, do you get a higher price for doing the "extra stuff"? Yes, because the price for not doing it is less and there are fewer buyers for product that doesn't meet the new specifications. As we have seen in the pork industry and to a lesser extent in beef, if one company requires something, the others are not far behind. The challenge is to make sure that the requirement is important and not simply window dressing. Important issues that are not addressed will cause consumers to choose a competitor. Ten years ago that

meant switching from beef to chicken. Today it may be switching from Bob's beef to Brenda's beef, or at a minimum some calves are acceptable to one feedlot but not another.

Before you panic about market access, refer to Table 1 and the list of retailers. There are companies on the list that will continue to sell commodity beef and a lot of it. There is a significant market share of consumers that are only interested in safe affordable beef with minimal concerns beyond taste and tenderness. Commodity beef with some increased minimums will continue to be the largest share of the US beef industry. However, I do believe that we will continue to see growth in more differentiated beef products and higher standard of proof that "trust-me" to back the claims.

If the increased requirements become the new minimum standard then the industry continues to operate as a commodity, but one with higher minimum and higher costs. Increasing requirements to meet consumer demands may result in more work and perhaps more out of pocket expense. If you approach it as a commodity and try to do the minimum required to meet the new specification then expect an increase in cost. However, if the added requirement helps define it as a different product then the added costs can be at least partially recovered in a price difference or cost reduction. If you see the requirement as a need for more management rather than more labor, expect to receive dividends from better overall management of the operation.

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Meeting Consumer Demands Through Genetic Selection: The NCBA Carcass Merit Project

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Introduction

It is well documented that tenderness is one of the most important attributes of higher-value beef cuts. Equally well documented is that genetic variation exists both between and within breeds for this important trait. However, tenderness is difficult and expensive to measure, and market incentives to improve tenderness are limited. Accordingly, it has been ignored in most selection programs. Left purely to chance, the beef industry is fortunate that a majority of cattle harvested have acceptable tenderness, but the fact remains that a significant portion of the population is unacceptable. It is hard to imagine that any industry would ignore the primary criterion by which their product is evaluated by consumers.

In 1998, the US cattle industry initiated the Carcass Merit Project (CMP), a large multi-breed study to evaluate the genetics of tenderness in the US beef cattle population. The project was jointly funded by the $1 per head beef checkoff, and the participating breed associations. The objectives of the project were:

- Generate data from which genetic evaluations for tenderness and sensory traits can be computed.
- Develop methodology and procedures for collection of information necessary for further development of EPDs for carcass traits.
- Validate DNA markers discovered in previous checkoff-funded research for use in industry-wide marker-assisted selection programs for improvement of carcass traits.
- Measure costs and returns of implementing EPDs for carcass traits for the alternative genetic selection programs and combinations of management × genetic improvement of carcass traits.
- Breed comparison was strictly precluded from being an objective.

Project Design

All US beef breeds were invited to participate in CMP, and the following chose to do so:

Angus	Maine-Anjou
Brahman	Red Angus
Brangus	Salers
Charolais	Shorthorn
Gelbvieh	Simmental
Hereford	Simbrah
Limousin	South Devon

Commercial cows were inseminated to several of the most widely used AI sires of each of the breed associations cooperating and supporting the research project. Each breed association selected the sires and provided the leadership and all costs associated with nominating cattle for the study, including semen, AI, collecting feedlot performance data, blood sampling/collection, carcass data collection, shipping of blood samples and the development of EPDs for their respective breeds. Breed identity was coded to prevent breed associations and/or breeders from comparing breeds.

Ten bulls from each breed were designated as "DNA sires." Fifty progeny of each of these sires were used for DNA analysis and shear force observations. Five of those DNA sires were further designated as "Sensory Sires", and all fifty of their progeny were also used in sensory panel assessments of tenderness, juiciness and flavor. In addition to the sensory sires, breeds were allocated a number of "EPD sires", of whom 25 progeny would be evaluated for shear force, but no DNA samples would be collected. The number of EPD sires allocated was based on the historical number of registrations by the respective breed associations.

Progeny were fed at numerous commercial feedyards and ultimately slaughtered at several cooperating packers. Breed associations were encouraged to minimize the number of contemporary groups and harvest each group in its entirety, whenever possible. Decisions on days fed, rations, implant and health protocols, and other management considerations were made by the breed associations in consultation with feedlot personnel, and were uniform within contemporary group.

The project was not designed to provide comparisons between breeds and consequently, no valid breed comparisons can be made from these data. A breed's average relative to the overall project average can be due to

management of that breed's groups as much as genetics. Furthermore, some breed associations bred their sires to cows of the their breed, while other breeds used cows of breeds believed to excel for tenderness. There is no reasonable statistical approach to adjust for the nesting of contemporary group effects within breeds, nor for the differences in genetics of the dams.

Phenotypic Results

Analysis of the phenotypic data showed significant variation among all breeds for shear force. Ranges of sire progeny means for shear force within breed varied from 1.90 to 6.62 lb., indicating that every breed has significant variation in tenderness, and opportunity to improve. Warner-Bratzler shear force was strongly correlated with trained sensory panel tenderness scores, but the relationship between shear force and marbling score was weak at best. These results indicate that Warner-Bratzler shear force is an excellent predictor of consumer experience for tenderness, and that selection for marbling alone will not significantly improve tenderness. Heritability estimates for shear force were variable across breeds, but were moderate or higher in some breeds, consistent with other studies. If adequate amounts of phenotypic shear force data can be collected, significant improvement in tenderness is possible through selection.

Greater than 7200 progeny of 279 sires representing 14 breeds were harvested for collection of carcass and meat quality data. There were 7015 progeny used in carcass and WBSF analyses and 2401 progeny with sensory panel data. Carcass traits of the project cattle were representative of the beef industry with average hot carcass weight of 771 lb, fat thickness of 0.48 in, ribeye area of 13.2 in^2, yield grade of 2.8 and marbling score of Small[20]. Although the cattle were young, mostly from AI sires, and managed optimally, 26% of the steaks had WBSF values > 11.0 lb (considered tough) and 19.4% had sensory panel tenderness scores of < 5.0 (5 = slightly tender; 4 = slightly tough).

Data from four of the breeds for shear force and marbling were used to estimate heritabilities and genetic correlations (Minick et al., in press). In these data, the phenotypic correlation between shear force and sensory score overall tenderness is high, indicating shear force is a useful predictor of consumer satisfaction. Furthermore, shear force is a heritable characteristic, and hence, will respond to selection. Therefore, EPDs for shear force can be computed for all sires in the CMP and can be generated on an ongoing basis if new phenotypic information is generated.

By April 2004, four breeds (Simmental, Simbrah, Shorthorn, and Hereford) had calculated and publicly released shear force EPDs on over 200 sires. Breeds not calculating or not releasing shear force EPDs report several reasons for not doing so. The most common reason cited is that there appears to be limited opportunity to collect shear force data on progeny of new sires. While three of the four largest packers, as well as many smaller plants were very accommodating of this project, there seems to be less willingness by packers to allow steak retrieval for shear force analysis in the future. Accordingly, a release of shear force EPDs might be limited to mostly project sires, with the many of the newest sires in the breed unevaluated. However, such an analysis would describe the amount of variation in the breed, and identify sire lines that are more or less favorable for this important, heritable trait. While some project sires may be past the time when they are widely used, their sons and grandsons are now some of the most important sires in their respective breeds. Some project sires have thousands of recorded progeny in their respective breed associations.

Evaluation of Marker Data

The objectives of the DNA component of the CMP were to validate and characterize 11 quantitative trait loci (QTL) for carcass and meat quality traits that were discovered in previous beef checkoff-funded research at Texas A&M University (the Angleton Project). The Angleton Project used a resource population comprised of greater than 600 progeny in large full-sib families (produced by embryo transfer) of a double reciprocal backcross design between Angus and Brahman.

Validation of QTL discovery projects is necessary because of the substantial risk of false positive results, even in large, well-designed projects. However, failure to validate a QTL does not necessarily imply that the QTL was a false positive; it may simply have been segregating in the resource population used for discovery, but not in the population used for validation. In other words, it is possible that in the Angleton population, all Angus were homozygous for one allele, and all Brahmans were homozygous for a different allele, so segregation was found in the designed crosses, but might not be found in any single breed in the CMP. Characterization of QTL involves determining which QTL are segregating in each breed, how many sires per breed appear to be segregating each QTL, and which traits are affected by each QTL. In other words, characterization seeks to determine the potential utility of the QTL in genetic improvement programs.

Segregation of QTL occurs within paternal half-sib families. Some sires segregate QTL, but many are homozygous at the QTL. The QTL analysis involved 70 sires with 2516 progeny with DNA marker data and phenotypes in 210 contemporary groups. There were 1458 progeny with sensory data and DNA marker data.

While preliminary analyses appear promising, at the time this article was written, the marker data collected in CMP was undergoing final analysis. Those results will be presented in the Thursday morning general session, with details to follow in the Emerging Technologies committee meeting. As that information becomes available, this

document will be updated with that information and will be available on the BIF website.

Economic Considerations

The economic portion of the project also revealed useful findings. Improvement of tenderness has the potential to significantly increase market price, quantity and revenue of fresh beef sales. Improvement of tenderness both increases the value of beef and stimulates greater demand leading to higher consumer expenditures. A ten percent improvement in tenderness would result in approximately a one percent improvement in industry revenue, although the cost of such an improvement is unknown.

How Can Cattle Breeders Use the Results?

The most direct and immediate way is for breed associations to compute and publish EPDs for shear force and sensory traits from the data generated by the CMP. Use of the DNA results is contingent on a partner commercializing tests based on the QTL. This could be done either in the form of direct tests or linked markers.

The existing linked markers could be used to select among progeny and grandprogeny of the 70 legacy bulls that were evaluated in the DNA component of the CMP. While this may seem to be a small number of bulls, these 70 bulls were very influential in their respective breeds and have produced a tremendous number of progeny and grandprogeny.

Linked markers could be commercialized quickly with relatively little development cost and could be used to improve accuracy of selection among progeny of the CMP sires. The technology would probably be used effectively by only a small proportion of the breeders in any breed, but the improved selection response in those herds would likely benefit the entire breed. Some additional development of statistical/computational methods would be required to include marker information in national cattle evaluation.

This approach would also require continued collection of phenotypes and marker data on progeny groups for the approach to be sustainable long term. However, fewer phenotypes would be required than without the markers and accurate genetic evaluations could be obtained earlier in life (prior to breeding decisions).

Although there are several scenarios under which the CMP QTL could be used as linked markers, most commercial interest is in association or functional tests. Therefore, the most promising QTL should be converted into association tests based on single nucleotide polymorphisms. While this is no small task, the large number of animals measured with DNA samples represents an excellent population for further discovery and refinement.

Conclusions

The primary objectives of the NCBA Carcass Merit Project were to collect data for carcass merit EPDs, including tenderness, and to attempt to validate previously discovered QTL for carcass merit in the U.S. cattle population. Both of those objectives were accomplished, but much work remains to be done in these areas.

Besides the stated objectives, several other benefits have resulted from the Carcass Merit Project, both tangible and intangible. The project represents a considerable cooperative effort among U.S. beef breed associations. Experiences gained and goodwill generated in this project will facilitate further cooperative research by breeds, benefiting the entire beef industry. The project has raised the awareness of marker-assisted selection and genomics in the beef industry, and has tested and refined methodology to evaluate results of such studies. The considerable publicity received and educational efforts undertaken by the project have moved the industry closer to embracing selection aided by DNA tests, and have improved the understanding of issues with these technologies. In addition, the project has revealed the considerable cost and coordination required for shear force data collection.

Likely the most significant result of the Carcass Merit Project is the sizeable database of phenotypic information and DNA samples stored for a wide cross section of US beef germplasm. Already, data and samples stored by breed associations are being used to validate gene tests marketed to cattle producers. The potential to further mine this resource to refine the positions of QTL and create association tests for them should accelerate the genetic improvement of carcass merit in beef cattle. The building of a large unbiased multi-breed database to use in discovery and validation alone justifies the industry's investment in this project, and stands to be the project's greatest legacy.

Genetic Prediction Committee

Larry Cundiff, Chair

Diagnostics and edits for genetic evaluations
Dorian Garrick, Colorado State University

Identification and utilization of QTL in the Angus breed
Jerry Taylor, University of Missouri

Software to estimate breeding value combining phenotypic and genotypic data
Kathy Hanford USDA-MARC

Across breed EPD Update
Dale Van Vleck, USDA-MARC

Mating plans for multi-breed and QTL evaluation in the Germplasm Evaluation Program at MARC
R. Mark Thallman, USDA-MARC

Across-Breed EPD Tables for the Year 2004 Adjusted to Breed Differences for Birth Year of 2002

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Introduction

This report is the year 2004 update of estimates of sire breed means from data of the Germplasm Evaluation (GPE) project at the U.S. Meat Animal Research Center (USMARC) adjusted to a year 2002 base using EPDs from the most recent national cattle evaluations. Factors to adjust EPD of 17 breeds to a common birth year of 2002 were calculated and reported in Tables 1-3 for birth weight, weaning weight, and yearling weight and in Table 4 for 15 breeds for the MILK component of maternal weaning weight.

Some changes from the 2003 update (Van Vleck and Cundiff, 2003) are as follows:

Records from USMARC for birth, weaning, and yearling weights were the same as last year with important exceptions that will be noted. The EPDs from the Limousin national cattle evaluations were computed with a new base which causes major changes in the across-breed adjustment factors for Limousin weights. A change in base and genetic parameters for Charolais EPD resulted in some changes in adjustment factors for Charolais weights. A change to a multibreed genetic evaluation by the American Salers Association resulted in some changes in adjustment factors for Salers weights.

A considerable number of maternal records (weaning weights of grandprogeny) were added this year, ranging from about 160 for Hereford and Angus to about 75 for Simmental, Limousin, Charolais, Gelbvieh, and Red Angus.

1) a) For BWT, a Beefmaster sire (1 of 21) with 9 calves (of 214) was added but resulted in little change in the across-breed adjustment.
   b) The new Limousin base resulted in a change in the across-breed adjustment factor from 5.8 to 4.5 lb.
2) For WWT, the USMARC records were the same as last year so that any changes from the analysis will be due to the EPD reported by the breed associations.
   a) The new Limousin base changed the adjustment factor from 23.5 to 1.8 lb.
   b) The new Charolais base and genetic parameters changed the adjustment factor
   factor from 41.1 to 38.4 lb.
   c) The Salers adjustment factor changed nearly as much. The change follows that seen last year as the 2002, 2003, 2004 across-breed adjustments were: 26.1 to 28.4 to 30.7 lb in the 2004 update.
3) Last year, due to the earlier deadline for reports to be included in the BIF proceedings, weights taken at USMARC in 2003 which were converted to yearling weights were taken in mid-March rather than as usual in mid-April. This year no new yearling records were added to USMARC data but the mid-April weights for 2003 were available and were used to calculate yearling weights for the 2004 update. The breeds affected were Hereford, Angus, Brangus and Beefmaster. Hereford and Angus were affected slightly because the 2003 records comprised only a small proportion of their yearling weight records. The impact was greater for Brangus and Beefmaster because one-half of their YWT records were obtained in 2003.
   a) The effect of the warmer month was to add 7 to 10 lb to the solutions for Beefmaster and Brangus compared with the base breed of Angus. The new solutions changed the across-breed adjustments from 11.1 to 20.4 lb for Brangus and from 29.7 to 37.9 lb for Beefmaster. The yearling weights of two Brangus and three Beefmaster calves which were removed this year and which should have been removed last year, would also have contributed to the increases of about 20 lb for the unadjusted averages of both breeds.
   b) The new Limousin base resulted in a change in the across-breed adjustment from 20.5 to -19.9 lb.
   c) The changes in the Charolais NCE resulted in the adjustment changing from 57.8 to 53.4 lb.
   d) As with weaning weight for Salers, the adjustment factor for yearling weight also changed; from 40.6 to 46.1 lb.
4) a) About 160 maternal weaning weights for both Hereford and Angus grandsires and about 75 for Simmental, Limousin, Charolais, Gelbvieh and Red Angus grandsires were added to the maternal (MILK). Changes in the across-breed adjustments were not large except for that due to the Limousin base change: from 0.2 to -15.9 lb for Limousin, 3.8 to 1.7 lb for Gelbvieh, 11.3 to 9.0 lb for Salers, and -10.7 to -7.8 lb for Red Angus.
   b) The first crop of Brangus and Beefmaster sired heifers had calves with weaning weights available this year but the numbers (about 20 of each) were

considered too small to analyze this year as half of the heifers had been moved to an experiment in Louisiana.

The across-breed table adjustments apply **only** to EPDs for most recent (in most cases; spring, 2004) national cattle evaluations. Serious biases can occur if the table adjustments are used with earlier EPDs which may have been calculated with a different within-breed base.

Materials and Methods

Adjustment for heterosis

The philosophy underlying the calculations has been that bulls compared using the across-breed adjustment factors will be used in a crossbreeding situation. Thus calves and cows would generally exhibit 100% of both direct and maternal heterozygosity for the MILK analysis and 100% of direct heterozygosity for the BWT, WWT, and YWT analyses. The use of the MARC III composite (1/4 each of Pinzgauer, Red Poll, Hereford, and Angus) as a dam breed for Angus, Brangus, Hereford and Red Angus sires requires a small adjustment for level of heterozygosity for analyses of calves for BWT, WWT and YWT and for cows for maternal weaning weight. Some sires (all multiple sire pasture mated) mated to the F1 cows are also crossbred so that adjustment for direct heterozygosity for the maternal analysis is required. Two approaches for accounting for differences in breed heterozygosity have been tried which resulted in similar final table adjustments. One approach was to include level of heterozygosity in the statistical models which essentially adjusts to a basis of no heterozygosity. The other approach was based on the original logic that bulls will be mated to another breed or line of dam so that progeny will exhibit 100% heterozygosity. Most of the lack of heterozygosity in the data results from homozygosity of Hereford or Angus genes from pure Hereford or Angus matings and also from Red Angus by Angus and from Hereford, Angus or Red Angus sires mated with MARC III composite dams (1/4 each, Pinzgauer, Red Poll, Hereford, and Angus). Consequently, the second approach was followed with estimates of heterosis obtained from analyses of BWT, WWT, YWT, and MWWT using only records from the imbedded diallel experiments with Hereford and Angus. Red Angus by Angus matings were assumed not to result in heterosis. With Brangus representing 5/8 and 3/8 inheritance from Angus and Brahman genes, records of Brangus sired calves were also adjusted to a full F1 basis when dams were Angus cows and MARC III cows (1/4 Angus). The adjustment for calves with Beefmaster (1/2 Brahman, 1/4 Shorthorn, 1/4 Hereford) sires was only when dams were MARC III cows (1/4 Hereford) as Beefmaster sires were not mated to Hereford cows.

The steps were:

1) Analyze records from H-A diallel experiments to estimate direct heterosis effects for BWT, WWT, YWT (1,326, 1,279, and 1,249 records for BWT, WWT, and YWT, respectively, representing 152 sires). The H-A diallel experiments were conducted as part of Cycle I (1970-1972 calf crops), Cycle II (1973-1974), Cycle IV (1986-1990) and Cycle VII (1999-2001) of the GPE program at MARC.
2) Adjust maternal weaning weight (MWWT) records of calves of the H-A cows from the diallel for estimates of direct heterosis from 1) and then estimate maternal heterosis effects from 3,255 weaning weight records of 776 daughters representing 171 Hereford and Angus maternal grandsires.
3) Adjust all records used for analyses of BWT, WWT and YWT for lack of direct heterozygosity using estimates from 1), and
4) Adjust all records used for analysis of MWWT for lack of both direct and maternal heterozygosity using estimates from 1) and 2).

Models for the analyses to estimate heterosis were the same as for the across-breed analyses with the obvious changes in breed of sire and breed of dam effects.

Estimates of direct heterosis were 3.01, 14.70, and 30.39 lb for BWT, WWT and YWT, respectively. The estimate of maternal heterosis was 23.05 lb for MWWT. As an example of step 3), birth weight of an H by H calf would have 3.01 added. A Red Angus by MARC III calf would have (1/4) (3.01) added to its birth weight. A Red Poll sired calf of an Angus by MARC III dam would have (1/8) (14.70) plus (1/4) (23.05) added to its weaning weight record to adjust to 100% heterozygosity for both direct and maternal components of weaning weight.

After these adjustments, all calculations were as outlined in the 1996 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), and Van Vleck and Cundiff (1997–2003). All calculations were done with programs written in Fortran language with estimates of variance components, regression coefficients, and breed effects obtained with 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 EPDs are relative to Angus.

For completeness, the basic steps in the calculations will be repeated.

Models for Analysis of MARC Records

Fixed effects in the models for birth weight, weaning weight (205-d) and yearling weight (365-d) were: breed of sire (17), dam line (Hereford, Angus, MARC III composite) by sex (female, male) by age of dam (2, 3, 4, 5-9, ≥10 yr) combination (49), year of birth (21) of dam (1970-76, 86-90, 92-94 and 97-99, 2000-02) by damline combination (101) and a separate covariate for day of year at birth of calf for each of the three breeds of dam. Cows from the Hereford selection lines were used in Cycle IV of GPE. To account for differences from the original Hereford cows, Hereford dams were subdivided into the selection lines and others. That refinement of the model had little effect on breed of sire solutions. Dam of calf was included as a random effect to account for correlated maternal effects for cows with more than one calf (4,630 dams for BWT, 4,395 for WWT, 4,243 for YWT). For estimation of variance components and to estimate breed of sire effects, sire of calf was also used as a random effect (650).

Variance components were estimated with a derivative-free REML algorithm. At convergence, the breed of sire solutions were obtained as were the sampling variances of the estimates to use in constructing prediction error variances for pairs of bulls of different breeds.

For estimation of coefficients of regression of progeny performance on EPD of sire, the random sire effect was dropped from the model. Pooled regression coefficients, and regression coefficients by sire breed, by dam line, and by sex of calf 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 later to adjust for genetic trend and bulls used at MARC.

The fixed effects for the analysis of maternal effects included breed of maternal grandsire (15), maternal granddam line (Hereford, Angus, MARC III), breed of natural service mating sire (17), sex of calf (2), birth year-GPE cycle-age of dam subclass (79), and mating sire breed by GPE cycle by age of dam subclass (43) with a covariate for day of year of birth. The subclasses are used to account for confounding of years, mating sire breeds, and ages of dams. Ages of dam classes were (2, 3, 4, 5-9, ≥10 yr). For estimation of variance components and estimation of breed of maternal grandsire effects, random effects were maternal grandsire (573) and dam (3,017 daughters of the maternal grandsires). Mating sires were unknown within breed. For estimation of regression coefficients of grandprogeny weaning weight on maternal grandsire EPD for weaning weight and milk, random effects of both maternal grandsire and dam (daughter of MGS) were dropped from the model.

Adjustment of MARC Solutions

The calculations of across-breed adjustment factors rely on solutions for breed of sire or breed of maternal grandsire from records at MARC and on averages of within-breed EPDs. The records from MARC are not used in calculation of within-breed EPD by the breed associations. The basic calculations for BWT, WWT, and YWT are as follows:

MARC breed of sire solution adjusted for genetic trend (as if bulls born in the base year had been used rather than the bulls actually used).

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

Breed table factor 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,

MARC(i) is solution from mixed model equations with MARC data for sire breed i,

EPD(i)_{YY} is the average within-breed EPD for breed i for animals born in the base year (YY, which is two years before the update; e.g., YY = 2002 for the 2004 update),

EPD(i)_{MARC} is the weighted (by number of progeny at MARC)

average of EPD of bulls of breed i having progeny with records at MARC,

b is the pooled coefficient of regression of progeny performance at MARC on EPD of sire (for 2004: 1.05, 0.86, and 1.13 for BWT, WWT, YWT),

i denotes sire breed i, and

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

The calculations to arrive at the Breed Table Factor for milk are more complicated because of the need to separate the direct effect of the maternal grandsire breed from the maternal (milk) effect of the breed.

MARC breed of maternal grandsire solution for WWT adjusted for genetic trend:

$$\text{MWWT(i)} = \text{MARC(i)}_{MGS} + b_{wwt}[\text{EPD(i)}_{YYWWT} - \text{EPD(i)}_{MARCWWT}] + b_{MLK}[\text{EPD(i)}_{YYMLK} - \text{EPD(i)}_{MARCMLK}]$$

MARC breed of maternal grandsire solution adjusted for genetic trend and direct genetic effect:

$$\text{MILK(i)} = [\text{MWWT(i)} - 0.5\ \text{M(i)}] - [\overline{\text{MWWT}} - 0.5\ \overline{\text{M}}]$$

Breed table factor to add to EPD for MILK for bull of breed i:

$$A_i = [\text{MILK(i)} - \text{MILK(x)}] - [\text{EPD(i)}_{YYMLK} - \text{EPD(i)}_{MARCMLK}]$$

where,

$MARC(i)_{MGS}$ is solution from mixed model equations with MARC data for MGS breed i for WWT,

$EPD(i)_{YYWWT}$ is the average within-breed EPD for WWT for breed i for animals born in base year (YY),

$EPD(i)_{MARCWWT}$ is the weighted (by number of grandprogeny at MARC) average of EPD for WWT of MGS of breed i having grandprogeny with records at MARC,

$EPD(i)_{YYMLK}$ is the average within-breed EPD for MILK for breed i for animals born in base year (YY),

$EPD(i)_{MARCMLK}$ is the weighted (by number of grandprogeny at MARC) average of EPD for MILK of MGS of breed i having grandprogeny with records at MARC,

b_{WWT}, b_{MLK} are the coefficients of regression of performance of MARC grandprogeny on MGS EPD for WWT and MILK (for 2004: 0.59 and 1.13),

$M(i) = M_i$ is the MARC breed of sire solution from the first analysis of direct breed of sire effects for WWT adjusted for genetic trend,

$\overline{MWWT}$ and $\overline{M}$ are unneeded constants corresponding to unweighted averages of MWWT(i) and M(i) for i = 1,..., n, the number of sire (maternal grandsire) breeds included in the analysis.

Results

Tables 1, 2, and 3 (for BWT, WWT and YWT) summarize the data from, and results of, MARC analyses to estimate breed of sire differences and the adjustments to the breed of sire effects to a year 2002 base. The last column of each table corresponds to the "breed table" factor for that trait.

The general result shown in Tables 1-4 is that many breeds are continuing to become more similar to the arbitrary base breed, Angus. Most of the other breeds have not changed much relative to each other. Column 7 of Tables 1-3 and column 10 of Table 4 represent the best estimates of breed differences for calves born in 2002. These pairs of differences minus the corresponding differences in average EPD for animals born in 2002 result in the last column of the tables to be used as adjustment factors for pairs of sires with within-breed EPD.

Birth Weight

The range in estimated breed of sire differences for BWT relative to Angus is large: from 1.5 lb for Red Angus to 9.4 lb for Charolais and 12.5 lb for Brahman. The relatively heavy birth weights of Brahman sired progeny would be expected to be completely 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. Differences from Angus were only slightly changed from the 2003 update but most of the changes were generally to slightly smaller differences from Angus.

Suppose the EPD for birth weight for a Charolais bull is +2.0 (which is above the year 2002 average of 1.5 for Charolais) and for a Hereford bull is also +2.0 (which is below the year 2002 average of 3.8 for Herefords). The across-breed adjustment factors in the last column of Table 1 are 3.5 for Hereford and 10.5 for Charolais. Then the adjusted EPD for the Charolais bull is 10.5 + 2.0 = 12.5 and for the Hereford bull is 3.5 + 2.0 = 5.5. The expected birth weight difference when both are mated to another breed of cow, e.g., Angus, would be 12.5 - 5.5 = 7.0 lb.

Weaning Weight

Weaning weights also seem to be becoming more similar for the breeds when used as sire breeds. Most of the changes between the year 2003 and 2004 updates were less than 2 lb. All except three sire breed means for WWT adjusted to year of birth of 2002 are within about 10 lb of the Angus mean.

Yearling Weight

Changes in adjusted differences from Angus from the 2003 update were generally small: 1 to 2 lb. The major exceptions were for Brangus and Beefmaster where two and three records which should have been removed from the data base last year were removed this year. More importantly, April weights rather than March weights were available for use this year for the 2002 calf crop which would be less affected by adverse effects of cold weather on postweaning growth rate of progeny with Brahman influenced sires. The result was that the adjusted differences from Angus for the current base year went from -18.4 to -11.1 lb for Brangus and from -22.2 to -16.0 lb for Beefmaster. Adjusted to a base year of 2002, Angus have heavier yearling weights than 11 breeds (11.1 to 44.1 lb), lighter yearling weights than 2 breeds (14.7 and 20.4 lb) and nearly the same as 3 breeds (-0.7 to 0.1 lb).

Milk

The greatest changes from last year for MILK compared to Angus for the current base year were for breeds that added about 75 grandprogeny: -3.5, -2.7, -2.7, and +3.0 lb for Limousin, Charolais, Gelbvieh, and Red Angus, respectively. Red Angus added 74 records to the previous

112 records. The other 3 breeds generally added less than 10% more maternal weaning weight records. The comparison of Hereford and Angus changed very little although both added about 160 weaning weights to the analysis for milk. For MILK with breeds adjusted to the current base year, Angus were within 2.3 lb of 4 breeds, exceeded 8 breeds (2.9 to 15.2 lb) and trailed only 2 breeds (4.8 for Braunvieh and 15.0 lb for Brahman). The greatest changes in the across-breed adjustment factors were for Limousin which has changed its base and for Red Angus which changed somewhat due to the additional grandprogeny weaning weights.

Table 5 summarizes the average BIF accuracy for bulls with progeny at MARC weighted appropriately by number of progeny or grandprogeny. South Devon bulls had relatively small accuracy for all traits as did Hereford, Brahman, and Maine-Anjou bulls. Braunvieh bulls had low accuracy for milk. The accuracy values for Brangus are relatively high. Table 6 reports the estimates of variance components from the records that were used in the mixed model equations to obtain breed of sire and breed of MGS solutions. Neither Table 5 nor Table 6 changed much from the 2003 report.

Table 7 updates the coefficients of regression of records of MARC 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 1.05 for BWT, 0.86 for WWT, and 1.13 for YWT were used to adjust breed of sire solutions to the base year of 2002. These regression coefficients are reasonably close to expected values of 1.0. Deviations from 1.0 are believed to be due to scaling differences between performance of progeny in the MARC herd and of progeny in herds contributing to the national genetic evaluations of the 17 breeds.

The regression coefficient for female progeny on sire EPD for YWT was 0.93 compared to 1.30 for steers. These differences are probably expected because postweaning average daily gains for heifers have been significantly less than those for steers. The females were fed relatively high roughage diets to support average daily gains of 1.6 lb per day while the steers were fed relatively high energy growing and finishing diets supporting average daily gains of about 3.4 lb per day. For reasons that have never been clear, the regressions for sex used to fluctuate widely from year to year, but for the past six years the pattern has been fairly consistent (female estimates have ranged from 0.93 to 1.02; while male estimates have ranged from 1.26 to 1.32).

The coefficients of regression of records of grandprogeny on MGS EPD for WWT and MILK are shown in Table 8. Several sire (MGS) breeds have regression coefficients considerably different from the theoretical expected values of 0.50 for WWT and 1.00 for MILK. The standard errors for the regression coefficients by breed are large except for Angus and Hereford. The standard errors for regression coefficients over all breeds of grandsires associated with heifers and steers overlap for milk EPD. Again, the pooled regression coefficients of 0.59 for MWWT and 1.13 for MILK are reasonably close to the expected regression coefficients of 0.50 and 1.00, respectively.

Prediction Error Variances of Across-Breed EPD

The standard errors of differences in the solutions for breed of sire and breed of MGS differences from the MARC records can be adjusted by theoretical approximations to obtain variances of adjusted breed differences (Van Vleck, 1994; Van Vleck and Cundiff, 1994). These variances of estimated breed differences can be added to prediction error variances of within-breed EPDs to obtain prediction error variances (PEV) or equivalently standard errors of prediction (SEP) for across-breed EPDs (Van Vleck and Cundiff 1994, 1995). The variances of adjusted breed differences are given in the upper triangular part of Table 9 for BWT, lower triangular part of Table 9 for YWT, upper triangular part of Table 10 for direct WWT, and lower triangular part of Table 10 for MILK. How to use these to calculate standard errors of prediction for expected progeny differences of pairs of bulls of the same or different breeds was discussed in the 1995 BIF proceedings (Van Vleck and Cundiff, 1995).

Even though the variances of estimates of adjusted breed differences look large, especially for YWT and MILK, they generally contribute a relatively small amount to standard errors of predicted differences. For example, suppose for WWT, a Salers bull has an EPD of 15.0 with prediction error variance of 75 and a Hereford bull has an EPD of 30.0 with PEV of 50. The difference in predicted progeny performance is (Salers adjustment + Salers bull's EPD) - (Hereford adjustment + Hereford bull's EPD):

$$(30.7 + 15.0) - (-2.0 + 30.0) = 45.7 - 28.0 = 17.7.$$

The prediction error variance for this difference is (use the 18.0 in the upper part of Table 10 at intersection of row for HE and column for SA):

V(Salers breed - Hereford breed) + PEV(Salers bull) + PEV(Hereford bull):

$$18 + 75 + 50 = 143$$

with

standard error of prediction, $\sqrt{143} = 12$.

If the difference between the Salers and Hereford breeds in the year 2002 could be estimated perfectly, the

variance of the estimate of the breed difference would be 0 and the standard error of prediction between the two bulls would be:

$\sqrt{0+75+50} = 11.2$ which is only slightly smaller than 12.0.

Implications

Bulls of different breeds can be compared on a common EPD scale by adding the appropriate table factor to expected progeny differences (EPDs) produced in the most recent genetic evaluations for each of the 17 breeds. The across-breed EPDs are most useful to commercial producers purchasing bulls of two or more breeds to use in systematic crossbreeding programs. Uniformity in across-breed EPDs should be emphasized for rotational crossing. Divergence in across-breed EPDs 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 EPDs depends primarily upon the accuracy of the within-breed EPDs of individual bulls being compared.

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Table 1. Breed of sire solutions from MARC, mean breed and MARC EPDs used to adjust for genetic trend to 2002 base and factors to adjust within breed EPDs to Angus equivalent - BIRTH WEIGHT (lb)

Breed	Number Sires	Number Progeny	Raw MARC Mean (1)	Ave. Base EPD Breed 2002 (2)	Ave. Base EPD MARC Bulls (3)	Breed Soln at MARC + Ang vs Ang (4)	Breed Soln at MARC + Ang vs Ang (5)	Adjust to 2002 Base + Ang vs Ang (6)	Adjust to 2002 Base + Ang vs Ang (7)	Factor to adjust EPD to Angus (8)
Hereford	113	1817	87	3.8	2.4	88	3.6	89	4.6	3.4
Angus	105	1421	84	2.6	2.2	84	0.0	84	0.0	0.0
Shorthorn	25	181	87	1.8	0.9	90	6.4	91	7.0	7.8
South Devon	15	153	80	0.0	-0.2	88	4.3	89	4.1	6.7
Brahman	40	589	98	2.1	0.7	96	11.6	97	12.5	13.0
Simmental	48	623	87	1.9	2.7	91	7.0	90	5.7	6.4
Limousin	40	589	83	2.4	0.7	87	3.0	89	4.3	4.5
Charolais	75	675	89	1.5	0.5	93	8.8	94	9.4	10.5
Maine-Anjou	18	218	94	2.5	5.9	95	10.6	91	6.6	6.7
Gelbvieh	48	595	89	1.0	0.9	88	4.1	88	3.8	5.4
Pinzgauer	16	435	84	-0.1	-0.4	89	5.2	89	5.0	7.7
Tarentaise	7	199	80	2.2	1.8	87	3.2	88	3.2	3.6
Salers	27	189	85	1.1	1.7	88	4.4	88	3.4	4.9
Red Angus	21	206	85	0.5	-0.7	85	0.6	86	1.5	3.6
Braunvieh	7	188	88	1.1	0.8	89	5.1	89	5.0	6.5
Brangus	21	215	91	2.0	2.4	90	5.9	90	5.1	5.7
Beefmaster	21	214	96	0.4	0.8	92	8.3	92	7.5	9.7

Calculations:
(4) = (5) + (1, Angus)
(6) = (4) + b[(2) - (3)] with b = 1.05
(7) = (6) - (6, Angus)
(8) = (7) - (7, Angus) - [(2) - (2, Angus)]

Table 2. Breed of sire solutions from MARC, mean breed and MARC EPDs used to adjust for genetic trend to 2002 base and factors to adjust within breed EPDs to Angus equivalent - WEANING WEIGHT (lb)

Breed	Number Sires	Number Progeny	Raw MARC Mean (1)	Ave. Base EPD Breed 2002 (2)	Ave. Base EPD MARC Bulls (3)	Breed Soln at MARC + Ang vs Ang (4)	Breed Soln at MARC + Ang vs Ang (5)	Adjust to 2002 Base + Ang vs Ang (6)	Adjust to 2002 Base + Ang vs Ang (7)	Factor to adjust EPD to Angus (8)
Hereford	112	1712	503	35.0	22.5	501	-2.7	512	-2.0	-2.0
Angus	106	1315	504	35.0	23.3	504	0.0	514	0.0	0.0
Shorthorn	25	170	521	13.0	6.7	518	14.1	523	9.4	31.4
South Devon	15	134	443	17.1	0.2	503	-0.6	518	3.8	21.7
Brahman	40	509	532	16.1	4.6	520	16.1	530	15.9	34.8
Simmental	47	564	505	33.6	23.5	526	22.4	535	21.0	22.4
Limousin	40	533	477	33.8	20.4	503	-0.8	514	0.6	1.8
Charolais	74	600	514	18.2	8.5	527	23.3	535	21.6	38.4
Maine-Anjou	18	197	459	15.9	23.6	519	15.1	513	-1.5	17.6
Gelbvieh	48	559	507	36.4	31.4	518	14.3	522	8.5	7.1
Pinzgauer	16	415	478	0.6	-4.1	504	-0.1	508	-6.1	28.3
Tarentaise	7	191	476	12.0	-4.8	507	2.7	521	7.1	30.1
Salers	27	176	525	12.0	5.0	516	11.7	522	7.7	30.7
Red Angus	21	199	535	28.0	27.2	505	1.0	506	-8.4	-1.4
Braunvieh	7	183	451	6.6	7.0	516	12.0	516	1.6	30.0
Brangus	21	208	550	20.9	26.1	524	20.3	520	5.9	20.0
Beefmaster	22	215	563	6.0	13.3	530	26.3	524	10.0	39.0

Calculations:
(4) = (5) + (1, Angus)
(6) = (4) + b[(2) - (3)] with b = 0.86
(7) = (6) - (6, Angus)
(8) = (7) - (7, Angus) - [(2) - (2, Angus)]

Table 3. Breed of sire solutions from MARC, mean breed and MARC EPDs used to adjust for genetic trend to 2002 base and factors to adjust within breed EPDs to Angus equivalent - YEARLING WEIGHT (lb)

Breed	Number Sires	Number Progeny	Raw MARC Mean (1)	Ave. Base EPD Breed 2002 (2)	Ave. Base EPD MARC Bulls (3)	Breed Soln at MARC + Ang vs Ang (4)	Breed Soln at MARC + Ang vs Ang (5)	Adjust to 2002 Base + Ang vs Ang (6)	Adjust to 2002 Base + Ang vs Ang (7)	Factor to adjust EPD to Angus (8)
Hereford	112	1627	852	60.0	38.4	852	-20.0	876	-18.7	-13.7
Angus	106	1257	872	65.0	44.4	872	0.0	895	0.0	0.0
Shorthorn	25	168	918	20.0	13.2	887	15.0	895	-0.5	44.5
South Devon	15	134	744	23.5	0.3	868	-3.7	894	-0.7	40.8
Brahman	40	438	838	26.3	8.4	832	-40.1	852	-43.1	-4.4
Simmental	47	528	852	57.8	39.0	889	16.7	910	14.7	21.9
Limousin	40	527	797	63.5	41.2	849	-23.3	874	-21.4	-19.9
Charolais	74	566	882	32.0	15.6	897	25.1	916	20.4	53.4
Maine-Anjou	18	196	787	31.1	46.6	884	12.3	867	-28.4	5.5
Gelbvieh	48	555	849	68.9	56.7	864	-7.8	878	-17.2	-21.1
Pinzgauer	16	347	838	0.7	-8.0	847	-25.3	856	-38.8	25.5
Tarentaise	7	189	807	23.0	-3.4	837	-35.2	867	-28.6	13.4
Salers	27	173	899	19.0	5.3	880	7.8	895	0.1	46.1
Red Angus	21	194	916	48.0	46.7	877	5.4	879	-16.3	0.7
Braunvieh	7	182	737	7.0	10.9	856	-16.4	851	-44.1	13.9
Brangus	21	152	977	33.5	44.2	896	24.1	884	-11.1	20.4
Beefmaster	22	157	991	11.1	23.3	893	20.9	879	-16.0	37.9

Calculations:
(4) = (5) + (1, Angus)
(6) = (4) + b[(2) - (3)] with b = 1.13
(7) = (6) - (6, Angus)
(8) = (7) - (7, Angus) - [(2) - (2, Angus)]

Table 4. Breed of maternal grandsire solutions from MARC, mean breed and MARC EPDs used to adjust for genetic trend to 2002 base and factors to adjust within-breed EPDs to Angus equivalent - MILK (lb)

		Number		Raw MARC Mean	Mean EPD Breed		MARC		Breed Soln at MARC MWWT + Ang vs Ang		Adjust to 2002 Base MWWT + Ang vs Ang			Factor to Adjust MILK EPD to Angus
Breed	MGS	Gpr	Daughters	(1)	WWT (2)	MILK (3)	WWT (4)	MILK (5)	(6)	(7)	(8)	(9)	(10)	(11)
Hereford	103	2565	668	473	35.0	13.0	19.4	6.1	470	-19.5	487	-22.8	-17.7	-17.8
Angus	101	1826	488	490	35.0	17.0	17.7	8.1	490	0.0	510	0.0	4.1	0.0
Shorthorn	22	251	69	527	13.0	2.0	6.7	7.0	514	24.0	512	1.8	1.2	12.1
South Devon	14	347	69	488	17.1	6.2	0.1	5.4	494	4.0	505	-5.4	-3.2	3.5
Brahman	40	880	216	522	16.1	7.4	4.8	3.0	522	31.6	533	23.0	19.1	24.6
Simmental	47	983	239	510	33.6	5.6	20.0	8.3	514	24.4	519	9.1	2.7	10.0
Limousin	40	952	238	475	33.8	17.7	16.7	15.4	483	-7.3	495	-14.9	-11.1	-15.9
Charolais	68	894	235	499	18.2	5.7	5.5	2.5	501	11.3	512	2.1	-4.6	2.6
Maine-Anjou	17	485	86	533	15.9	3.5	22.9	4.7	509	19.1	504	-6.7	-1.8	7.6
Gelbvieh	46	843	231	526	36.4	17.3	30.9	17.3	513	23.3	517	6.3	6.1	1.7
Pinzgauer	15	545	133	504	0.6	-1.0	-1.7	6.4	502	12.4	495	-14.9	-7.7	6.1
Tarentaise	6	341	78	513	12.0	1.5	-6.0	4.7	509	19.2	516	5.8	6.4	17.8
Salers	25	351	87	534	12.0	8.0	3.5	12.0	514	23.7	514	3.9	4.1	9.0
Red Angus	21	186	88	465	28.0	14.0	27.3	14.3	495	5.2	495	-14.9	-6.6	-7.8
Braunvieh	7	502	92	542	6.6	-0.4	7.7	-0.8	516	26.1	516	5.6	8.9	22.2

Calculations:
(6) = (7) + (1, Angus)
(8) = (6) + b_{WWT} [(2) - (4)] + b_{MLK} [(3) - (5)] with b_{WWT} = 0.59 and b_{MLK} = 1.13
(9) = (8) - (8, Angus)
(10) = [(9) - Average (9)] - 0.5[(7, Table 2) - Average (7, Table 2)]
(11) = [(10) - (10, Angus)] - [(3) - (3, Angus)]

Table 5. Mean weighted[a] accuracies for birth weight (BWT), weaning weight (WWT), yearling weight (YWT), maternal weaning weight (MWWT) and milk (MILK) for bulls used at MARC

Breed	BWT	WWT	YWT	MWWT	MILK
Hereford	0.56	0.53	0.48	0.49	0.47
Angus	0.87	0.87	0.84	0.83	0.82
Shorthorn	0.82	0.80	0.74	0.81	0.78
South Devon	0.37	0.39	0.37	0.41	0.42
Brahman	0.50	0.54	0.37	0.55	0.42
Simmental	0.94	0.93	0.93	0.95	0.94
Limousin	0.92	0.88	0.82	0.90	0.85
Charolais	0.71	0.65	0.56	0.63	0.54
Maine-Anjou	0.72	0.71	0.71	0.71	0.71
Gelbvieh	0.72	0.65	0.52	0.68	0.56
Pinzgauer	0.85	0.68	0.62	0.70	0.64
Tarentaise	0.95	0.95	0.94	0.95	0.95
Salers	0.83	0.82	0.77	0.82	0.83
Red Angus	0.87	0.84	0.84	0.84	0.80
Braunvieh	0.84	0.85	0.83	0.85	0.77
Brangus	0.76	0.75	0.61	–	–
Beefmaster	0.63	0.72	0.57	–	–

[a]Weighted by number of progeny at MARC for BWT, WWT, and YWT and by number of grandprogeny for MWWT and MILK.

Table 6. REML estimates of variance components (lb^2) for birth weight (BWT), weaning weight (WWT), yearling weight (YWT), and maternal weaning weight (MWWT) from mixed model analyses

	Direct			Maternal
Analysis[a]	BWT	WWT	YWT	MWWT
Direct				
Sires (650) within breed (17)	11.4	152	631	
Dams (4395) within breed (3)	26.6	876	1233	
Residual	68.2	1535	4037	
Maternal				
MGS (573) within MGS breed (15)				192
Daughters within MGS (3017)				916
Residual				1303

[a]Numbers for weaning weight.

Table 7. Pooled regression coefficients (lb/lb) for weights at birth (BWT), 205 days (WWT), and 365 days (YWT) of F_1 progeny on sire expected progeny difference and by sire breed, dam breed, and sex of calf

	BWT	WWT	YWT
Pooled	1.05 ± 0.05	0.86 ± 0.05	1.13 ± 0.05
Sire breed			
Hereford	1.16 ± 0.08	0.78 ± 0.07	1.12 ± 0.07
Angus	1.02 ± 0.11	0.80 ± 0.10	1.16 ± 0.08
Shorthorn	0.64 ± 0.48	0.75 ± 0.42	1.15 ± 0.34
South Devon	0.92 ± 0.58	-0.18 ± 0.37	-0.06 ± 0.41
Brahman	1.82 ± 0.27	1.11 ± 0.27	0.69 ± 0.24
Simmental	1.05 ± 0.22	1.23 ± 0.17	1.27 ± 0.15
Limousin	0.68 ± 0.17	0.55 ± 0.16	1.16 ± 0.15
Charolais	1.01 ± 0.14	0.95 ± 0.14	0.92 ± 0.13
Maine-Anjou	1.08 ± 0.37	0.55 ± 0.49	0.15 ± 0.50
Gelbvieh	1.01 ± 0.16	1.27 ± 0.27	1.34 ± 0.22
Pinzgauer	1.26 ± 0.17	1.49 ± 0.21	1.66 ± 0.16
Tarentaise	0.67 ± 0.89	0.76 ± 0.55	1.38 ± 0.61
Salers	1.20 ± 0.39	0.98 ± 0.45	0.80 ± 0.45
Red Angus	0.55 ± 0.19	0.55 ± 0.34	0.77 ± 0.30
Braunvieh	0.46 ± 0.37	0.78 ± 0.76	1.97 ± 0.53
Brangus	1.25 ± 0.32	0.81 ± 0.46	0.39 ± 0.41
Beefmaster	1.61 ± 0.57	1.48 ± 0.38	1.60 ± 0.43
Dam breed			
Hereford	0.98 ± 0.08	0.79 ± 0.08	1.00 ± 0.07
Angus	1.12 ± 0.06	0.89 ± 0.07	1.17 ± 0.06
MARC III	.99 ± 0.08	0.86 ± 0.09	1.20 ± 0.09
Sex of calf			
Heifers	1.03 ± 0.06	0.96 ± 0.06	0.93 ± 0.06
Steers	1.06 ± 0.06	0.76 ± 0.06	1.30 ±.0 06

Table 8. Pooled regression coefficients (lb/lb) for progeny performance on maternal grandsire EPD for weaning weight (MWWT) and milk (MILK) and by breed of maternal grandsire, breed of maternal grandam, and sex of calf

Type of regression	MWWT	MILK
Pooled	0.59 ± 0.04	1.13 ± 0.06
Breed of maternal grandsire		
Hereford	0.57 ± 0.06	1.14 ± 0.11
Angus	0.60 ± 0.09	1.07 ± 0.13
Shorthorn	0.30 ± 0.36	0.83 ± 0.49
South Devon	0.31 ± 0.25	-1.16 ± 0.82
Brahman	0.44 ± 0.21	0.54 ± 0.33
Simmental	0.73 ± 0.18	1.08 ± 0.44
Limousin	1.12 ± 0.14	2.00 ± 0.26
Charolais	0.44 ± 0.12	1.39 ± 0.22
Maine-Anjou	0.13 ± 0.34	0.47 ± 0.38
Gelbvieh	0.96 ± 0.25	1.56 ± 0.33
Pinzgauer	0.71 ± 0.19	0.28 ± 0.58
Tarentaise	0.20 ± 0.67	0.76 ± 0.81
Salers	0.89 ± 0.32	2.24 ± 0.35
Red Angus	0.71 ± 0.36	1.34 ± 0.39
Braunvieh	0.00 ± –	2.83 ± –
Breed of maternal grandam		
Hereford	0.57 ± 0.06	1.51 ± 0.10
Angus	0.63 ± 0.05	1.18 ± 0.09
MARC III	0.52 ± 0.08	0.80 ± 0.12
Sex of calf		
Heifers	0.60 ± 0.05	1.13 ± 0.08
Steers	0.58 ± 0.05	1.12 ± 0.08

Table 9. Variances (lb^2) of adjusted breed differences to add to sum of within breed prediction error variances to obtain variance of differences of across breed EPDs for bulls of two different breeds[a]. Birth weight above diagonal and yearling weight below the diagonal.

Breed	HE	AN	SH	SD	BR	SI	LI	CH	MA	GE	PI	TA	SA	RA	BV	BS	BM
HE	0.0	0.2	0.8	1.4	0.5	0.5	0.5	0.4	1.0	0.4	0.8	2.6	0.8	0.8	1.2	0.9	1.0
AN	14	0.0	0.9	1.4	0.5	0.5	0.5	0.4	1.1	0.5	0.9	2.6	0.8	0.8	1.2	0.9	1.0
SH	53	54	0.0	2.0	1.2	1.1	1.2	1.0	1.6	1.0	1.3	3.1	1.1	1.4	1.7	1.7	1.7
SD	83	83	122	0.0	1.7	1.3	1.4	1.3	2.1	1.6	2.0	3.7	1.9	1.8	2.3	2.2	2.3
BR	36	37	78	110	0.0	0.9	0.9	0.8	1.3	0.8	0.9	2.6	1.1	1.2	1.5	1.3	1.4
SI	28	29	69	80	56	0.0	0.5	0.5	1.3	0.6	1.1	2.8	1.1	0.8	1.4	1.3	1.3
LI	31	31	72	83	58	30	0.0	0.5	1.3	0.7	1.1	2.9	1.1	0.9	1.5	1.3	1.4
CJ	24	25	61	81	52	29	31	0.0	1.2	0.5	1.0	2.7	0.9	0.8	1.3	1.2	1.3
MA	62	64	97	128	86	75	78	72	0.0	1.0	1.5	3.2	1.5	1.6	1.1	1.9	1.9
GE	28	29	64	95	54	38	39	34	62	0.0	1.0	2.8	0.9	0.8	1.2	1.2	1.3
PI	53	55	85	123	65	69	72	64	94	64	0.0	2.6	1.3	1.4	1.6	1.7	1.7
TA	151	154	188	220	158	167	170	163	191	164	156	0.0	3.1	3.2	3.4	3.4	3.5
SA	49	50	70	118	74	66	68	57	93	60	83	184	0.0	1.4	1.7	1.6	1.7
RA	46	46	88	111	75	49	51	48	95	52	89	188	84	0.0	1.7	1.5	1.6
BV	69	71	105	135	93	83	85	79	68	69	102	198	101	102	0.0	2.0	2.1
BS	66	65	114	142	97	86	88	83	123	86	114	213	110	100	130	0.0	1.0
BM	66	66	115	142	97	86	89	83	123	87	115	213	111	102	131	78	0.0

[a]For example, a Hereford bull has within breed PEV of 300 for YWT and that for a Shorthorn bull is 200. Then the PEV for the difference in EPDs for the two bulls is 53 + 300 + 200 = 553 with SEP $= \sqrt{553} = 23.5$.

Table 10. Variances (lb^2) of adjusted breed differences to add to sum of within breed prediction error variances to obtain variance of difference of across breed EPDs for bulls of two different breeds. Weaning weight direct above diagonal and MILK below the diagonal.

Breed	HE	AN	SH	SD	BR	SI	LI	CH	MA	GE	PI	TA	SA	RA	BV	BS	BM
HE	0	4	19	28	11	9	10	8	22	9	15	42	18	17	24	20	20
AN	14	0	20	28	11	10	10	8	23	9	16	43	18	17	25	20	20
SH	50	52	0	43	27	25	26	22	36	23	29	56	26	33	38	38	38
SD	58	59	97	0	36	27	28	27	45	32	40	66	42	39	47	46	46
BR	25	27	65	74	0	18	18	16	29	17	18	43	25	26	31	29	29
SI	26	27	65	60	42	0	10	9	27	12	21	48	24	18	29	27	27
LI	28	29	67	62	44	31	0	10	28	13	22	48	25	18	29	28	28
CJ	21	23	58	59	37	28	30	0	26	11	19	46	21	18	27	26	26
MA	54	57	91	100	69	68	70	63	0	22	31	58	35	35	24	41	41
GE	23	25	59	68	39	34	36	29	58	0	19	46	21	19	23	27	27
PI	50	53	84	97	57	66	67	60	82	61	0	41	27	29	33	34	34
TA	122	125	160	169	126	138	140	133	153	122	133	0	55	56	59	61	60
SA	41	44	69	88	57	57	58	49	82	50	69	148	0	31	37	37	37
RA	47	48	86	89	64	53	54	50	95	60	90	146	84	0	37	34	34
BV	81	83	118	126	96	95	96	90	97	83	115	187	100	115	0	43	42
BS	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0	21
BM	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0

Mean EPDs Reported by Different Breeds

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The mean non-parent EPDs are shown for growth traits in Table 1 for 17 different breeds. The mean EPDs for certain carcass traits are shown in Table 2 for 10 breeds. The mean EPDs for reproduction and certain other traits are shown in Table 3 for 10 breeds. Mean non-parent EPDs are useful only for making comparison within breeds. They can not be used to compare different breeds because EPDs are estimated from separate analyses for each breed. These estimates are from the most current genetic evaluation conducted by each breed. They are presented here primarily to show the traits included in genetic evaluations of various breeds.

Table 1. 2002 non-parent average EPDs from 2004 evaluations.

Breed	Birth wt.	Weaning wt.	Yearling wt.	Milk
Angus	2.6	35	65	17
Hereford	3.8	35	60	13
Red Angus	0.5	28.0	48.0	14.0
Shorthorn	1.8	13.0	20.0	2.0
S. Devon	0.0	17.1	23.5	6.2
Brahman	2.1	16.1	26.3	7.4
Limousin	2.39	33.83	63.46	17.72
Simmental	1.9	33.6	57.8	5.6
Charolais	1.5	18.2	32.0	5.7
Gelbvieh	.97	36.4	68.9	17.3
Maine Anjou	2.5	15.9	31.1	3.5
Salers	1.1	12.0	19.0	8.0
Tarentaise	2.2	12.0	23.0	1.5
Pinzgauer	-.1	0.6	0.7	-1.0
Braunvieh	1.089	6.56	6.96	-.39
Beefmaster	.35	6.0	11.1	2.0
Brangus	1.99	20.94	33.54	9.01

Table 2. 2002 non-parent average EPDs for carcass or body composition traits from 2004 evaluations.

Breed	Carcass weight	BF thickness	Ribeye area	Marbling	% retail product	Ultra-sound IMF %	Ultra-sound ribeye area	Ultra-sound BF thickness	Ultra-sound % retail product
Angus	4	.001	.12	.11	.07	.02	.08	.002	.01
Hereford						.00	.05	.00	
Red Angus		.03	.6	.6					
Shorthorn		0.00	-.02	-.03	0.00				
Limousin	14.19	.01	.10	-.01					
Simmental	.02	.01	.06	.08	.01				
Charolais	.17	.00	.04	.01					
Gelbvieh	1	-.02	.07	.02					
Maine Anjou	-4.4	.00	-.04	.05	0.0				
Salers	15.3	.00	.00	.1	0.0				

Table 3. Non-parent EPDs for other traits from 2004 evalutation.

Breed	Scrotal cicumference	Calving ease direct	Calving ease maternal	Stayability	Docility	Mature weight	Mature height
Angus	.23					4	.8
Hereford	.6	-.5	.4				
Red Angus		4	4				
S. Devon	.1						
Limousin	.18	5.17	3.39	15.5	11.67		
Simmental		5.8	2.4			.2	.03
Charolais	.52						
Gelbvieh	.4	103	104	4			
Salers	.1			0.0	5.6	14	
Beefmaster	.06						

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Frank Baker Biography

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

Frank H. Baker was born May 2, 1923, at Stroud, Oklahoma, and was reared on a farm in northeastern Oklahoma. He received his B.S. degree, with distinction, in Animal Husbandry from Oklahoma State University (OSU) in 1947, after 2½ years of military service with the US Army as a paratrooper in Europe, for which he was awarded the Purple Heart. After serving three years as county extension agent and veterans agriculture instructor in Oklahoma, Frank returned to OSU to complete his M.S. and Ph.D. degrees in Animal Nutrition.

Frank's professional positions included teaching and research positions at Kansas State University, 1953-55; the University of Kentucky, 1955-58; Extension Livestock Specialist at OSU, 1958-62; and Extension Animal Science Programs Coordinator, USDA, Washington, D.C., 1962-66. Frank left Nebraska in 1974 to become Dean of Agriculture at Oklahoma State University, a position he held until 1979, when he began service as International Agricultural Programs Officer and Professor of Animal Science at OSU. Frank joined Winrock International, Morrilton, Arkansas, in 1981, as Senior Program Officer and Director of the International Stockmen's School, where he remained until his retirement.

Frank served on advisory committees for the Angus, Hereford, and Polled Hereford beef breed associations, the National Cattlemen's Association, Performance Registry International, and the Livestock Conservation, Inc. His service and leadership to the American Society of Animal Science (ASAS) included many committees, election as vice-president and as president, 1973-74. Frank was elected an ASAS Honorary Fellow in 1977, he was a Fellow of the American Association for the Advancement of Science, and served the Council for Agricultural Science and Technology (CAST) as president in 1979.

Frank Baker received many awards in his career, crowned by having his portrait hung in the Saddle and Sirloin Club Gallery at the International Livestock Exposition, Louisville, Kentucky, on November 16, 1986. His ability as a statesman and diplomat for the livestock industry was to use his vision to call forth the collective best from all those around him. Frank was a "mover and shaker" who was skillful in turning "Ideas into Action" in the beef cattle performance movement. His unique leadership abilities earned him great respect among breeders and scientists alike. Frank died February 15, 1993, in Little Rock, Arkansas.

Frank Baker Memorial Scholarship Award Essays

The Genetic Improvement of Carcass Composition in Beef Cattle

Reynold Bergen, University of Guelph

Introduction

Although carcass trait selection programs have primarily focused on carcass marbling (quality grade), recent changes in the North American beef industry will very likely increase the economic importance of carcass composition (yield grade). Ultrasound technology is a valuable tool in these efforts. This review summarizes recent research pertaining to the role of ultrasound in improving carcass lean percentage in beef cattle. Incorporating commercial carcass data generated by new grading technologies to improve ultrasound-based genetic evaluations for carcass composition is discussed. The potential value of including genotype data from quantitative trait loci is addressed, as well as negative genetic correlations between carcass composition and other economically relevant traits in commercial beef production.

Literature Review

1. Echoes from the Past

Although carcass traits have received a great deal of attention in North America in recent years, the first well-documented selection for beef carcass value occurred in Britain in 1750 (Towne and Wentworth, 1955). Robert Bakewell's objective was to breed British Longhorn cattle with a high proportion of carcass weight in cuts with the greatest commercial value, and "particularly aimed at early maturity and readiness to put on fat" (Towne and Wentworth, 1955). Bakewell's methods were studied by Charles and Robert Colling and applied to Shorthorn cattle. Whether by accident or design, the efforts of Bakewell and the Colling brothers to improve carcass composition resulted in a dramatic increase in fatness rather than leanness. This fact is amply illustrated in the portraits of cattle bred and exhibited by the Colling brothers early in the 19th century (Figure 1).

In the days of Bakewell and the Collings, increased beef carcass fatness was not entirely negative since there was a genuine need for tallow in candle making during the industrial revolution (Epstein and Mason, 1984; Porter, 1991). The more vigorous lifestyle of that time also meant that people required greater levels of dietary energy (Towne and Wentworth, 1955). However, intensive selection for increased fatness reduced the milk production of the British Longhorn so drastically that it was no longer valued as a triple-purpose breed, and nearly became extinct in the 1800's (Porter, 1991). As we shall see, concerns regarding unfavorable genetic correlations among carcass composition and other production traits still apply today.

Then, as now, "a superior carcass is characterized by a high proportion of muscle, a low proportion of bone, and an optimal level of fatness" (Berg and Butterfield, 1976). However, the "optimal level of fatness" has changed over the years. Since the days of Bakewell and the Colling brothers, the development of petroleum products has greatly reduced the value of tallow. Increased mechanization and a more sedentary lifestyle have also reduced the need for fat in consumer diets. For many years, researchers have recognized that "consumers generally do not wish to eat fat because they believe this may well result in a plumper figure and a shorter life, both of which are undesirable to them" (Brady, 1957). The relatively recent rise and continued popularity and expansion of the fast food industry notwithstanding, the observations of Brady (1957) still apply today.

Voluntary federal beef carcass quality grading started in the U.S. in 1926 (Taylor and Field, 1999) and in Canada in 1928 (Nielson and Prociuk, 1998). However, many packers maintained their own "house grades" until mandatory federal grading was instituted during World War II to ensure product quality standards during wartime price controls (Ewing, 1995). Yield grades estimating the percentage of saleable lean beef in the carcass were introduced in the U.S. in 1965 (Taylor and Field, 1999) and in Canada in 1972 (Nielson and Prociuk, 1998).

Price signals to discourage the production of over-fat beef are communicated to feedlot operators through discounts for fatter (high yield grade) carcasses. These price discounts are relatively small until carcasses reach yield grade 4 (U.S.) or Canada 3 since packers prefer high levels of marbling due to it's association with beef eating quality and tenderness (Barkhouse et al., 1996; Reverter et al., 2003). High quality and yield grades come at a high cost. Fat deposition increases feedlot production costs. Carcass fabrication costs also rise since excess external and seam fat must be trimmed from retail beef cuts to improve consumer appeal. Identifying cattle with the genetic potential to attain high quality grades while maintaining high carcass lean percentage (low yield grades) would benefit the feedlot and packing industries.

Carcass lean percentage has also been largely neglected due to the complex structure of the beef industry. The beef production traits that are important to one level of the industry may be of less (or negative) value to other industry segments. For example, cow-calf producers may prefer

moderate birth weights in order to minimize calving difficulty and to maintain a 365 day calving interval. However, calves with low birth weights often tend to have somewhat lower post-weaning feedlot growth performance (Koots et al., 1994). Similarly, although lean carcasses might be preferred by packers and feedlot operators provided that quality grade is not compromised, cow-calf operators often prefer cows with natural fleshing ability in order to reduce winter feed costs and optimize reproductive performance (Broring et al., 2002). Consequently, beef sire purchasing decisions made by cow-calf producers seeking to maximize their own profit may not result in commercial cattle with ideal carcass lean percentage.

Convincing cow-calf producers of the need to improve carcass composition is therefore problematic. Very few cow calf producers retain ownership of their calves through to slaughter; most weaned calves are sold at auction marts to order buyers acting on behalf of backgrounding or finishing feedlots (Small and McCaughey, 1999). These calves are commonly re-tagged upon arrival at the feedlot and co-mingled with calves from numerous other sources. Consequently, the herd of origin and identity of these calves is lost, along with the ability to communicate feedlot performance or carcass data to the primary producer. Efforts to communicate carcass information among the various sectors of the industry is further complicated by the practice of selling finished cattle to the packer on a live basis, in which case the packer is not obligated to provide any carcass data to the previous owner. Even when cattle are sold rail-grade, individual carcass weight and grade data may be returned to the feedlot, but individual animal identification numbers may not since brands and ear tags are removed with the hide. These factors make it extremely difficult for seedstock breeders to obtain information regarding the carcass merit of the commercial cattle generated by their selection programs.

Although yield grades have been in place for nearly 40 years, genetic selection for carcass traits was also largely ignored until recently for another important reason. When beef carcass grading was introduced in the mid 1960's, the simplest way to increase carcass value was by crossbreeding. This requires explanation, since heterosis generally benefits low-heritability traits such as fertility to a greater extent than moderate heritability traits such as carcass composition (Gregory et al., 1994). The importation of "exotic" beef breeds such as Charolais, Limousin and Simmental in the late 1960's to early 1970's meant that drastic improvements in yield grade could be achieved by selecting an appropriate sire breed without investing a great deal of effort in within breed selection. However, since there are few "new" breeds left to import, future genetic improvements will rely on the identification and selection of desirable alleles by within-breed selection rather than the introgression of new alleles from "exotic" breeds.

The intrepid seedstock breeders who did choose to include carcass traits in their breeding programs faced another serious challenge. Since actual carcass data cannot be measured without slaughtering the animal, the genetic improvement of carcass traits required extensive progeny testing. The rate of genetic improvement from progeny testing is relatively slow since progeny of a yearling bull would not produce carcass data until the sire was over three years of age. Structured progeny tests are also extremely expensive and carry a high risk of losing the offspring's unique identification or the carcass data itself. These challenge limited selection for carcass traits in seedstock selection programs (Wilson, 1992).

This was the industry and economic environment to which ultrasound technology specifically designed for collection of live animal carcass data in beef cattle was introduced in the early 1990's. Since then, two major upheavals in the North American beef industry have drastically changed the importance of carcass traits in beef cattle breeding programs.

The first major change was the reappearance of "house grades" in North American packing plants. These branded beef programs offer premiums for individual carcasses meeting specifications for weight, yield and quality grade. It is estimated that over fifty percent of Canadian beef is sold under a branded beef program (Beef Information Center, 2004). This growth in value-based marketing has led to an increase in vertical coordination among the different sectors of the beef industry. Consequently, carcass traits are becoming more important.

Secondly, the recent discovery of Bovine Spongiform Encephalopathy (BSE) in Canada and the U.S. are also altering the cost structure of the beef packing industry. Although beef consumption by domestic consumers has not decreased in response to BSE (Canadian Cattlemen's Association, 2003), the value of ruminant meat and bone meal certainly has (Cochrane, 2003). If market forces, or regulatory intervention or irrational fears cause other livestock industries to also stop using tallow as an energy supplement, a source of packer revenue would be eliminated while simultaneously increasing waste fat disposal costs. In this case, discounts or premiums based on carcass composition would become steeper.

2. Use of Ultrasound to Select for Beef Carcass Composition in North America

Ultrasound technology has become a valuable tool to evaluate carcass traits in seedstock selection programs. Since ultrasound allows 'carcass' measurements to be collected on live animals, this technology may allow breeders to reduce their reliance on actual carcass data (Wilson, 1992). Ultrasound therefore presents the potential to lower the cost and increase the rate of genetic improvement, with a higher confidence of maintaining correct animal identification. The last fifteen years have witnessed a great deal of research regarding the value of ultrasound measurements as predictors of carcass merit in beef cattle. This research is summarized below.

2.1. Repeatability and Accuracy of Ultrasound Measurements

The relationship between ultrasound measurements collected on the same animal on the same day (repeatability), and the relationship between ultrasound measurements collected on the live animal with carcass measurements collected after slaughter (accuracy) have been studied extensively. These studies concluded that trained and experienced ultrasound technicians are capable of obtaining highly repeatable ultrasound fat depth and l. dorsi area measurements (Bergen et al., 1996; Hassen et al., 1998; Herring et al., 1994b; Perkins et al., 1992b; Robinson et al., 1992). Accuracy statistics indicate that ultrasound measurements also compare reasonably well with the corresponding carcass measurements (Bergen et al. 1996; Charagu et al., 2000; Greiner et al., 2003b; Hassen et al., 1998; Herring et al., 1994b; Perkins et al., 1992b; Robinson et al., 1992). Although overall ultrasound accuracy statistics are acceptable, many of these studies have shown that ultrasound fat measurements under- and overestimated carcass fat depth on lean- and over-fat carcasses, respectively (Charagu et al., 2000; Hassen et al., 1998; Greiner et al., 2003b; Herring et al., 1994b; Robinson et al., 1992). Similarly, ultrasound measurements tended to overestimate muscle size on carcasses with small l. dorsi area, and underestimate muscle size on carcasses with large l. dorsi area (Charagu et al., 2000; Hassen et al., 1998; Herring et al., 1994b). Although ultrasound technician error plays some role in these discrepancies, factors such as hide removal, carcass hanging, shrouding, rigor mortis, and quartering also influence the relationship between live and carcass measurements (Perkins et al., 1992a; Robinson et al., 1992).

Regardless of the cause of live ultrasound vs. carcass discrepancies, these findings may impact genetic evaluations based primarily on ultrasound data from yearling bulls. Since young bulls tend to be leaner and more heavily muscled than typical commercial carcasses, they represent the very cases that are most likely to be in error. If ultrasound measurements do not detect the true degree of variation in fat depth and l. dorsi area in seedstock cattle, estimates of additive genetic (co)variance, heritabilities, genetic correlations, accuracy and the rate of genetic improvement may be adversely affected.

2.2. Using Ultrasound Measurements to Predict Carcass Composition

Although it is important that ultrasound measurements are repeatable and bear a reasonable relationship to subsequent post-slaughter carcass measurements, the real objective of measuring fat depth and l. dorsi area is to obtain an estimate of carcass lean percentage. Several studies have addressed this issue.

The majority of ultrasound measurements are collected at the 12/13th rib interface, since this is also the site of carcass grading. Most studies have found that ultrasound measurements collected at the 12/13th rib interface can predict carcass lean percentage nearly as precisely as the corresponding carcass measurements. Precision (R^2) of equations predicting carcass lean percentage based on 12/13th rib ultrasound (vs. carcass) measurements include 0.73 (vs. 0.69; Bergen et al. 1996), 0.64 (vs. 0.68; Greiner et al. 2003a), 0.49 (vs. 0.60; Herring et al. 1994a), 0.38 (vs. 0.40; Realini et al. 2001), and 0.18 (vs. 0.31; Williams et al. 1997). Furthermore, ultrasound fat depth is a much stronger predictor of beef carcass composition than ultrasound l. dorsi area. Partial r^2 values in the above studies indicate that fat measurements are three to eight times as important as l. dorsi area as predictors of carcass lean meat yield.

Since ultrasound measurements are not restricted to the 12/13th rib interface, efforts have been made to identify alternative scan sites that may improve predictions of carcass composition. These include depths of the body wall (Greiner et al., 2003a), rump fat (Greiner et al., 2003a; Realini et al., 2001), gluteus medius (Realini et al., 2001) and biceps femoris (Williams et al., 1997). The results of these papers indicate that the majority of variation in carcass composition is explained by 12/13th rib ultrasound fat and muscle measurements, and there is little benefit to adding additional ultrasound measurements. The possible exception to this is rump fat, which showed considerable benefit in the study of Williams et al. (1997), though not in the studies of Greiner et al. (2003a) or Realini et al. (2001).

2.3. Genetics of Carcass and Ultrasound Measurements

The effective use of ultrasound measurements in beef cattle breeding programs requires that ultrasound traits be heritable and genetically correlated to carcass traits measured in commercial offspring. Several recent reports have addressed this issue (Crews and Kemp, 2001 and 2002; Crews et al., 2003; Devitt and Wiltonk 2001; Moser et al., 1998; Reverter et. al., 2000). These papers generally agree that ultrasound traits are as heritable as the corresponding carcass traits, and that corresponding ultrasound and carcass traits are moderately correlated with each other (Figure 2). This suggests that selection based on live animal ultrasound indicator traits for carcass lean percentage should be reflected in the corresponding indicator traits of their commercial progeny.

These findings have led to the development of carcass trait EPDs based on ultrasound measurements collected from yearling seedstock bulls and heifers. Many seedstock producers are using these evaluations in their breeding programs, and a variety of private commercial interests have arisen to collect, interpret, and manage ultrasound data. The next section of this paper will address potential improvements that can be made to current ultrasound-based genetic evaluations for carcass composition.

3. Scanning the Horizon: Improving Genetic Evaluations for Beef Carcass Composition

Although several purebred beef breed associations have begun to include ultrasound carcass data in their genetic evaluations, more work is needed to take full advantage of the data. The main conundrum is that although carcass data collected from commercial cattle and ultrasound data collected from seedstock bulls and heifers are genetically correlated, they are not the same traits. Evidence that genetic correlations between seedstock ultrasound and commercial carcass measurements are less than 1.00 is illustrated in Figure 2. This is not surprising. Young bulls and heifers are frequently raised on diets designed to limit fat deposition and may not be able to fully express their genetic potential for fattening. In addition, unlike bulls and heifers, fat and muscle development in steers is unaffected by endogenous reproductive hormones. Finally, seedstock bulls and heifers evaluated at 365 days of age are likely at a different stage of physiological maturity than commercial cattle adjusted to a slaughter age of 440 days. Recent research has examined how to best deal with the separate but correlated carcass traits measured in live seedstock and commercial beef carcasses, and has provided preliminary answers to three important questions.

3.1. Should EPDs be reported as "seedstock ultrasound" or as a "commercial carcass" equivalent?

Although live ultrasound and carcass traits are not genetically identical, reporting separate evaluations for commercial carcass vs. seedstock ultrasound data risks information overload and confusion for the target audience of bull buyers. Consequently, combining commercial carcass data and live animal ultrasound measurements into a single evaluation for carcass merit will enhance the adoption of these genetic evaluations by the bull buying public.

The question then becomes whether genetic evaluations for carcass traits should be reported as a "live seedstock ultrasound" or as a "commercial carcass" EPD. Since the objective of the selection program is to improve commercial carcass value, EPDs should be reported as a "commercial carcass" EPD rather than as a "seedstock ultrasound" EPD. This distinction is important.

Since an EPD indicates the animal's expected average genetic contribution to it's progeny, a one-unit increase in sire EPD should result in a one-unit increase in progeny phenotype. Crews (2002) regressed progeny phenotype on sire EPD for progeny tested sires using carcass data from a structured Charolais progeny test. Regression coefficients for carcass weight, fat depth, l. dorsi area and marbling score did not differ from one, indicating that the carcass trait EPD functioned as expected. However, since ultrasound and abattoir carcass traits are not perfectly correlated, reporting carcass trait evaluations solely as live ultrasound data may give misleading results. Crews et al. (2004) showed that a sire fat depth EPD based solely on ultrasound data collected in Simmental seedstock tended to greatly underestimate the response seen in progeny carcass fat depth; a 1.00 mm increase in ultrasound fat depth EPD resulted in a 1.73 mm increase in carcass fat depth. This suggests that genetic evaluations for fat depth based exclusively on seedstock ultrasound data may underestimate the animal's genetic propensity for fat deposition. While this may not drastically affect sire rankings, it may undermine commercial producer confidence in the merit of an ultrasound-based genetic evaluation system. Crews et al. (2004) then scaled these ultrasound-based EPD to a carcass equivalent using genetic regression (Cameron, 1997):

$$EPD_{CFat} = \left[\frac{\delta_{gUSFat,CFat}}{\delta^2_{gUSFAT}} \right] \times EPD_{USFat}$$

where,

EPD_{CFat} = seedstock EPD for commercial carcass fat depth,

$\delta_{gUSFAT,CFAT}$ = genetic covariance between seedstock ultrasound and commercial carcass fat depth,

δ^2_{gUSFAT} = genetic variance of seedstock ultrasound fat depth, and

EPD_{USFat} = seedstock EPD for ultrasound fat depth.

After applying this genetic regression to the ultrasound EPDs, the regression of progeny phenotype on sire EPD produced coefficients equal to 1.00 for all ultrasound traits (Crews et al., 2004).

3.2. How can commercial carcass data be incorporated into ultrasound-based evaluations?

Although ultrasound data can be collected more economically and rapidly than carcass data with a higher confidence of maintaining correct animal identification, recent developments in the beef industry may conspire to drastically increase the amount of reliable carcass data available for genetic evaluations. Firstly, several video-based automated grading systems have been developed in Canada (Cannell et al., 2002) and the U.S. (Shackelford et al., 2003). These systems can predict carcass lean percentage more accurately and precisely than graders working at line speeds (Cannell et al., 2002), and would augment the development of databases containing individual carcass weight, fat depth, l. dorsi area and marbling score data. A great deal of work has also been invested to develop birth-to-slaughter animal tracking systems in Canada (Canadian Cattle Identification Agency, 2004) and the United States (Antosh, 2004) in response to human health and animal disease concerns. These identification programs have enormous potential value in collecting carcass data from commercial cattle, provided animal identification is maintained to the point of carcass grading, data ownership and security issues can be resolved, and commercial carcass

data collection can be linked to suitable genetic evaluation database.

Crews et al. (2003) combined live ultrasound data from Simmental bulls and replacement heifers and carcass data from commercial crossbred cattle as three separate but correlated traits in a multiple trait genetic evaluation. This approach makes the most efficient use of all available data, produces genetic evaluations for carcass traits much more quickly than progeny testing alone, and facilitates the evaluation of carcass traits at the level of the producing animal.

3.3. Should carcass trait EPD be reported for indicator traits or for the economically relevant trait?

As mentioned above, carcass traits should be evaluated at the level of the producing animal rather than seedstock. Similarly, it would be of value to evaluate the economically relevant trait (i.e. carcass lean percentage) rather than simply evaluating indicator traits (i.e. fat depth and l. dorsi area). Reporting separate evaluations for fat depth and l. dorsi area may imply that these traits are of equal value in predicting carcass composition, when results shown in section 2.2 indicates that this is clearly not the case.

To date, two studies have examined the relationship between live seedstock ultrasound measurements and commercial carcass lean percentage based on carcass dissection. Crews and Kemp (2001) examined these relationships in composite seedstock (404 bulls and 514 heifers) and partial carcass dissection data from 235 steers. Reverter et al. (2000) used ultrasound data from purebred Angus (4209 bulls and 3987 heifers) and Hereford (1793 bulls and 1612 heifers) and complete carcass dissection data from 604 Angus and 333 Hereford steers and heifers. Genetic correlations between live seedstock ultrasound and commercial carcass measurements with dissected lean percentage from Reverter et al. (2000) illustrated in Figure 2. These data indicate that seedstock ultrasound fat depth and l. dorsi area have a moderate genetic correlation with the dissected carcass lean percentage of commercial cattle.

We must then determine how to calculate a carcass lean percentage EPD in a genetic evaluation program. There are essentially two options.

3.3.1. Calculation of an ultrasound lean meat yield phenotype

Firstly, several equations predicting carcass lean percentage based on pre-slaughter ultrasound measurements are available in the literature (Bergen et al., 1996 and 2003; Greiner et al., 2003a; Herring et al., 1994a; Realini et al., 2001; Williams et al., 1997). Multiplying ultrasound fat depth and l. dorsi area measurements by their respective regression coefficients would generate a phenotype for carcass lean percentage. Genetic evaluations could then generate a single EPD for carcass lean percentage rather than separate evaluations for fat depth and l. dorsi area. If genetic (co)variances between seedstock ultrasonically predicted lean percentage and commercial carcass lean percentage were available, the genetic regression approach used by Crews et al. (2004) could be used to scale the seedstock ultrasound lean percentage EPD to a commercial carcass lean percentage EPD.

However, there is a potential weakness associated with using any regression equation to predict carcass lean percentage in the live animal. The regression coefficients for fat depth and l. dorsi area in any given equation each have their own standard errors. This suggests that although these are the "best" regression coefficients for the data set as a whole, many individuals might be better described by a slightly different set of regression coefficients. Consequently, applying a "one size fits all" equation to an entire breed may bias the genetic evaluations for animals that are not adequately described by the set of regression coefficients chosen.

3.3.2. Multiple trait evaluation of commercial carcass lean percentage

An alternative method to calculate EPD for commercial carcass lean percentage may be to use multiple trait evaluation. For example, a seven-trait evaluation would use seedstock ultrasound fat depth and l. dorsi area data (treating bull and heifer data as separate but correlated traits) and commercial carcass fat depth and l. dorsi area data as indicator traits to calculate an EPD for dissected lean meat percentage of the commercial carcass (which would not be routinely measured). Genetic (co)variances among bull and heifer ultrasound traits and commercial carcass lean percentage reported by Crews and Kemp (2001) and Reverter (2000) would be very valuable in these efforts.

This approach would efficiently use all available data and improve the accuracy of the genetic evaluation. However, a weakness analogous to that mentioned for the phenotypic pre-adjustment approach discussed in section 3.3.1 may also apply here, since "one size fits all" genetic (co)variances would be applied in all EPD calculations. Further investigation is needed to determine whether there are non-linear genetic correlations among the indicator traits with the economically relevant trait (i.e. dissected lean percentage of the commercial carcass). Additive genetic variances may also change across the range of the indicator traits, particularly at the extremes of the distribution. This would affect genetic parameters of the indicator traits and the accuracy of the genetic evaluation for carcass lean meat percentage. However, these issues are clearly beyond the scope of this review.

4. Additional Considerations Regarding the Evaluation of Beef Carcass Composition

Although this paper has concentrated on the use of ultrasound technology to identify animals with superior genetic potential for improved carcass lean percentage, several additional factors must be considered.

4.1. Unfavorable Genetic Correlations With Other Economically Relevant Traits

Given the near demise of the British Longhorn breed in the 19th century (Porter, 1991), It would be remiss not to briefly mention the potential costs associated with increasing leanness. Unintended and undesirable effects on reproductive traits (Bennett and Williams, 1994) as well as marbling and tenderness (Reverter et al., 2003) may result from selection for increased leanness. Fortunately, since these unfavorable genetic correlations are not -1.00, careful seedstock selection decisions and use of terminal crossbreeding systems should help to minimize the negative effects on other performance and quality traits.

4.2. Inclusion of Molecular Data in Genetic Evaluations for Beef Carcass Composition

Molecular genetics research has revealed several loci influencing carcass composition. Examples of these include leptin (Nkrumah et al., 2003) and myostatin (Wheeler et al., 2001). Since physiological roles of these loci have been determined, they can be considered "quantitative trait loci" (QTL) rather than simply linked markers. These QTL may allow valuable refinements to selection programs for carcass traits. Since traditional animal breeding is based on the infinitesimal model, it considers the average effect of all loci but ignores the specific effect of any given locus. In contrast, in the absence of pedigree information, QTL analyses examine the specific effect of a single locus, while ignoring the influence of all other loci in the genome. In order to take full advantage of all available genetic information, current animal models will need to be modified to report an EPD that accounts for the fixed effect of known QTL genotypes as well as the average effect of the remaining loci. Collection of QTL genotype data from seedstock and commercial livestock may be aided by the development of DNA-based animal tracing and parentage verification systems (Shaw, 2004).

5. Conclusions and Implications for the Genetic Improvement of Beef Cattle

Ongoing changes in the North American beef industry will likely cause carcass composition to become a more important trait in seedstock selection programs. Although ultrasound technology has made an important contribution to the genetic improvement of carcass composition, the manner in which genetic evaluations incorporate and report ultrasound data can be improved. In particular, EPD should be reported for the economically relevant trait (carcass lean percentage) rather than indicator traits (fat depth and l. dorsi area), and should be expressed as a commercial carcass equivalent EPD (rather than as a seedstock ultrasound EPD). Development of birth to slaughter animal identification programs and automated grading technologies present the opportunity to greatly increase the amount of commercial carcass data available for genetic evaluations. However, close attention needs to be paid to the impact of genetic selection for increased carcass leanness on other beef production and quality traits. Additional improvements in the genetic evaluation of carcass composition will likely be gained through the incorporation of QTL data as it becomes more widely available.

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Figure 1. "A White Short Horned Heifer, 7 Years Old" (left) painted by Thomas Weaver in 1811, and "The Durham Ox" (right) painted by John Boultbee in 1802. These cattle were bred and raised by Charles and Robert Colling. Images obtained from http://www.ruralhistory.org/online_exhibitions/livestok/cat_ls.html, with permission from the Museum of English Rural Life.

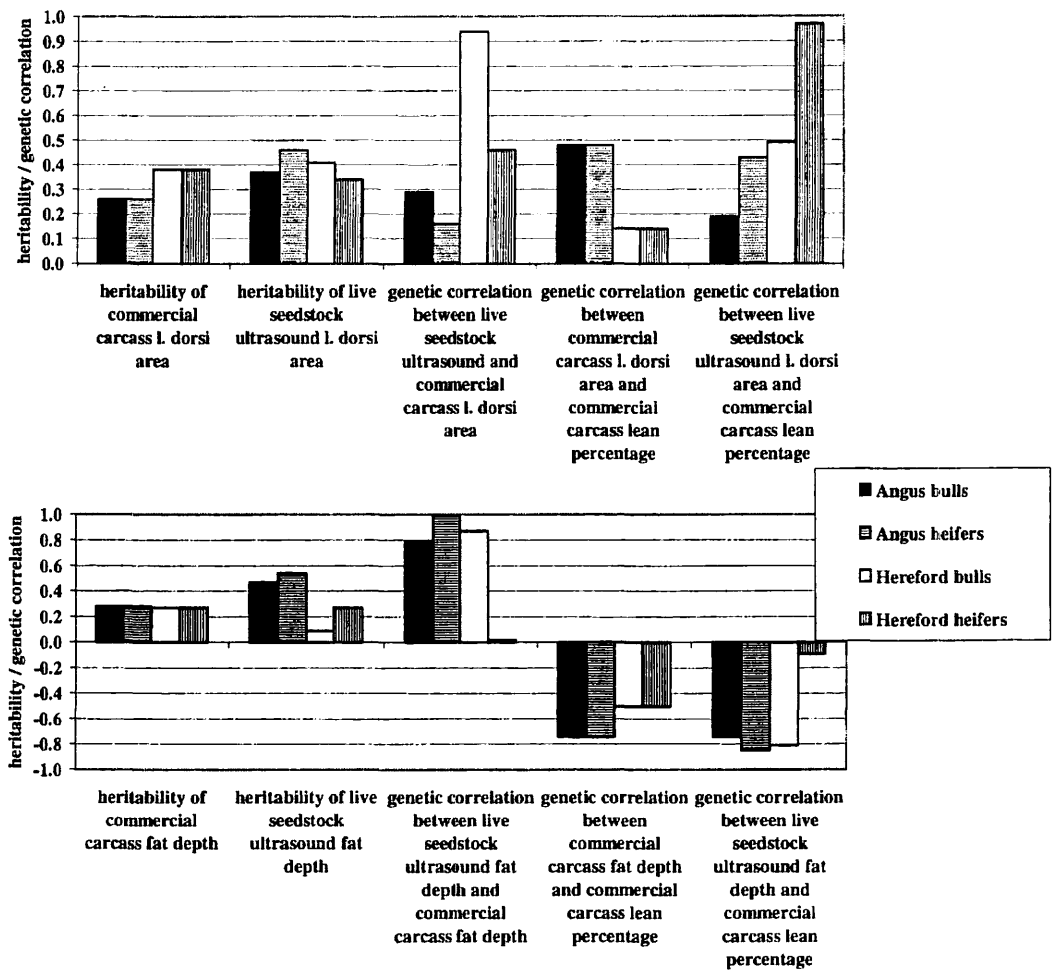

Figure 2. Heritabilities and genetic correlations among commercial carcass and live seedstock ultrasound indicator traits and dissected commercial carcass lean percentage in Angus and Hereford bulls, heifers and commercial cattle (data from Reverter et al., 2000).

Frank Baker Memorial Scholarship Award Essays

Genetic Evaluation of Carcass Traits: Looking at the Effects of Slaughter End Points

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Introduction

An exhaustive review of estimates of heritability ($\mathbf{h^2}$) for a broad spectrum of beef production traits published in the scientific literature from 1945 to 1991 was conducted by Koots et al. (1994), but their review did not include other important carcass traits (e.g., kidney, pelvic, and heart fat percentage, yield grade, fat weight) and due to the purpose of their study, individual estimates of h^2 for the traits reviewed were not reported, but only the weighted and unweighted averages. On the other hand, the review by Marshall (1994) reported estimates of h^2 for some additional carcass traits, but only for cattle reared under U.S. conditions and, basically, estimates presented were on an age-constant basis. In addition, due to few estimates for the additional traits at that time, averages of estimates of h^2 for several carcass traits were based on only one to three observations. Neither of the two reviews focused on the effect of end point on estimates of h^2. In the last ten years, as a consequence of the increased interest of many beef producers on carcass yield and quality to satisfy consumer demand, numerous studies of carcass traits have published estimates of h^2 and genetic correlations ($\mathbf{r_g}$), doubling, at least, the number of estimates for many carcass traits. This review was conducted to present estimates of h^2 and r_g for carcass traits published in the scientific literature from 1962 to 2004. Because animals are slaughtered at, or carcass traits are adjusted to, different end points, the effects of adjusting for age, weight or fat depth on such estimates are also discussed.

Review of Literature

Estimates of Heritability

Table 1 provides estimates of h^2, numbers of estimates and unweighted means of estimates of h^2 for 14 carcass traits measured at, or adjusted to, constant age, weight or backfat thickness (**BT**) end points. References repeated in two or three categories compared estimates adjusted to two or three different end points; otherwise, only one kind of adjustment was performed. The exception is Fouilloux et al. (1999), who reported estimates of h^2 for dressing percentage at constant age and at constant weight, but estimates were for different breeds. The age-constant category includes estimates on an age-constant or time-on-feed-constant basis. Those in the weight-constant category are estimates that were adjusted for weight at slaughter or for carcass weight.

Carcass Weight (CW). CW had many estimates of h^2 (n=56) in the literature. Estimates were adjusted for age, weight, or BT, with averages of 0.42 (n=36), 0.37 (n=8) and 0.35 (n=12), respectively. Age-constant estimates of h^2 were greater than weight- and BT-constant estimates; although, fewer estimates were on a weight- and BT-constant basis. Mean estimate across end points was 0.40, which indicates that CW would respond well to selection. Large variation existed in estimates of h^2. Range of estimates was from 0.09, obtained by paternal half-sib analysis with REML with a BT adjustment (Johnston et al., 1992) to 0.92, obtained by paternal half-sibs analysis with Henderson's Method 2 with an age adjustment (Blackwell et al., 1962), but most estimates were moderate. Wulf et al. (1996) for crossbred steers and heifers, Wheeler et al. (1996) for crossbred steers, Oikawa et al. (2000) for Japanese Black (Wagyu) steers, Morris et al. (1990) for crossbred steers, and Benyshek et al. (1988) for Hereford cattle reported low h^2 estimates (0.10, 0.15, 0.15, 0.17 and 0.19, respectively). Koch et al. (1982) for crossbred steers, MacNeil et al. (1984) for purebred and crossbred steers, Elzo et al. (1998) for Angus steers, and Benyshek (1981) for Hereford steers and heifers reported moderate estimates (0.43, 0.44, 0.46 and 0.48, respectively). Large estimates (0.59, 0.60 and 0.68) were obtained by Moser et al. (1998) for Brangus steers and heifers, Pariacote et al. (1998) for American Shorthorn steers, and Koch (1978) for Hereford heifers.

Only three studies compared estimates of h^2 for CW adjusted for age or for BT. Differences in estimates of h^2 with these two adjustments were variable. For crossbred steers representing 11 cattle breeds that were slaughtered at 20 months of age, Morris et al. (1990) found that CW adjusted to a constant age had a larger estimate of h^2 than CW adjusted to a constant BT (0.28 vs 0.17). In a recent study, Devitt and Wilton (2001), using crossbred steers, also obtained differences between age- and BT-constant estimates of h^2 for CW, but the estimate adjusted for BT was larger than the estimate adjusted for age (0.57 vs 0.47). The reduction in the estimate of genetic variance caused by age adjustment relative to that for BT (522 vs 1,051 kg^2) could explain most of this difference, because phenotypic

variances were not much different with the two adjustments. In contrast, Shanks et al. (2001) found no significant difference between age- and BT-constant estimates of h^2 (0.32 vs 0.33) for CW of Simmental and percentage Simmental steers.

Dressing Percentage (DP). The number (32) of h^2 estimates for DP found in the literature was about half of that found for CW. Most estimates of h^2 were adjusted for age (n=18), which had a mean of 0.28. Fewer estimates adjusted for BT (n=3) had a mean of 0.36. Eleven weight-constant h^2 estimates had a mean of 0.38. Average estimate of h^2 was 0.32 across end points, indicating that DP is lowly to moderately heritable, which suggests that response to selection would be possible. Estimates of h^2 for DP ranged from very low (0.01) estimated as twice the son on sire regression coefficient on an age-constant basis (Reynolds et al., 1991), to very high (0.97) obtained with a paternal half-sib analysis on a weight-constant basis (Hinks and Bech Andersen, 1969). This range includes estimates of 0.06, 0.12, 0.37, 0.39, 0.50 and 0.69 reported by Wheeler et al. (1996), Lee et al. (2000), Robinson et al. (1998), Kim et al. (1998), Fouilloux et al. (1999) and Renand et al. (1985), revealing significant variability among estimates, which may reflect the relatively limited number of records in most studies. Few studies in the scientific literature compared estimates of h^2 for DP adjusted for different end points. Veseth et al. (1993), by a paternal half-sib model with Henderson's Method 3, obtained similar estimates of h^2 with age (0.25) or weight (0.26) as covariates in the model. Also, Koots et al. (1994), in their review of h^2 estimates, found that weighted average of h^2 estimates for DP were about the same on a weight- or age-constant basis (0.38 and 0.39, respectively). In a recent study (Lee et al., 2000), estimates of h^2 to age- and weight-constants were similar (0.12 and 0.16, respectively), but somewhat larger than estimates of h^2 to BT-constant (0.09).

Backfat Thickness. BT also had many estimates of h^2 (n=63) in the literature. Most of the estimates were to an age-constant (n=34), followed by many to a weight-constant (n=23). Few estimates of h^2 were to a BT-constant (n=6). Averages of estimates of h^2 were 0.39, 0.33 and 0.29, respectively. The average across end points was 0.36, which suggests that genetic progress to single trait selection would be possible if records were available. Across end points, estimates of h^2 ranged from 0.03 (Morris et al., 1990, REML analysis with a sire model) to 0.94 (Dunn et al., 1970, paternal half-sib analysis). These two extreme estimates were for carcasses of crossbred steers adjusted for age. Estimates of h^2 were small (0.07, 0.14 and 0.15) by Hoque et al. (2002), Gilbert et al. (1993) and Oikawa et al. (2000), and large (0.63, 0.68 and 0.84) by Riley et al. (2002), Koch (1978) and Wheeler et al. (2001), respectively. Moderate estimates of h^2 (0.43, 0.44, and 0.46) were reported by Brackelsberg et al. (1971), Yoon et al. (2002) and Pariacote et al. (1998). Five studies (Shelby et al., 1963; Cundiff et al., 1969; Hirooka et al., 1998; Shanks et al., 2001; Devitt and Wilton, 2001) compared estimates of h^2 for BT adjusted for age or weight. All agreed that estimates were similar regardless of the type of covariate used.

Longissimus Muscle Area (LMA). LMA was the carcass trait with the most h^2 estimates (n=66) reported, reflecting its relative importance and easy measurement. Averages of h^2 estimates were 0.41 (n=36), 0.37 (n=19) and 0.41 (n=11) with age, weight or BT constants, respectively. The average of estimates of h^2 (0.40) over all end points indicates that LMA is moderately heritable and genetic gain might be achieved through selection. However, estimates of h^2 vary significantly among studies. Estimates ranged from almost the minimum (0.01, Reynolds et al., 1991, Hereford bulls, son on sire regression analysis) to almost the maximum for h^2 (0.97, Pariacote et al., 1998, American Shorthorn steers, REML analysis with a sire model). Estimates of h^2 for LMA adjusted for age or weight reported by Benyshek (1981) for Hereford steers and heifers, Morris et al. (1990) for crossbred steers, and Hirooka et al. (1996) for Japanese Brown steers, indicate no significant effect of end point on estimates. In contrast, Shelby et al. (1963) reported that the h^2 estimate for LMA increased from 0.26 to 0.46 when the adjustment was made for slaughter weight instead of age. In a study using Hanwoo (Korean Native) cattle, Lee et al. (2000) reported that age- (0.17) and BT-constant (0.18) estimates of h^2 were slightly smaller than the weight-constant estimate (0.24). Similar differences between weight- and BT-adjusted h^2 estimates were obtained by other authors; although, the differences had opposite sign. In a more recent study (Shanks et al., 2001) that included Simmental and percentage Simmental cattle, the age- and BT-constant h^2 were estimated to be slightly larger than the weight-constant h^2 (0.26 and 0.29 vs 0.22, respectively). Larger estimates of h^2 with a weight-constant (0.45) or a BT-constant (0.52) basis were reported by Devitt and Wilton (2001), but the difference (0.07) between estimates was of the same magnitude. More recently, Kemp et al. (2002), after adding weight to a model that included age as a covariate, obtained a much smaller h^2 estimate for LMA (0.45 vs 0.36).

Kidney, Pelvic, and Heart Fat Percentage (KPH). Comparatively few estimates of h^2 (n=14) were found in the literature for KPH. Eight estimates were adjusted for age with an average of 0.48, two were adjusted for weight with an average of 0.19, and four were adjusted for BT with an average of 0.34. The overall average was 0.40. Estimates of h^2 ranged from 0.00 (Wilson et al., 1976, paternal half-sib analysis) on a weight-constant basis to 0.83 (Koch et al., 1982, paternal half-sibs analysis with Henderson's Method 3) on an age-constant basis. Elzo et al. (1998) and Wheeler et al. (2001) reported h^2 estimates of 0.03 and 0.28, Wheeler et al. (1996) and Riley et al. (2002) obtained moderate estimates (0.32 and 0.46) and Brackelsberg et al. (1971) and Nephawe et al. (2004) reported high estimates of 0.72 and 0.65, respectively. Only Veseth et al. (1993) contrasted estimates of h^2 for KPH adjusted for different covariates but

estimates where similar when age (0.37) or weight (0.38) were used as covariates in a model based on paternal half-sibs.

Marbling Score (MS). MS is one of the most genetically evaluated carcass traits. Age-, weight- and BT-constant estimates averaged 0.45 (n=29), 0.29 (n=15) and 0.30 (n=12), respectively. The average across end points was 0.37. Similar to estimates of h^2 for carcass traits discussed previously, estimates of h^2 for MS were highly variable across studies with a large range, from 0.01 (Lee et al., 2000, DFREML analysis with an animal model) using weight as a covariate to 0.88 (Pariacote et al., 1998, REML analysis with a sire model) using age. Most estimates, however, were moderate within a range of 0.30 to 0.57. For example, Devitt and Wilton (2001), Lamb et al. (1990), Splan et al. (2002), Fernandes et al. (2002), Benyshek et al. (1988), Barkhouse et al. (1996), Kemp et al. (2002), Van Vleck et al. (1992), Gregory et al. (1995), O'Connor et al. (1997) and Yoon et al. (2002) reported estimates of 0.30, 0.33, 0.35, 0.37, 0.38, 0.40, 0.42, 0.43, 0.48, 0.52 and 0.57, respectively. Few (3) studies in the literature have compared estimates of h^2 for MS obtained by adjusting for age, weight or BT. Using field records of the American Simmental Association, Shanks et al. (2001) reported similar estimates of h^2 for MS adjusted for age (0.12), weight (0.12) or BT (0.13) for bulls, steers and heifers. Similarly, Hirooka et al. (1996) concluded that choice of covariate in the model (slaughter age vs slaughter weight) had little effect on h^2 estimates for MS. In contrast, Devitt and Wilton (2001), for crossbred steers, reported that weight-constant h^2 (0.43) was significantly larger than BT-constant h^2 (0.30), and was slightly larger than age-constant h^2 (0.35).

Yield Grade (YG). Only six estimates of h^2 for YG were reported in the literature, four with data adjusted for age and two for BT, with averages of 0.60 and 0.74, respectively. Average of estimates of h^2 was 0.64 across the two end points, indicating that this trait is highly heritable and genetic merit might be improved by selection. In studies conducted to a constant age, low (0.24, Hereford bulls) and moderate (0.54, American Shorthorn steers) estimates of h^2 were obtained by Lamb et al. (1990) and Pariacote et al. (1998), respectively. However, on a BT-constant basis, Wulf et al. (1996) for crossbred steers and heifers and Riley et al. (2002) for Brahman steers and heifers reported estimates of 0.76 and 0.71, and on an age-constant basis, Wheeler et al. (1996) and Wheeler et al. (2001) for crossbred steers obtained larger estimates of 0.76 and 0.85, respectively. No reports were found that compared estimates of h^2 for YG adjusted to constant age, weight or BT.

Predicted Percentage of Retail Product (ER). The column labeled as ER in Table 1 lists estimates of h^2 for various cut-out-type traits, which are cited as predicted percentage of retail product in this review. Few (n=17) estimates of h^2 for ER have been published in the literature relative to estimates for actual carcass traits. More estimates found were on an age- (n=8) than on a weight- (n=6) or BT-constant basis (n=3), with averages of 0.28, 0.41 and 0.48, respectively. Across end points, average of estimates was 0.36. Estimates of h^2 for ER were in a low-to-high range, from 0.07 (age-constant) obtained with DFREML analysis with an animal model by Hassen et al. (1999) for Angus- and Simmental-sired steers and bulls, to 0.71 (BT-constant) estimated with animal model with DFREML analysis by Riley et al. (2002) for Brahman steers and heifers. Examples of moderate estimates of h^2 included: at constant age, 0.53 by Mukai et al. (1995) for Japanese Black steers and heifers; at constant weight, 0.44 by Wilson et al. (1976) for crossbred steers and heifers; and at constant BT, 0.55 by Gilbert et al. (1993) for Canadian Angus and Hereford bulls. Estimates of h^2 for ER adjusted to different end points were found in only two reports. In an early genetic study (Cundiff et al., 1971), the h^2 estimate for ER increased somewhat in the moderate range when data were adjusted to a constant weight relative to adjustment to a constant age (0.28 vs 0.35). Similarly, Shanks et al. (2001) obtained somewhat larger estimates of h^2 for ER adjusted for BT or for weight than when adjusted for age (0.17 and 0.12 vs 0.09).

Retail Product Weight (RW). Of the 13 estimates of h^2 for RW found in the literature most (n=11) were adjusted for age; and one each for BT and weight. Age-constant estimates of h^2 ranged from low to moderate (0.28) for purebred and composite steers (Gregory et al., 1995, Henderson's Method 3 with a sire model) to high (0.66) for purebred, composite and F_1 crossbred steers (Shackelford et al., 1995, DFREML with an animal model). Estimates of h^2 on an age-constant basis averaged 0.51. Estimates at constant weight or BT were 0.42 and 0.50 by Cundiff et al. (1969) and Riley et al. (2002), respectively. The average of age-constant estimates and weight- and BT-constant estimates of h^2 imply that significant genetic variation exists to improve RW by selection. Estimates of h^2 for RW based on different covariates were published in only one report (Cundiff et al., 1969), which found that the estimate of h^2 using age as the covariate in the model was larger than the estimate using weight as the covariate (0.64 vs 0.42).

Fat Weight (FW). Only nine estimates of h^2 for FW were found in the literature. Seven estimates were with adjustment to constant age, one to constant weight and one to constant BT. Estimates of h^2 adjusted for age averaged 0.52 and ranged from low to moderate (0.30) for purebred and crossbred steers and heifers (Morris et al., 1999, animal model and REML) to high (0.94) for Hereford heifers (Koch, 1978, sire model and Henderson's Method 2). Almost all estimates, however, were moderate, except those obtained by Koch (1978) and Shackelford et al. (1995). The estimates of h^2 at constant weight or BT found in the literature were by Cundiff et al. (1969) and Brackelsberg et al. (1971), who reported estimates of 0.37 and 0.50, respectively. The average of estimates of h^2 across end points was 0.50, suggesting that selection against FW or to an intermediate level, for example, would respond well to

selection. Only one report (Cundiff et al., 1969) compared estimates of h^2 for FW obtained with different covariates; the age-constant estimate of h^2 was larger than the weigh-constant estimate (0.46 vs 0.37).

*Bone Weight (**BW**).* Seven estimates of h^2 for BW were found in the literature; six adjusted to constant age, and one to constant weight, with none for constant BT. For a constant age, the average was 0.51; all estimates were moderate to large (0.38, Cundiff et al., 1969; 0.39, Gregory et al., 1995; 0.51, Morris et al., 1999; 0.56, Koch, 1978; 0.57, Koch et al., 1982; 0.62, Shackelford et al., 1995). The h^2 estimate of 0.39 for BW adjusted to a weight-constant basis was reported by Cundiff et al. (1969), who also reported an estimate of 0.38 adjusted to a common age.

*Actual Retail Product Percent (**RP**).* The numbers of estimates of h^2 for RP in the scientific literature were 9 on an age-constant basis and 8 on a weight-constant basis. Estimates of h^2 on an age-constant basis averaged 0.54, and ranged from moderate (0.33, Morris et al., 1999, REML analysis with an animal model) to high (0.67, Shackelford et al., 1995, DFREML analysis with an animal model), but most estimates were moderate. On a weight-constant basis, the average of estimates (0.50) was similar to that on an age-constant basis, but estimates ranged from low (0.18) for Danish Red males (Hinks and Bech Andersen, 1969, paternal half-sib analysis) to high (0.71) for bulls of Holstein Friesian and Brown Swiss sires (Jensen et al., 1991, REML analysis with a sire model). No comparisons of estimates of h^2 for RP obtained using different covariates in the same study were found.

*Fat Percent (**FP**).* Seven estimates of h^2 for FP in the literature were age-constant estimates. Estimates averaged 0.51 and ranged from moderate (0.35) for purebred and composite steers (Gregory et al., 1995) to high (0.65) for purebred, composite and F_1 crossbred steers (Shackelford et al., 1995). This range also includes estimates of h^2 of 0.39, 0.49, 0.53, 0.57 and 0.59 reported by Morris et al. (1999), Splan et al. (2002), Nephawe et al. (2004), Koch et al. (1982) and Wheeler et al. (1997), respectively. The two estimates on a weight-constant basis were very different: 0.12 by Hinks and Bech Andersen (1969) for Danish Red males and 0.89 by Jensen et al. (1991) for Holstein Friesian and Brown Swiss bulls, respectively. No comparisons of estimates of h^2 for FP evaluated at different end points in the same study were found.

*Bone Percent (**BP**).* All estimates of h^2 (n=8) for BP were adjusted for age, except the weight-constant estimate of 0.35 reported by Hinks and Bech Andersen (1969) for Danish Red males. In general, the estimates of h^2 indicate that BP is moderately heritable, averaging 0.44. The range was from 0.21 (Gregory et al., 1995) to 0.69 (Shackelford et al., 1995). Most estimates in this range were moderate: 0.31, 0.44, 0.48, 0.52, and 0.53 by Morris et al. (1999), Wheeler et al. (1997), Splan et al. (2002), Nephawe et al. (2004) and Koch et al. (1982), respectively. No reports of estimates of h^2 for BP adjusted for different covariates in the same study were found.

Estimates of Genetic Correlations

Estimates, unweighted means, minima, and maxima of r_g among carcass traits are displayed in Tables 2 (constant age or constant time-on-feed), 3 (constant slaughter weight or constant CW) and 4 (constant BT). Papers repeated in two or three Tables compared the effect of two or three different end points on estimates of r_g among carcass traits. Estimates of r_g on an age-constant or time-on-feed-constant basis will be referred as age-constant estimates and those on a slaughter weight-constant or CW-constant basis as weight-constant estimates. Table 5 contains minima, maxima and unweighted averages of estimates of r_g among carcass traits over the three end points. The column labeled as ER in the Tables refers to various cutability-type traits, which are cited as predicted percentage of retail product in this review. Extensive information is given in the Tables, but due to space restrictions discussion is limited to most important trait combinations and with the most number of observations.

Almost all (n=7) the estimates of r_g between CW and DP were on an age-constant basis and averaged 0.38, indicating that these two traits are moderately associated. Estimates were in a low-to-high range from 0.04 (Reynolds et al., 1991, son-sire regression analysis) for Hereford bulls to 0.65 (Pariacote et al., 1998, REML analysis with a sire model) for American Shorthorn steers. The other estimates within this range were 0.19, 0.32, 0.35, 0.52 and 0.62 by Yoon et al. (2002), Veseth et al. (1993), Shelby et al. (1963), Morris et al. (1999) and Hoque et al. (2002), showing significant variability among estimates. The only estimate of r_g for CW and DP of 0.47 obtained at constant BT (median=10 mm) was published by Riley et al. (2002) for 504 Brahman steers and heifers in central Florida.

Most (n=21) estimates of r_g for CW and BT were adjusted for age, followed by weight- and BT-constant estimates with four reports. Means of estimates were 0.13, -0.10 and 0.21, respectively. The overall average was 0.11, suggesting that the two traits are lowly associated. Estimates were highly variable within each end point. At constant age, for example, estimates ranged from -0.85, obtained by REML with a sire model (Morris et al., 1990, 1908 crossbred steers), to 0.95, obtained by Henderson's Method 2 with a sire model (Koch, 1978, 377 Hereford heifers). Estimates of -0.37, -0.22 and -0.10 by Shanks et al. (2001), Pariacote et al. (1998) and Moser et al. (1998), respectively, are other negative estimates. Other positive estimates by Wheeler et al. (1996), Cundiff et al. (1971) and Hoque et al. (2002) were 0.24, 0.34 and 0.42, respectively.

Of the 34 estimates of the r_g between CW and LMA 23 were for common age, 4 for common weight, and 7 for common BT. Estimates adjusted for age, weight and BT were, respectively, 0.44, 0.05 and 0.53. The mean of the 34 estimates was 0.41, revealing a moderate genetic

association. Estimates with equal age or equal weight end points were more variable than those with equal BT, but at equal weight the range included not only positive, but negative estimates. The positive estimates on an age constant basis ranged from very low (0.02) for 377 Hereford heifers (Koch, 1978) to very high (0.82) for 161 Hanwoo steers (Hoque et al., 2002), including variable estimates of 0.11, 0.23, 0.44, 0.58 and 0.76 by Wheeler et al. (2001), Mukai et al. (1995), Koch et al. (1982), Kemp et al. (2002) and Hassen et al. (1999), respectively. With constant BT, estimates were in a positive moderate-to-high range from 0.40 (Elzo et al., 1998) for Brahman steers to 0.69 (Devitt and Wilton, 2001) for Canadian crossbred steers. The estimates at constant weight by Reverter et al. (2003) for Belmont Red, Santa Gertrudis and Brahman, Benyshek et al. (1988) for Hereford cattle, Arnold et al. (1990) for Hereford steers and Reverter et al. (2003) for Murray Grey, Shorthorn, Angus and Hereford were -0.28, -0.07, 0.09 and 0.45, respectively. Only two studies evaluated the effects of age and BT end points on estimates of r_g between CW and LMA. Using Simmental field records, Shanks et al. (2001) reported that the estimate of the r_g was slightly reduced from 0.57 to 0.49 using age as a covariate in the model instead of BT. For Canadian crossbred steers, a larger difference was obtained by Devitt and Wilton (2001), who reported that the estimate adjusted for age (0.42) was significantly less than the estimate adjusted for BT (0.69).

Age- (n=16), weight- (n=4) and BT-constant estimates (n=9) of r_g for CW and MS were found. Mean estimates by end point were 0.16, 0.08 and 0.15, respectively. The 29 estimates had a mean of 0.14, indicating a weak genetic association between the two traits. Estimates were highly variable with positive and negative signs within each end point. With fixed age, estimates ranged from -0.33 for Hereford heifers (Koch, 1978) to 0.64 for Hereford bulls (Lamb et al., 1990); with fixed weight, the range was from -0.20 for Murray Grey, Shorthorn, Angus and Hereford (Reverter et al., 2003) to 0.35 (Benyshek et a., 1988) for Hereford cattle; and with fixed BT, was from -0.31 for Charolais steers and heifers (Johnston et al., 1992) to 0.67 for Charolais- and Limousin-sired steers and heifers (Wulf et al., 1996). Two studies compared estimates of r_g for CW and MS for different end points. Devitt and Wilton (2001), using Canadian carcass data, reported that the genetic correlation was much stronger at constant age than at constant BT (-0.30 vs -0.03). Similarly, Shanks et al. (2001) found that estimate of r_g was slightly greater with constant age than with constant BT (0.30 vs 0.20), but the estimates had different (positive) sign than those by Devitt and Wilton (2001).

Mean estimate of r_g between CW and ER on an age-constant (-0.10) or a BT-constant basis (0.25) indicate a low genetic correlation, but the sign of the estimated correlation did change with different end points. Shanks et al. (2001) reported negative estimates for the r_g between CW and ER, but the estimate adjusted for age was significantly larger than the estimate adjusted for bakcfat thickness (-0.21 vs -0.05).

On average, CW was highly positively correlated genetically with RW, FW and BW (0.84, 0.64 and 0.75 respectively) as expected on an age-constant basis. Estimates of r_g for these three pairs of traits were much less variable than estimates of r_g discussed previously. No estimates of r_g with constant weight or constant BT were in the literature. In contrast, averages of estimates of r_g of CW with RP (-0.06), FP (0.02) and BP (-0.04) at common age indicate little genetic association with these traits.

Few estimates of r_g for DP and BT were in the literature; most were adjusted for age (n=6) with one estimate each adjusted for weight and BT. Mean of age-constant estimates was 0.28. Reported estimates were -0.16, 0.02, 0.31, 0.36, 0.52, 0.61 by Pariacote et al. (1998), Oikawa et al. (2000), Yoon et al. (2002), Kuchida et al. (1990), Hoque et al. (2002) and Shelby et al. (1963), showing significant variation. The weight- (0.25) and BT-constant (0.42) estimates were reported by Dinkel and Busch (1973) and Riley et al. (2002). The mean (0.29) over all end points indicates a small genetic association.

Averages of estimates of r_g between DP and LMA suggest changes in magnitude and sign with different end points. Means were: 0.36 (n=9) at constant age, 0.62 (n=3) at constant weight and -0.05 (n=2) at constant BT. Estimates for age end point were variable, ranging from lowly negative (-0.11) for 411 Hereford bulls (Veseth et al., 1993, Henderson's Method 3 with paternal half-sibs) to highly positive (0.92) for 535 Japanese Black (Wagyu) steers (Oikawa et al., 2000, REML fitting an animal model). Only one study (Lee et al., 2000) assessed the effects of end point on estimates of r_g for DP and LMA. Changes in magnitude and sign were reported with different end points. The estimate of r_g was nearly zero (0.01) at constant age, nearly one (0.91) at constant weight and lowly negative (-0.11) at constant BT.

Averages of estimates of r_g between DP and MS were -0.32, 0.24 and 0.01 with constant age, weight and BT, suggesting possible changes in sign and magnitude with different end points, although these averages are based on few studies and observations (n=7, 2 and 3, respectively). Lee et al. (2000), for Korean Native (Hanwoo) cattle, found significant effects on magnitude of estimates of r_g for DP and MS reporting much larger estimates when adjusted for age and BT than when adjusted for weight (-0.88 and -0.99 vs -0.03).

Most of the estimates of r_g for BT and LMA were with common age (n=24) with fewer with common weight (n=8) and common BT (n=5). Means of estimates of r_g were -0.16, -0.28 and -0.06, respectively. Regardless of end point, the overall mean (-0.17) suggests that the two traits are lowly and negatively correlated genetically. Estimates obtained on an age-constant basis were more variable than estimates on a weight- or BT-constant basis. Estimates with constant age ranged from -1.00 for Japanese Black (Oikawa et al., 2000,

n=535 steers) to 0.38 for Hanwoo (Hoque et al., 2002, n=161 steers). Two recent studies (Shanks et al., 2001; Devitt and Wilton, 2001) concluded that age and weight end points had no significant effect on estimates of r_g for BT and LMA.

About half (n=19) of the 33 estimates of r_g for BT and MS were at constant age. Fewer estimates were at constant weight (n=8) and constant BT (n=6). Averages of estimates indicate the r_g at equal age (0.24), weight (0.23) or BT (0.21) are similar to each other. The average of estimates (0.20) across the three end points indicates BT and MS are lowly and positively genetically correlated. Shanks et al. (2001) reported similar estimates of r_g for BT and MS at constant age (0.17) and constant weight (0.18). Devitt and Wilton (2001) reported the weight-constant estimate was somewhat larger than the age-constant estimate (0.41 vs 0.30). All estimates with constant weight were positive, whereas four and two estimates were negative with constant age and constant BT, respectively. The near-to-zero estimate (0.01) by Wheeler et al. (1996) suggests that selection for increased MS would not affect BT. Average of BT-constant estimates does not include the estimate (-0.83) by Gilbert et al. (1993). This estimate should be interpreted with care because the scale of measurement for MS increased with decreased levels of marbling, i.e., higher levels of marbling were associated with increased BT. More variability was observed among estimates at constant age or constant BT than at constant weight. Range of estimates was from -0.42 (Kuchida et al., 1990) to 1.00 (Dunn et al., 1970) with fixed age and from -0.19 (Fernandes et al., 2002) to 0.62 (Brackelsberg et al., 1971) with fixed BT.

Few estimates of r_g between BT and ER for each end point ($n \leq 4$) were in the literature. Overall mean (-0.76) indicates BT and ER are highly and negatively correlated genetically. Estimates within each end point were less variable compared to estimates of r_g for combinations of traits discussed previously. The only study (Shanks et al., 2001) that contrasted estimates of r_g for BT and ER reported a larger estimate using weight as a covariate in the model than using age (-0.53 vs -0.29).

The r_g of LMA with MS had the most estimates (n=40) reported in the literature. Twenty were on an age-, 9 on a weight- and 11 on a BT-constant basis, which averaged 0.06, -0.07 and 0.05. Over the 40 estimates the mean was 0.03, indicating little genetic association with the implication that selection for increased LMA would not decrease marbling. At any slaughter end point, estimates had important variability. With common age, the range of estimates was from -0.61 for Canadian crossbred steers (Devitt and Wilton, 2001) to 0.83 for Wagyu steers (Oikawa et al., 2000), including estimates of -0.40, -0.36, -0.17, -0.10, 0.02, 0.12, and 0.49 by Van Vleck et al. (1992), Wheeler et al. (2001), Pariacote et al. (1998), Kemp et al. (2002), Mukai et al. (1995), Hirooka et al. (1996) and Kim et al. (1998), respectively. With common weight, estimates ranged from -0.38 for steers and heifers of Hereford sires and Angus-Holstein cows (Wilson et al., 1976) to 0.39 for Korean Native cattle (Lee et al., 2000). Other estimates reported by Reverter et al. (2003), Dinkel and Busch (1973), Benyshek et al. (1988) and Shanks et al. (2001) were -0.23, -0.17, 0.04 and 0.26, respectively. End point had a significant effect on the estimates of r_g of LMA with MS in each of three recent studies. Lee et al. (2000) found that estimates were different depending on the covariate used as the end point: 0.20 with BT, and 0.39 and 0.47 with slaughter weight and slaughter age covariates. Shanks et al. (2001) concluded that the estimates of r_g were moderate at age (0.46) and BT (0.48) end points but smaller on a weight-constant basis (0.26). Estimates reported by Devitt and Wilton (2001) were -0.61, -0.37 and -0.35 when using age, BT or weight end points, respectively.

The first insight into the effects of slaughter end points on estimates of r_g among carcass traits was by Cundiff et al. (1969). They reported a change in magnitude and direction of the r_g between RW and FW with constant age (0.55) or with constant weight (-0.90) end points. Two years later, Cundiff et al. (1971) reported that age end point caused a significant reduction in estimates of r_g of MS with RW, FW and BW relative to weight end point. Estimates were -0.13, 0.82 and -0.27 with constant age and -0.89, 0.98 and -0.78 with constant weight, respectively.

Conclusions and Implications

The review of estimates of h^2 and r_g published in the scientific literature during the last 42 years revealed that most estimates were on an age-constant basis. The traits with the most estimates of h^2 were CW, BT, LMA and MS. The average estimates for these traits indicate that they are similarly and moderately heritable. In contrast, the number of estimates of h^2 for DP was about half or less than half of those for carcass traits listed above. The average estimate also indicates that DP is moderately heritable. Fewest estimates of h^2 reported in the literature were for traits that require the most effort to measure: KPH, YG, ER, RW, FW, BW, RP, FP, and BP. The estimates, however, indicate they are more heritable, except for KPH and ER, than the more frequently studied carcass traits. The smallest number of estimates was for YG, which also had the largest estimates of h^2. Estimates of h^2 and r_g for most carcass traits varied greatly, which could be due to differences in breed groups, methods of estimation, effects in the model, number of observations, measurement errors, sex, and management differences. Few studies have compared h^2 and r_g estimates for carcass traits adjusted to different end points. Results from those few studies were inconsistent although some studies revealed that h^2 and r_g estimates for several traits were sensitive to the covariate (end point) included in the model implying that direct and correlated responses to selection would be different for some traits depending on slaughter end point. The effect of different end points on estimates of h^2 and r_g has not been studied for several

carcass traits. Estimates averaged over slaughter end points suggests that BT is highly correlated genetically with YG and ER, indicating that selection for reduced BT would be most efficient for improving YG and increasing ER. Carcass quality, however, would be affected negatively because of the positive estimate of r_g between MS and BT across end points. These relationships could discourage beef producers who desire to improve quality grade without increasing BT. Other researchers (Bertrand et al., 1993; Vieselmeyer et al., 1996), however, have demonstrated that marbling can be increased without increasing BT through selection based on estimated progeny differences. Based on age-constant estimates, an alternative would be to select for increased LMA, which could improve YG and increase ER without altering marbling.

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Table 1. Estimates of heritability (%) for carcass traits measured at, or adjusted to, different end points reported in the scientific literature from 1962 to 2004.

Author	Carcass trait[a]													
	CW	DP	FT	LA	KF	MS	YG	ER	RW	FW	BW	RP	FP	BP
Constant age														
Blackwell et al. (1962)	92	25												
Shelby et al. (1963)	57	57	24	26										
Cundiff et al. (1964)			43	73				40						
Cundiff et al. (1969)									64	46	38			
Dunn et al. (1970)[b]			39	60		42			59					
Dunn et al. (1970)			94	2					65					
Cundiff et al. (1971)	56		50	41		31		28						
Koch (1978)	68		68	28		34			38	94	56			
Benyshek (1981)	48	31	52	40		47		49	45					
Koch et al. (1982)	43		41	56	83	40			58	47	57	63	57	53
MacNeil et al. (1984)	44								45	50				
Hanset et al. (1987)		53												
More O'Ferrall et al. (1989)	32													
Lamb et al. (1990)	31		24	28		33	24	23						
Morris et al. (1990)[c]	28	14	3	30										
Morris et al. (1990)	44	39	37	29										
Kuchida et al. (1990)		15	62	65		86								
MacNeil et al. (1991)			52											
Reynolds et al. (1991)	33	1		1										
Van Vleck et al. (1992)				62		43								
Woodward et al. (1992)						23		18						
Wilson et al. (1993)	31		26	32		26								
Veseth et al. (1993)	38	25		51	37	31								
Gregory et al. (1994)			30			52						50		
Shackelford et al. (1994)												45		
Shackelford et al. (1995)									66	65	62	67	65	69
Gregory et al. (1995)	23	19	25	22		48			28	32	39	47	35	21
Mukai et al. (1995)	39		55	47		52		53						
Barkhouse et al. (1996)						40								
Wheeler et al. (1996)	15	6	56	65	32	73	76							
Hirooka et al. (1996)	37		35	38		40								
Wheeler et al. (1997)									50			62	59	44
Pariacote et al. (1998)	60	49	46	97	45	88	54							
Moser et al. (1998)	59		27	39										
Kim et al. (1998)		39	34	49	30	78								
Hassen et al. (1999)	33		14	15				7						

Table 1 (continued). Estimates of heritability (%) for carcass traits measured at, or adjusted to, different end points reported in the scientific literature from 1962 to 2004.

	Carcass trait[a]													
Author	CW	DP	FT	LA	KF	MS	YG	ER	RW	FW	BW	RP	FP	BP
Morris et al. (1999)	48	31		42					48	30	51	33	39	31
Fouilloux et al. (1999)[d]		50												
Lee et al. (2000)		12		17		8								
Oikawa et al. (2000)[e]	15		15	2		49								
Reverter et al. (2000)[f]	31													
Reverter et al. (2000)	54													
Wheeler et al. (2001)	33		84	69	28	57	85							
Shanks et al. (2001)	32		10	26		12		9						
Devitt and Wilton (2001)	47		41	45		35								
Splan et al. (2002)	49		46	58	60	35						58	49	48
Pitchford et al. (2002)[g]	36		26											
Kemp et al. (2002)	48		35	45		42								
Fouilloux et al. (2002)	35													
Yoon et al. (2002)	29	17	44	39		57								
Hoque et al. (2002)	37	19	7	18										
Crews et al. (2003)	48		35	46		54								
Nephawe et al. (2004)	52		46	57	65	46						59	53	52
n	**36**	**18**	**34**	**36**	**8**	**29**	**4**	**8**	**11**	**7**	**6**	**9**	**7**	**7**
Unweighted mean	**42**	**28**	**39**	**41**	**48**	**45**	**60**	**28**	**51**	**52**	**51**	**54**	**51**	**45**
Constant weight														
Shelby et al. (1963)			22	46										
DuBose and Cartwright (1967)	65													
Cundiff et al. (1969)									42	37	39			
Hinks and Bech Andersen (1969)		97										18	12	35
Cundiff et al. (1971)			53	32		33		35						
Wilson et al. (1971)			18	47		9								
Dinkel and Bush (1973)		15	57	25		31		66						
Wilson et al. (1976)			41	42	0			44						
Benyshek (1981)		35	51	41		46		48						
Renand et al. (1985)[h]		27		33										
Renand et al. (1985)		69												
Benyshek et al. (1988)	19		44	44		38								
Morris et al. (1990)[c]			11	28										
Morris et al. (1990)			42	28										

Table 1 (continued). Estimates of heritability (%) for carcass traits measured at, or adjusted to, different end points reported in the scientific literature from 1962 to 2004.

Author	Carcass trait[a]													
	CW	DP	FT	LA	KF	MS	YG	ER	RW	FW	BW	RP	FP	BP
Arnold et al. (1991)	24		49	46		35								
Jensen et al. (1991)		33										71	89	
Johnston et al. (1992)			24	44		22								
Veseth et al. (1993)		26			38	28								
Hirooka et al. (1996)			33	42		42								
Robinson et al. (1998)[g,i]		37	18											
Robinson et al. (1998)		15	29											
Fouilloux et al. (1999)		43												
Reverter et al. (2000)[f]			28									68		
Reverter et al. (2000)			27									36		
Lee et al. (2000)		16		24		1								
Shanks et al. (2001)			14	22		12		12						
Devitt and Wilton (2001)			38	45		43								
Crews and Kemp (2001)[j]	38		46	54		55		42						
Newman et al. (2002)[g,k]	35		28									53		
Newman et al. (2002)	40		24									44		
Reverter et al. (2003)[l]	36		41	32		25						50		
Reverter et al. (2003)	39		27	30		17						57		
n	**8**	**11**	**23**	**19**	**2**	**15**	**0**	**6**	**1**	**1**	**1**	**8**	**2**	**1**
Unweighted mean	**37**	**38**	**33**	**37**	**19**	**29**	**-**	**41**	**42**	**37**	**39**	**50**	**51**	**35**
Constant fat thickness														
Cunningham and Broderick (1969)	52													
Brackelsberg et al. (1971)[m]			43	40	72	73				50				
Morris et al. (1990)[c]	17													
Morris et al. (1990)	51													
Johnston et al. (1992)	9			38		26								
Gilbert et al. (1993)	26		14	48		28		55						
Wulf et al. (1996)	10	21		52		16	76							
O'Connor et al. (1997)						52								
Elzo et al. (1998)[n]	46		14	42	3	14								
Elzo et al. (1998)	39		24	53	14	16								
Lee et al. (2000)		9		18		10								
Shanks et al. (2001)	33			29		13		17						
Devitt and Wilton (2001)	57			52		30								

Table 1 (continued). Estimates of heritability (%) for carcass traits measured at, or adjusted to, different end points reported in the scientific literature from 1962 to 2004.

Author	Carcass trait[a]													
	CW	DP	FT	LA	KF	MS	YG	ER	RW	FW	BW	RP	FP	BP
Fernandes et al. (2002)	30		17	40		37								
Riley et al. (2002)	55	77	63	44	46	44	71	71	50					
n	**12**	**3**	**6**	**11**	**4**	**12**	**2**	**3**	**1**	**1**	**0**	**0**	**0**	**0**
Unweighted mean	**35**	**36**	**29**	**41**	**34**	**30**	**74**	**48**	**50**	**50**	-	-	-	-
Total n	**56**	**32**	**63**	**66**	**14**	**56**	**6**	**17**	**13**	**9**	**7**	**17**	**9**	**8**
Minimum	**9**	**1**	**3**	**1**	**0**	**1**	**24**	**7**	**28**	**30**	**38**	**18**	**12**	**21**
Maximum	**92**	**97**	**94**	**97**	**83**	**88**	**85**	**71**	**66**	**94**	**62**	**71**	**89**	**69**
Total mean	**40**	**32**	**36**	**40**	**40**	**37**	**64**	**36**	**51**	**50**	**49**	**52**	**51**	**44**

[a]CW=carcass weight, DP=dressing percentage, FT=backfat thickness, LA=longissimus muscle area, KF=kidney, pelvic, and heart fat percentage, MS=marbling score, YG=yield grade, ER=predicted percentage of retail product, RW=retail product weight, FW=fat weight, BW=bone weight, RP=actual retail product percent, FP=fat percent, BP=bone percent.

[b]First row of estimates for Dunn et al. (1970) is for purebreds; second row is for crossbreds.

[c]First row of estimates for Morris et al. (1990) is for animals slaughtered at 20 mo of age; second row is for animals slaughtered at 31 mo of age.

[d]Age-constant estimate for Fouilloux et al. (1999) is for Limousin; weight-constant estimate is for Charolais.

[e]LA and MS without covariate (nonsignificant), and DP and FT heritabilities are age-constant estimates.

[f]First row of estimates for Reverter et al. (2000) is for Angus; second row is for Hereford.

[g]FT is fat depth over the rump at the P8 site.

[h]First and second rows of estimates for Renand et al. (1985) are for two different stations.

[i]First row of estimates for Robinson et al. (1998) is for tropical breeds; second row is for temperate breeds.

[j]Animals slaughtered when live weight and fat depth reached minimums of 500 kg and 7mm, respectively.

[k]First row of estimates for Newman et al. (2002) is for purebreds; second row is for crossbreds.

[l]First row of estimates for Reverter et al. (2003) is for tropical breeds; second row is for temperate breeds.

[m]Animals slaughtered at a constant quality-grade end point.

[n]First row of estimates for Elzo et al. (1998) is for Angus; second row is for Brahman.

Table 2. Estimates of genetic correlations among carcass traits measured at, or adjusted to, constant age or constant time-on-feed reported in the scientific literature[a].

	Carcass trait[b]												
	DP	FT	LA	KF	MS	YG	ER	RW	FW	BW	RP	FP	BP
CW													
Shelby et al. (1963)	.35	.47	.15										
Cundiff et al. (1971)		.34	.66		.23		-.33	.94	.80	.86			
Koch (1978)		.95	.02		-.33			.80	.90	.57			
Koch et al. (1982)		.08	.44	.22	.25			.81	.45	.71	-.11	.13	-.20
Morris et al. (1990)[c]		-.85	.09										
Morris et al. (1990)		-.30	.09										
Lamb et al. (1990)		.14	.68		.64								
Reynolds et al. (1991)	.04												
Veseth et al. (1993)	.32		.80	.21	.38								
Wilson et al. (1993)		.38	.47		-.06								
Mukai et al. (1995)		.39	.23		.36		-.08						
Gregory et al. (1995)		.13	.66		.31			.76	.51	.75	-.12	.08	.18
Hirooka et al. (1996)		.39	.23		-.05								
Wheeler et al. (1996)		.24	.25		-.03	.18							
Wheeler et al. (1997)								.73			.19	-.19	.08
Moser et al. (1998)		-.10	.12										
Pariacote et al. (1998)	.65	-.22	.70	-.30	-.10	-.39							
Morris et al. (1999)	.52		.75					.98	.54	.85	-.20	.06	-.21
Hassen et al. (1999)		.25	.76				.24						
Shanks et al. (2001)		-.37	.49		.30		-.21						
Devitt and Wilton (2001)		.15	.42		-.32								
Wheeler et al. (2001)		.06	.11		.44	.23							
Kemp et al. (2002)		.17	.58		.27								
Hoque et al. (2002)	.62	.42	.82										
Yoon et al. (2002)	.19	-.02	.65		.20								
Minimum	**.04**	**-.85**	**.02**	**-.30**	**-.33**	**-.39**	**-.33**	**.73**	**.45**	**.57**	**-.20**	**-.19**	**-.21**
Maximum	**.65**	**.95**	**.82**	**.22**	**.64**	**.23**	**.24**	**.98**	**.90**	**.86**	**.19**	**.13**	**.18**
Unweighted mean	**.38**	**.13**	**.44**	**.04**	**.16**	**.01**	**-.10**	**.84**	**.64**	**.75**	**-.06**	**.02**	**-.04**
DP													
Shelby et al. (1963)		.61	.40										
Kuchida et al. (1990)		.36	.20		-.18								
Veseth et al. (1993)			-.11	-.06	.00								
Pariacote et al. (1998)		-.16	.79	-.10	.08	-.56							
Kim et al. (1998)					-.20								
Morris et al. (1999)			.40					.57	.35	.18	.24	.09	-.58
Lee et al. (2000)			.01		-.88								
Oikawa et al. (2000)		.02	.92		-1.0								

Table 2 (continued). Estimates of genetic correlations among carcass traits measured at, or adjusted to, constant age or constant time-on-feed reported in the scientific literature[a].

	Carcass trait[b]											
	DP	FT	LA	KF	MS	YG	ER	RW	FW	BW	RP	FP	BP
Hoque et al. (2002)		.52	.68										
Yoon et al. (2002)		.31	-.07		-.05								
Minimum		**-.16**	**-.11**	**-.10**	**-1.0**	**-.56**	**-**	**.57**	**.35**	**.18**	**.24**	**.09**	**-.58**
Maximum		**.61**	**.92**	**-.06**	**.08**	**-.56**	**-**	**.57**	**.35**	**.18**	**.24**	**.09**	**-.58**
Unweighted mean		**.28**	**.36**	**-.08**	**-.32**	**-.56**	**-**	**.57**	**.35**	**.18**	**.24**	**.09**	**-.58**
FT													
Shelby et al. (1963)			.30										
Cundiff et al. (1964)			.08				-.95						
Dunn et al. (1970)			-.27		1.0			-.24					
Koch (1978)			.03		.73			.65	.95	.30			
Koch et al. (1982)			-.44	.10	.16			-.34	.74	-.30	-.74	.78	-.52
Morris et al. (1990)[c]			-.07										
Morris et al. (1990)			-.07										
Lamb et al. (1990)			-.04		.73								
Kuchida et al. (1990)			-.11		-.42								
Wilson et al. (1993)			-.06		-.13								
Gregory et al. (1994)					.32						-.76		
Mukai et al. (1995)			-.33		-.04		-.76						
Gregory et al. (1995)			-.06		.44			-.48	.80	-.05	-.76	.82	-.27
Hirooka et al. (1996)			-.12		-.12								
Wheeler et al. (1996)			-.43		.01	.86							
Wheeler et al. (1997)								-.29			-.62	.66	-.53
Moser et al. (1998)			-.05										
Pariacote et al. (1998)			-.31	-.21	.26	.67							
Kim et al. (1998)					.12								
Hassen et al. (1999)			-.30				-.74						
Oikawa et al. (2000)			-1.0		.15								
Shanks et al. (2001)			-.06		.17		-.29						
Devitt and Wilton (2001)			.02		.30								
Wheeler et al. (2001)			-.42		.42	.89							
Kemp et al. (2002)			-.20		.38								
Hoque et al. (2002)			.38										
Yoon et al. (2002)			-.28		.17								
Minimum			**-1.0**	**-.21**	**-.13**	**.67**	**-.95**	**-.48**	**.74**	**-.30**	**-.76**	**.66**	**-.53**
Maximum			**.38**	**.10**	**1.0**	**.89**	**-.29**	**.65**	**.95**	**.30**	**-.62**	**.82**	**-.27**
Unweighted mean			**-.16**	**-.06**	**.24**	**.81**	**-.69**	**-.14**	**.83**	**-.02**	**-.72**	**.75**	**-.44**

Table 2 (continued). Estimates of genetic correlations among carcass traits measured at, or adjusted to, constant age or constant time-on-feed reported in the scientific literature[a].

	Carcass trait[b]											
	DP	FT	LA	KF	MS	YG	ER	RW	FW	BW	RP	FP	BP
LA													
Cundiff et al. (1964)							.28						
Dunn et al. (1970)					-.38			.95					
Koch (1978)								-.02	.10	-.36			
Koch et al. (1982)				.01	-.14			.72	-.28	.35	.53	-.48	-.04
Lamb et al. (1990)					.57								
Kuchida et al. (1990)					.43								
Van Vleck et al. (1992)					-.40								
Veseth et al. (1993)				.36	.51								
Wilson et al. (1993)					-.04								
Mukai et al. (1995)					.02		.75						
Gregory et al. (1995)					-.02			.86	.07	.31	.32	-.26	-.25
Hirooka et al. (1996)					.12								
Wheeler et al. (1996)					-.37	-.79							
Wheeler et al. (1997)								.67			.76	-.75	.37
Pariacote et al. (1998)				-.31	-.17	-.85							
Kim et al. (1998)					.49								
Morris et al. (1999)								.74	.02	.59	-.08	-.51	-.39
Hassen et al. (1999)							.57						
Lee et al. (2000)					.47								
Oikawa et al. (2000)					.83								
Shanks et al. (2001)					.46		.75						
Devitt and Wilton (2001)					-.61								
Wheeler et al. (2001)					-.36	-.72							
Kemp et al. (2002)					-.10								
Yoon et al. (2002)					-.10								
Minimum				**-.31**	**-.61**	**-.85**	**.28**	**-.02**	**-.28**	**-.36**	**-.08**	**-.75**	**-.39**
Maximum				**.36**	**.83**	**-.72**	**.75**	**.95**	**.10**	**.59**	**.76**	**-.26**	**.37**
Unweighted mean				**.02**	**.06**	**-.79**	**.59**	**.65**	**-.02**	**.22**	**.38**	**-.50**	**-.08**
KF													
Koch et al. (1982)					.29			-.04	.48	-.05	-.43	.46	-.33
Veseth et al. (1993)					.59								
Pariacote et al. (1998)					.10	.22							
Kim et al. (1998)					.22								
Minimum					**.10**	**.22**	-	**-.04**	**.48**	**-.05**	**-.43**	**.46**	**-.33**
Maximum					**.59**	**.22**	-	**-04**	**.48**	**-.05**	**-.43**	**.46**	**-.33**
Unweighted mean					**.30**	**.22**	-	**-.04**	**.48**	**-.05**	**-.43**	**.46**	**-.33**

Table 2 (continued). Estimates of genetic correlations among carcass traits measured at, or adjusted to, constant age or constant time-on-feed reported in the scientific literature[a].

	Carcass trait[b]												
	DP	FT	LA	KF	MS	YG	ER	RW	FW	BW	RP	FP	BP
MS													
Dunn et al. (1970)								-.48					
Cundiff et al. (1971)								-.13	.82	-.27			
Koch (1978)									.33				
Koch et al. (1982)								-.02	.42	.15	-.37	.34	-.04
Lamb et al. (1990)						.32	-.36						
Woodward et al. (1992)							-.12						
Gregory et al. (1994)											-.56		
Mukai et al. (1995)							.09						
Gregory et al. (1995)								-.12	.65	.08	-.60	.66	-.28
Wheeler et al. (1996)						.19							
Wheeler et al. (1997)								-.24			-.36	.32	-.01
Pariacote et al. (1998)						.26							
Shanks et al. (2001)							.01						
Wheeler et al. (2001)						.60							
Minimum						**.19**	**-.36**	**-.48**	**.33**	**-.27**	**-.60**	**.32**	**-.28**
Maximum						**.60**	**.09**	**-.02**	**.82**	**.15**	**-.36**	**.66**	**-.01**
Unweighted mean						**.34**	**-.10**	**-.20**	**.56**	**-.01**	**-.47**	**.44**	**-.11**
YG													
Wheeler et al. (1997)							-	-.41	-	-	-.76	.78	-.53
ER													
Cundiff et al. (1971)								-.08	-.85	.17	-	-	-
RW													
Cundiff et al. (1969)									.55	.98			
Koch (1978)									.46	.78			
Koch et al. (1982)									-.12	.72	.46	-.44	.03
Gregory et al. (1995)									-.16	.54	.56	-.59	.19
Wheeler et al. (1997)											.80	-.77	.30
Morris et al. (1999)									.28	.79	.17	-.22	-.29
Minimum									**-.16**	**.54**	**.17**	**-.77**	**-.29**
Maximum									**.55**	**.98**	**.80**	**-.22**	**.30**
Unweighted mean									**.20**	**.76**	**.50**	**-.51**	**.06**
FW													
Cundiff et al. (1969)										.38			
Koch (1978)										.22			

Table 2 (continued). Estimates of genetic correlations among carcass traits measured at, or adjusted to, constant age or constant time-on-feed reported in the scientific literature[a].

	Carcass trait[b]												
	DP	FT	LA	KF	MS	YG	ER	RW	FW	BW	RP	FP	BP
Koch et al. (1982)										.03	-.91	.94	-.51
Gregory et al. (1995)										.35	-.88	.90	-.07
Morris et al. (1999)										.39	-.85	.94	-.28
Minimum										**.03**	**-.91**	**.90**	**-.51**
Maximum										**.39**	**-.85**	**.94**	**-.07**
Unweighted mean										**.27**	**-.88**	**.93**	**-.29**
BW													
Koch et al. (1982)											.14	-.25	.54
Gregory et al. (1995)											-.20	.03	.79
Morris et al. (1999)											-.34	-.02	.48
Minimum											**-.34**	**-.25**	**.48**
Maximum											**.14**	**.03**	**.79**
Unweighted mean											**-.13**	**-.08**	**.60**
RP													
Koch et al. (1982)												-.98	.35
Gregory et al. (1995)												-.98	.08
Wheeler et al. (1997)												-.98	.47
Morris et al. (1999)												-.94	-.21
Minimum												**-.98**	**-.21**
Maximum												**-.94**	**.47**
Unweighted mean												**-.97**	**.17**
FP													
Koch et al. (1982)													-.51
Gregory et al. (1995)													-.14
Wheeler et al. (1997)													-.63
Morris et al. (1999)													-.19
Minimum													**-.63**
Maximum													**-.14**
Unweighted mean													**-.37**

[a] "-" indicates no estimates found.

[b] CW=carcass weight, DP=dressing percentage, FT=backfat thickness, LA=longissimus muscle area, KF=kidney, pelvic, and heart fat percentage, MS=marbling score, YG=yield grade, ER=predicted percentage of retail product, RW=retail product weight, FW=fat weight, BW=bone weight, RP=actual retail product percent, FP=fat percent, BP=bone percent.

[c] First row of estimates for Morris et al. (1990) is for animals slaughtered at 20 months of age; second row is for animals slaughtered at 31 months of age.

Table 3. Estimates of genetic correlations among carcass traits measured at, or adjusted to, constant weight reported in the scientific literature[a].

	Carcass trait[b]												
	DP	FT	LA	KF	MS	YG	ER	RW	FW	BW	RP	FP	BP
CW													
Benyshek et al. (1988)		.04	-.07		.35								
Arnold et al. (1991)		.36	.09		.33								
Reverter et al. (2003)[c]		-.39	.45		-.15						.06		
Reverter et al. (2003)		-.42	-.28		-.20						.16		
Minimum	-	**-.42**	**-.28**	-	**-.20**	-	-	-	-	-	**.06**	-	-
Maximum	-	**.36**	**.45**	-	**.35**	-	-	-	-	-	**.16**	-	-
Unweighted mean	-	**-.10**	**.05**	-	**.08**	-	-	-	-	-	**.11**	-	-
DP													
Dinkel and Busch (1973)		.25	.47		.50		-.23						
Renand et al. (1985)			.47										
Jensen et al. (1991)											.04	.01	
Lee et al. (2000)			.91		-.03								
Minimum		**.25**	**.47**	-	**-.03**	-	**-.23**	-	-	-	**.04**	**.01**	-
Maximum		**.25**	**.91**	-	**.50**	-	**-.23**	-	-	-	**.04**	**.01**	-
Unweighted mean		**.25**	**.62**	-	**.24**	-	**-.23**	-	-	-	**.04**	**.01**	-
FT													
Dinkel and Busch (1973)			-.59		.38		-.75						
Wilson et al. (1976)			-.47		.37		-.95						
Benyshek et al. (1988)			-.52		.08								
Arnold et al. (1991)			-.37		.19								
Reverter et al. (2000)[d]											-.74		
Reverter et al. (2000)											-.50		
Shanks et al. (2001)			-.03		.18		-.53						
Devitt and Wilton (2001)			-.03		.41								
Reverter et al. (2003)[c]			-.13		.12						-.65		
Reverter et al. (2003)			-.10		.13						-.29		
Minimum			**-.59**	-	**.08**	-	**-.95**	-	-	-	**-.74**	-	-
Maximum			**-.03**	-	**.41**	-	**-.53**	-	-	-	**-.29**	-	-
Unweighted mean			**-.28**	-	**.23**	-	**-.74**	-	-	-	**-.55**	-	-
LA													
Dinkel and Busch (1973)					-.17		.72						
Wilson et al. (1976)					-.38		.87						
Benyshek et al. (1988)					.04								
Arnold et al. (1991)					-.01								
Lee et al. (2000)					.39								
Shanks et al. (2001)					.26		.75						
Devitt and Wilton (2001)					-.35								

Table 3 (continued). Estimates of genetic correlations among carcass traits measured at, or adjusted to, constant weight reported in the scientific literature[a].

	Carcass trait[b]												
	DP	FT	LA	KF	MS	YG	ER	RW	FW	BW	RP	FP	BP
Reverter et al. (2003)[c]					-.14						.44		
Reverter et al. (2003)					-.23						.25		
Minimum				-	**-.38**	-	**.72**	-	-	-	**.25**	-	-
Maximum					**.39**		**.87**				**.44**		
Unweighted mean				-	**-.07**	-	**.78**	-	-	-	**.35**	-	-
KF					-	-	-	-	-	-	-	-	-
MS													
Cundiff et al. (1971)								-.89	.98	-.78			
Dinkel and Busch (1973)							.26						
Wilson et al. (1976)							-.20						
Shanks et al. (2001)							.05						
Reverter et al. (2003)[c]											-.39		
Reverter et al. (2003)											-.56		
Minimum						-	**-.20**	**-.89**	**.98**	**-.78**	**-.56**	-	-
Maximum						-	**.26**	**-.89**	**.98**	**-.78**	**-.39**	-	-
Unweighted mean						-	**.04**	**-.89**	**.98**	**-.78**	**-.48**	-	-
YG							-	-	-	-	-	-	-
ER													
Cundiff et al. (1971)								.80	-	.89	-	-	-
RW													
Cundiff et al. (1969)									-.90	.96	-	-	-
FW													
Cundiff et al. (1969)										-.99	-	-	-
BW											-	-	-
RP													
Jensen et al. (1991)												-.92	-
FP													-

[a] "-" indicates no estimates found.

[b] CW=hot carcass weight, DP=dressing percentage, FT=backfat thickness, LA=longissimus muscle area, KF=kidney, pelvic, and heart fat percentage, MS=marbling score, YG=yield grade, ER=predicted percentage of retail product, RW=retail product weight, FW=fat weight, BW=bone weight, RP=actual retail product percent, FP=fat percent, BP=bone percent.

[c] First row of estimates for Reverter et al. (2003) is for temperate breeds; second row is for tropical breeds.

[d] First row of estimates for Reverter et al. (2000) is for Angus; second row is for Hereford.

Table 4. Estimates of genetic correlations among carcass traits measured at, or adjusted to, constant backfat thickness reported in the scientific literature[a].

	Carcass trait[b]												
	DP	FT	LA	KF	MS	YG	ER	RW	FW	BW	RP	FP	BP
CW													
Johnston et al. (1992)			.45		-.31								
Gilbert et al. (1993)					.55								
Wulf et al. (1996)					.67								
Elzo et al. (1998)[c]		.06	.45	-.03	-.15								
Elzo et al. (1998)		-.01	.40	.05	.11								
Shanks et al. (2001)			.57		.20		-.05						
Devitt and Wilton (2001)			.69		-.03								
Riley et al. (2002)	.47	.60	.52	.27	.39	.56	.55						
Fernandes et al. (2002)		.17	.62		-.10								
Minimum	**.47**	**-.01**	**.40**	**-.03**	**-.31**	**.56**	**-.05**	-	-	-	-	-	-
Maximum	**.47**	**.60**	**.69**	**.27**	**.67**	**.56**	**.55**						
Unweighted mean	**.47**	**.21**	**.53**	**.10**	**.15**	**.56**	**.25**	-	-	-	-	-	-
DP													
Wulf et al. (1996)					.68								
Lee et al. (2000)			-.11		-.99								
Riley et al. (2002)		.42	.02	.24	.35	.48	-.48						
Minimum		**.42**	**-.11**	**.24**	**-.99**	**.48**	**-.48**	-	-	-	-	-	-
Maximum		**.42**	**.02**	**.24**	**.68**	**.48**	**-.48**	-	-	-	-	-	-
Unweighted mean		**.42**	**-.05**	**.24**	**.01**	**.48**	**-.48**	-	-	-	-	-	-
FT													
Brackelsberg et al. (1971)			-.09	.87	.62				.97				
Gilbert et al. (1993)					-.83		-.98						
Elzo et al. (1998)[c]			.02	-.02	.05								
Elzo et al. (1998)			-.03	.03	.03								
Riley et al. (2002)			.02	.63	.56	.93	-.93						
Fernandes et al. (2002)			-.22		-.19								
Minimum			**-.22**	**-.02**	**-.19**	**.93**	**-.98**	-	**.97**	-	-	-	-
Maximum			**.02**	**.87**	**.62**	**.93**	**-.93**	-	**.97**	-	-	-	-
Unweighted mean			**-.06**	**.38**	**.04**	**.93**	**-.96**	-	**.97**	-	-	-	-
LA													
Brackelsberg et al. (1971)				-.35	-.12				-.53				
Johnston et al. (1992)					-.24								
Gilbert et al. (1993)					.63								
Wulf et al. (1996)					.13								
Elzo et al. (1998)[c]				-.02	-.11								
Elzo et al. (1998)				.03	-.01								

Table 4 (continued). Estimates of genetic correlations among carcass traits measured at, or adjusted to, constant backfat thickness reported in the scientific literature[a].

	Carcass trait[b]												
	DP	FT	LA	KF	MS	YG	ER	RW	FW	BW	RP	FP	BP
Lee et al. (2000)					.20								
Shanks et al. (2001)					.48		.81						
Devitt and Wilton (2001)					-.37								
Riley et al. (2002)				.18	.44	.26	.23						
Fernandes et al. (2002)					-.48								
Minimum				**-.35**	**-.48**	**.26**	**.23**	-	**-.53**	-	-	-	-
Maximum				**.18**	**.63**	**.26**	**.81**	-	**-.53**	-	-	-	-
Unweighted mean				**-.04**	**.05**	**.26**	**.52**	-	**-.53**	-	-	-	-
KF													
Brackelsberg et al. (1971)					.63				.81				
Elzo et al. (1998)[c]					.07								
Elzo et al. (1998)					.03								
Riley et al. (2002)					.27	.60	-.67						
Minimum					**.03**	**.60**	**-.67**	-	**.81**	-	-	-	-
Maximum					**.63**	**.60**	**-.67**	-	**.81**	-	-	-	-
Unweighted mean					**.25**	**.60**	**-.67**	-	**.81**	-	-	-	-
MS													
Brackelsberg et al. (1971)									.54				
Gilbert et al. (1993)							.63						
Wulf et al. (1996)						.04							
Shanks et al. (2001)							.06						
Riley et al. (2002)						.45	-.43						
Minimum						**.04**	**-.43**	-	**.54**	-	-	-	-
Maximum						**.45**	**.63**	-	**.54**	-	-	-	-
Unweighted mean						**.25**	**.09**	-	**.54**	-	-	-	-
YG													
Riley et al. (2002)							-.99	-	-	-	-	-	-
ER								-	-	-	-	-	-
RW									-	-	-	-	-
FW										-	-	-	-
BW											-	-	-
RP												-	-
FP													-

[a] "-" indicates no estimates found.

[b] CW=carcass weight, DP=dressing percentage, FT=backfat thickness, LA=longissimus muscle area, KF=kidney, pelvic, and heart fat percentage, MS=marbling score, YG=yield grade, ER=predicted percentage of retail product, RW=retail product weight, FW=fat weight, BW=bone weight, RP=actual retail product percent, FP=fat percent, BP=bone percent.

[c] First row of estimates for Elzo et al. (1998) is for Angus; second row is for Brahman.

Table 5. Minimum, maximum and unweighted average of estimates of genetic correlations among carcass traits for all end points published in the scientific literature from 1963 to 2003[a].

	Carcass trait[b]												
	DP	FT	LA	KF	MS	YG	ER	RW	FW	BW	RP	FP	BP
CW													
Minimum	.04	-.85	-.28	-.30	-.33	-.39	-.33	.73	.45	.57	-.20	-.19	-.21
Maximum	.65	.95	.82	.27	.67	.56	.55	.98	.90	.86	.19	.13	.18
Mean	.40	.11	.41	.07	.14	.15	.02	.84	.64	.75	-.003	.02	-.04
DP													
Minimum		-.16	-.11	-.10	-1.0	-.56	-.48	.57	.35	.18	.04	.01	-.58
Maximum		.61	.92	.24	.68	.48	-.23	.57	.35	.18	.24	.09	-.58
Mean		.29	.36	.03	-.14	-.04	-.36	.57	.35	.18	.14	.05	-.58
FT													
Minimum			-1.0	-.21	-.19	.67	-.98	-.48	.74	-.30	-.76	.66	-.53
Maximum			.38	.87	1.0	.93	-.29	.65	.97	.30	-.29	.82	-.27
Mean			-.17	.23	.24	.84	-.76	-.14	.87	-.02	-.63	.75	-.44
LA													
Minimum				-.35	-.61	-.85	.23	-.02	-.53	-.36	-.08	-.75	-.39
Maximum				.36	.83	.26	.87	.95	.10	.59	.76	-.26	.37
Mean				-.01	.03	-.53	.64	.65	-.12	.22	.37	-.50	-.08
KF													
Minimum					.03	.22	-.67	-.04	.48	-.05	-.43	.46	-.33
Maximum					.63	.60	-.67	-.04	.81	-.05	-.43	.46	-.33
Mean					.28	.41	-.67	-.04	.65	-.05	-.43	.46	-.33
MS													
Minimum						.04	-.43	-.89	.33	-.78	-.60	.32	-.28
Maximum						.60	.63	-.02	.98	.15	-.36	.66	-.01
Mean						.31	-.001	-.31	.62	-.21	-.47	.44	-.11
YG													
Minimum							-.99	-.41	-	-	-.76	.78	-.53
Maximum							-.99	-.41	-	-	-.76	.78	-.53
Mean							-.99	-.41	-	-	-.76	.78	-.53
ER													
Minimum								-.08	-.85	.17	-	-	-
Maximum								.80	-.85	.89	-	-	-
Mean								.36	-.85	.53	-	-	-

Table 5 (continued). Minimum, maximum and unweighted average of estimates of genetic correlations among carcass traits for all end points published in the scientific literature from 1963 to 2003[a].

	Carcass trait[b]												
	DP	FT	LA	KF	MS	YG	ER	RW	FW	BW	RP	FP	BP
RW													
Minimum									-.90	.54	.17	-.77	-.29
Maximum									.55	.98	.80	-.22	.30
Mean									.02	.80	.50	-.51	.06
FW													
Minimum										-.99	-.91	.90	-.51
Maximum										.39	-.85	.94	-.07
Mean										.06	-.88	.93	-.29
BW													
Minimum											-.34	-.25	.48
Maximum											.14	.03	.79
Mean											-.13	-.08	.60
RP													
Minimum												-.98	-.21
Maximum												-.94	.47
Mean												-.97	.17
FP													
Minimum													-.63
Maximum													-.14
Mean													-.37

[a] "-" indicates no estimates found.

[b] CW=carcass weight, DP=dressing percentage, FT=backfat thickness, LA=longissimus muscle area, KF=kidney, pelvic, and heart fat percentage, MS=marbling score, YG=yield grade, ER=predicted percentage of retail product, RW=retail product weight, FW=fat weight, BW=bone weight, RP=actual retail product percent, FP=fat percent, BP=bone percent.

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John Bruner ..... SD 1983
Leness Hall ..... WA 1983
Ric Hoyt ..... OR 1983
E.A. Keithley ..... MO 1983
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Eldon & Richard Wiese ..... MN 1987
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Harold Dickson ..... MO..... 1992
Tom Drake ..... OK 1992
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Dick Montague ..... CA.....1992
Bill Rea ..... PA 1992
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Miles P. "Buck" Pangburn ..... IA 1993
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Ted Seely ..... WY.....1993
Collin Sander ..... SD 1993
Harrell Watts ..... AL.....1993
Bob Zarn ..... MN.....1993
Ken & Bonnie Bieber ..... SD 1994
John Blankers ..... MN.....1994
Jere Caldwell ..... KY 1994
Mary Howe di'Zerega ..... VA 1994
Ron & Wayne Hanson ..... CAN...1994
Bobby F. Hayes ..... AL.....1994
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Bruce Orvis ..... CA.....1994
John Pfeiffer Family ..... OK 1994
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Bobby Aldridge ..... NC.....1995
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Frank Schiefelbein ..... MN.....1996
Ingrid & Willy Volk ..... NC.....1996
William A. Womack, Jr. ..... AL.....1996

Alan Albers	KS	1997
Gregg & Diane Butman	MN	1997
Blaine & Pauline Canning	CAN	1997
Jim & JoAnn Enos	IL	1997
Harold Pate	AL	1997
E. David Pease	CAN	1997
Juan Reyes	WY	1997
James I. Smith	NC	1997
Darel Spader	SD	1997
Bob & Gloria Thomas	OR	1997
Nicholas Wehrmann	VA	1997
Richard McClung	VA	1997
James D. Bennett Family	VA	1998
Dick & Bonnie Helms	NE	1998
Dallis & Tammy Basel	SD	1998
Duane L. Kruse Family	IL	1998
Abilgail & Mark Nelson	CA	1998
Airey Family	MB	1998
Dave & Cindy Judd	KS	1998
Earl & Nedra McKarns	OH	1998
Tom Shaw	ID	1998
Wilbur & Melva Stewart	AB	1998
Adrian Weaver & Family	CO	1998
Kelly & Lori Darr	WY	1999
Kent Klineman	SD	1999
Steve Munger	SD	1999
John Kluge	VA	1999
Kramer Farms	IL	1999
Noller & Frank Charolais	IA	1999
Lynn & Gary Pelton	KS	1999
Rausch Herefords	SD	1999
Duane Schieffer	MT	1999
Terry O'Neill	MT	1999
Tony Walden	AL	1999
Ralph Blalock, Sr. & Jr., & David Blalock	NC	2000
Larry & Jean Croissant	CO	2000
John C. Curtin	IL	2000
Galen, Lori & Megan Fink	KS	2000
Harlin & Susan Hecht	MN	2000
Banks & Margo Herndon	AL	2000
Kent Klineman & Steve Munger	SD	2000
Jim & Janet Listen	WY	2000
Mike & T.K. McDowell	VA	2000
Vaughn Meyer & Family	SD	2000
Blane & Cindy Nagel	SD	2000
John & Betty Botert	MO	2000
Alan & Deb Vedvei	SD	2000
Bob & Nedra Funk	OK	2001
Steve Hillman & Family	IL	2001
Tom Lovell	AL	2001
McAllen Ranch	TX	2001
Kevin, Jessica, & Emily Moore	TX	2001
Blane & Cindy Nagel	SD	2001
Don & Priscilla Nielsen	CO	2001
George W. Lemm	VA	2001
Marvin & Katheryn Robertson	VA	2001
Dale, Don & Mike Spencer	NE	2001
Ken Stielow & Family	KS	2001
Eddie L. Sydenstricker	MO	2001
DeBruycker Charolais	MT	2002
Ellis Farm	IL	2002
Holly Hill Farm	VA	2002
Isa Cattle Co., Inc.	TX	2002
Lyons Ranch	KS	2002
Noller & Frank Charolais	IA	2002
Rishel Angus	NE	2002
Running Creek Ranch	CO	2002
Shamrock Angus	WY	2002
Stewart Angus	IN	2002
Triple "M" Farm	AL	2002
Bedwell Charolais	IA	2003
Boyd Farm	AL	2003
Camp Cooley Ranch	TX	2003
Hilltop Ranch	TX	2003
Moser Ranch	KS	2003
Mystic Hill Farms	VA	2003
Pingetzer's Six Iron Ranch	WY	2003
San Isabel Ranch	CO	2003
Shamrock Vale Farms	OH	2003

Seedstock Producer of the Year

John Crowe	CA	1972
Mrs. R. W. Jones, Jr.	GA	1973
Carlton Corbin	OK	1974
Leslie J. Holden	MT	1975
Jack Cooper	MT	1975
Jorgensen Brothers	SD	1976
Glen Burrows	NM	1977
James D. Bennett	VA	1978
Jim Wolfe	NE	1979
Bill Wolfe	OR	1980
Bob Dickinson	KS	1981
A.F. "Frankie" Flint	NM	1982
Bill Borror	CA	1983
Lee Nichols	IA	1984
Ric Hoyt	OR	1984
Leonard Lodden	ND	1986
Henry Gardiner	KS	1987
W. T. "Bill" Bennett	WA	1988
Glynn Debter	AL	1989
Douglas & Molly Hoff	SD	1990
Summitcrest Farms	OH	1991
Leonard Wulf & Sons	MN	1992
R. A. "Rob" Brown	TX	1993
J. David Nichols	IA	1993
Richard Janssen	KS	1994
Tom & Carolyn Perrier	KS	1995
Frank Felton	MO	1996
Bob & Gloria Thomas	OR	1997
Wehrmann Angus Ranch	VA	1997
Flying H Genetics	NE	1998
Knoll Crest Farms	VA	1998
Morven Farms	VA	1999
Fink Beef Genetics	KS	2000
Sydensticker Angus Farms	MO	2001
Dave Gust Family	MO	2002
Moser Ranch	KS	2003

Moser Ranch Receives the 2003 BIF Outstanding Seedstock Producer Award

In spring 1987 the Moser Ranch marketed four bulls as breeding stock to local cattlemen. In their 11th annual sale in 2003, 118 head of Simmental, Angus and Red Angus bulls sold into seven states and one Canadian province. Harry, is a native of North Dakota and a graduate of North Dakota State University. Lisa is a native of Kansas with a degree from Kansas State University. They've been in the cattle business all of their lives. Along with their children — Cameron (19), Kendra (16) and Kayla (11) — the Mosers own and manage the Moser Ranch, located approximately 40 miles northeast of Manhattan in the northern Flint Hills of Kansas.

With the use of proven, predictable genetics and an extensive artificial insemination (AI) and embryo transfer (ET) program, utilizing every available economic and performance measurement, the Mosers have built a strong genetic base, while developing a strong customer-service program. The Moser ranch cow herd consists of 150 spring- and 20 fall-calving Simmental females, 40 spring- and 10 fall-calving Angus, 25 Red Angus spring-calving females, and 50 fall-calving commercial Angus females. Seven producers are cooperator herds for the ET program, which began in 1991. This enables the Mosers to produce approximately 150 additional calves per year. Bulls are sold primarily to commercial cattlemen in the annual bull sale; females and embryos are sold private treaty.

The Mosers are very hands-on with respect to their entire operation. The family works together and utilizes the strengths each person brings to the operation, whether it be for day-to-day care of the cow herd, sire selection and mating decisions, heat detection and AI, weaning and development of bulls and replacements, putting up and grinding feed, sale management and promotion, financial and breed association bookwork, computer time and Web site updates, customer service and consultations, or developing marketing options and feeding alliances.

In the past five years, the commitment to helping market customer calves through various avenues has been especially rewarding. Two alliances with which they are involved provide feedlot and carcass data on each individual animal that goes through each program. In addition, a Moser Influence Preconditioned Calf Sale each fall gives still other customers a very lucrative option. Continued customer and consumer education is addressed regularly by holding seminars and hosting tours to enhance understanding of the beef industry.

2004 Seedstock Producer Award Nominees

Adams Angus Farm

Bob & Juliette Adams, Rob & Connie Adams, Alabama

Adams Angus Farm is a true family farm begun in 1939 by Sidney F. Adams, father of Bob Adams. The farm is located in southeast Alabama, seven miles east of Union Springs. Over the last 65 years, many things have changed as the farm has adapted to the ever-changing agricultural world. Today, cattle, timber and hunting leases are the only remaining sources of income left on this 925-acre farm. Now approximately 75 brood cows are maintained to calve within a 90-day calving season, beginning in late September for heifers and ending in late January for mature cows.

Bob Adams was a charter member of the Alabama Beef Cattle Improvement Association in 1964 and saw the need, as many others did, to begin collecting performance records on his cattle to determine which cattle were truly superior. As record keeping became more detailed, the American Angus Association's record keeping service known as AHIR was utilized. Adams Angus Farm has been actively evaluating their bloodlines through Alabama BCIA bull evaluations for years and are also utilizing carcass ultrasound on farm to collect carcass data. Artificial insemination was implemented on the farm in 1982, with the goal to produce at least 75% of calves by A.I. Today, the HeatWatch® estrus detection system is utilized with A.I. to produce calves with the best genetics possible. The ultimate goal is for Adams cattle to be known for their performance, but also that they will be efficient, easy fleshing, structurally sound cattle.

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

Byland Polled Shorthorns

Mrs. L. Eugene (Marilyn) Byers & Dr. Jeff Byers and Jon Byers, Ohio

The late Dr. Eugene Byers and his wife, Marilyn, started raising Shorthorn cattle in the 1950s with the purchase of one bred cow. Gene was a practicing veterinarian and thus was exposed to all breeds of cattle and knew well what each offered in terms of positives and negatives. Shorthorns were selected because of their mothering ability and their problem free nature. Currently the farm is operated by Dr. Gene Byers' two sons Jon and Jeff.

Marilyn Byers is currently serving in her twenty-sixth year as Ashland County Commissioner and Dr. Jeff Byers stays busy with his veterinary practice, so Jon Byers currently manages the day to day operations of Byland Polled Shorthorns. The farm will calve 160 cows in 2004, mostly spring calving with a few fall calving cows to facilitate the embryo transfer program. Acreage consists of approximately 150 acres of alfalfa, 140 acres of corn, 70-80 acres of soybeans, and a few acres in small grains with the rest of the 800 acres in pasture or woodland. Most of the crops produced are fed on the farm.

Byland Polled Shorthorns is a performance focused herd that strives to produce cattle both purebred and commercial producers find acceptable. Breeding cattle have been sold into nearly every state plus Canada and Australia. Many of these cattle, especially bulls, have gone on to be nationally and internationally successful for other breeders.

All of the bull and heifer calves that fail to meet the strict selection criteria to be offered for sale or used as replacements in the herd are fed in the feedlot located on the farm and harvested at a local USDA inspected packing facility.

Byland has been the largest contributor of carcass data in the Shorthorn breed through the years. The Byland prefix is found on over seven percent of the sires in the 2004 Shorthorn Carcass Sire listing, and the farm has bred or owns 62 total bulls in all sections of the Sire Summary.

The Ohio Cattlemen's Association and the American Shorthorn Association is proud to nominate Byland Polled Shorthorns.

Camp Cooley Ranch

Klaus Birkel and Mark Cowan, Texas

Camp Cooley Ranch is a progressive beef operation located east of Franklin, Texas. Set on gently rolling hills, the 11,750 acre ranch is picturesque and home to Brangus, Angus and Charolais cattle.

Klaus Birkel purchased Camp Cooley Ranch in October 1991. In 1993, he purchased the Brinks Brangus cowherd and moved the cattle from Kansas to Texas. Eventually, he added the complimentary genetics of Angus and Charolais cattle. Today, the Camp Cooley Ranch umbrella has grown to include nearly 1,500 registered, breeding age females at the ranch and an additional 1,000 breeding age females at joint ventures in Mexico, Bolivia, Argentina and Brazil.

The combination of Brangus, Angus and Charolais cattle offer Camp Cooley Ranch customers the opportunity to utilize the positive contributions of each breed in their programs. In rotational cross breeding systems, the three breed make up provides options of environmental adaptability, maternal genetics, carcass traits, and performance for our customers.

Camp Cooley Ranch has taken progressive measures to support and encourage ultrasound use by funding and participating in numerous research projects across the

nation. Today, they continue to stay on the forefront of the industry with carcass research and the collection and analysis of carcass data.

During the calendar year 2004, Camp Cooley Ranch will market over 1,000 bulls through their annual production sale and by private treaty. At the annual sale and throughout the year, efforts are made to provide learning/educational opportunities for customers and cooperators.

The International Brangus Breeders Association is proud to nominate Camp Cooley Ranch.

Eaton Charolais

Eaton Families, Lee Eaton, Montana

Our great-grandfather, Charles Eaton, and his three oldest sons left Iowa to homestead on the vast Eastern Montana prairie in 1909. Our parents Cecil and Esther purchased his 320 acres in 1942. They had ten children, five sons and five daughters. Sons, Elner, Lee and Tom, along with their sons and families run the Montana operation. Ben and his two sons manage the North Dakota operation and Ed is retired and lives in New Mexico. We have been running the family business since 1960, when our dad had a heart attack. We have expanded the family business to about 50,000 deeded acres and 25,000 leased; the majority is leased from the Bureau of Land Management. We purchased our first Charolais in 1965, at the time we had just a few cows. Since, we have expanded our Charolais herd to over 1,000 head of purebred cows and 1,000 commercial cows. We finish thousands of cattle at Dinklage Feedyards in Nebraska, of which we are part owners.

Our program is a linebred program using the best young bulls out of our best young cows back in our cowherd. We only calve in the spring, don't creep feed and breed our cows in single sire pastures. We haven't AI'd any cows for a long time, but do AI yearling heifers (to our own bulls) in our Montana feedlot.

All of the Eaton families are involved in the management and operation of the family business. The cowherd, both purebred and commercial, Charolais bulls, feeder cattle, extensive dry land wheat, barley and hay production, our trucking and equipment maintenance keeps the whole family busy.

The American-International Charolais Association is proud to nominate Eaton Charolais.

Flat Branch Cattle Company

J. Ben Curtin, Illinois

Flat Branch Cattle Company is owned and operated by J. Ben Curtin. The purebred Angus operation is located in Taylorville, Illinois, which is in Christian County. Others involved in this seedstock operation are Ben's father, Bill Curtin, wife, Linda, and two children, Lori and Jess. Flat Branch Cattle Company was the recipient of the IBA Seedstock Breeder of the Year Award on July 15, 2003.

The Curtin family has been raising registered Angus cattle for three generations. Bill started Flat Branch Cattle Company in 1934 as a ten year old 4-H member with an Angus cattle project. During the 1970s there was a brief shift to exotic cattle. They began raising Chianina, and Maine Anjou cattle as well, but still remained committed to the Angus breed with a small herd. Today this purebred Angus operation consists of 40 mature cows, 200 acres of pasture and hay fields, and 700 acres of corn and soybean fields.

For the purposes of this operation, calving season begins in early January and continues through the end of March. Calves spend anywhere from four to six months out on pasture and are then weaned during the months of June and July. The breeding program is completely based on artificial insemination with a large emphasis on performance.

The University of Illinois Extension is proud to nominate Flat Branch Cattle Company.

Judd Ranch, Inc.

Dave and Cindy Judd, Kansas

Judd Ranch, Inc. is a family owned and operated seedstock enterprise located on the northeastern edge of the Flint Hills just west of Pomona, Kansas. Dave and Cindy Judd purchased the operation, along with a Polled Hereford herd, in 1981 after Dave finished his Animal Science degree from Iowa State University. Brangus females bred to Gelbvieh bulls quickly were added to the herd. Impressed with the results of Gelbvieh-influenced calves, the Judds purchased a large number of half-blood and ¾ blood Gelbvieh females in 1982 and began working toward a purebred Gelbvieh herd. Gelbvieh was the breed of choice due to U.S. Meat Animal Research data showing Gelbvieh as number one for pounds of calf weaned per cow exposed.

Today, Judd Ranch consists of 572 registered Gelbvieh females and 100 recipeint females, with another 150 registered Gelbvieh heifers developed each year as replacements. A small group of Red Angus females is used to produce purebred Red Angus and Balancer bulls.

The Judd Ranch program has both fall (August 14 – October 1) and spring (January 25 – March 10) calving seasons. About 90% of the females are artificially inseminated (AI), with the remaining 10% pasture bred to Judd Ranch herd sires. A majority are the same AI sires used by fellow producers. For the past several years, a 100% calf crop has been weaned, with twins supplementing this percentage. In addition to its extensive AI program. Judd Ranch's top genetics are propagated via embryo transfer (ET), flushing 15-20 females three times a year.

Judd Ranch is comprised of 5,000 acres, 4,500 deeded acres and 500 leased acres. Of this, 626 acres are farmed, with the remaining being native grass.

The Kansas Livestock Association is proud to nominate Judd Ranch.

Rausch Herefords

Jerry, Vern, Shannon and Joel Rausch, South Dakota

Brothers Jerry and Vern, and Vern's sons, Shannon and Joel, run a purebred Hereford and commercial ranching operation in north central South Dakota. Jerry and Vern's older brothers and their father started the Hereford herd in 1946. The ranch runs 600 registered Hereford and 200 commercial baldy cows. They purchase top bull calves from other brothers' and nephews' registered herds at weaning and performance test and market them with their home-raised bulls. Seventy-five bulls and 150 replacement heifer calves are offered in the annual bull and female sale, which is in its 47th year. An additional 75 bulls are sold private treaty.

Rausch Herefords are nearing 400 females qualifying on the American Hereford Association's (AHA) Dams of Distinction list. They lead the nation annually in the total number of cows to qualify for the list the past 23 years. Qualifying females requires a heifer to calve early in life and maintain a calving interval no greater than one year. Other qualifications require reproductive efficiency and weaning weight ratios above 105 percent.

South Dakota has four pronounced seasons. Rausch cows are stressed through the winter and calved in the spring. They are then flushed on spring green growth and naturally bull bred on the prosperity of summer growth. The hardened fall growth adds pounds to the calves and fleshens the dams. We think these, along with proper culling, are some of the reasons we qualify cows on the Dams of Distinctions list.

Rausch Herefords have merchandised nearly 6,000 bulls and 6,000 females to the commercial cattle industry.

The American Hereford Association is proud to nominate Rausch Herefords.

Reynolds Ranch

Genie, Ric and Rod Reynolds, Colorado

Reynolds Ranch is located in the San Luis Valley of south, central Colorado. The ranch consists of hay meadows and farm land used to produce enough winter feed for approximately 450 mother cows. Limousin make up the majority of the cows, with Angus, Shorthorn, and Maine cows used in a cross breeding program primarily for show steers. The cattle summer in the mountains of Colorado and northern New Mexico at elevations of 8,000 to 10,500 feet.

Ric and I are the fourth generation of ranchers to work the cattle on the ranch. With a desire to produce cattle with more production, our father started a crossbreeding program using Brown Swiss bulls. This cross developed more milk and growth along with a better disposition in our cattle. With the inception of Limousin cattle into the United States over 30 years ago, we began using them through Artificial Insemination. We then began to market these cattle as seedstock and now sell about 100-120 bulls annually along with a select group of females.

We are a hands on, no frills operation that has worked long and hard to develop cattle that work for us, our neighbors, and the industry in general.

The Colorado Cattlemen's Association is proud to nominate Reynolds Ranch.

Silveira Brothers Angus and Diversified Farming

Darrell and Dudley Silveira and Rick Silveira Blanchard, California

Silveira Brothers is located in the Central San Joaquin Valley in the towns of Mendota and Firebaugh, California and has been farming row crops and raising Angus cattle for over 30 years. This operation started with two small farms that Darrell and his wife Carole, started with son, Rick, and grew from a hobby to a full time cattle operation which included Darrell's brother, Dudley, who is the controller accountant and Darrell's son, Rick, who is now a managing partner on the ranch in Firebaugh, CA. The business consists of 300 spring and fall calving mother cows and using embryo transfer and A.I. along with natural breeding. We have two production sales a year, September for bull sale, October for the female sale as well as participation in the Signature Collection Sale in Wilton, CA in June and the Show Girl Revue Sale in Reno, Nevada in April. This operation only exists through two families dedication and passion for our cattle business which we have breathed and co-existed with every day of our lives.

The California BCIA is proud to nominate Silveira Brothers Angus.

Symens Brothers Limousin

Irwin, Paul and John Symens, South Dakota

Symens Brothers Limousin is located in northeast South Dakota at Amherst. The partnership began in 1966 when father Wilbert retired, and is currently owned by brothers, Irwin, Paul and John. The operation consists of 1,500 acres of cropland raising corn, alfalfa, and soybeans; a feedlot, feeding about 2,000 head per year; and a purebred Limousin herd of 300 registered Limousin cows with 240 spring calvers and 60 fall calvers.

The original cowherd consisted of 120 crossbred cows from Red Angus, Shorthorn and Hereford. In the late 60s, some of the cows were A.I.ed to Charolais, then Limousin, Chianina, Normandy, and Maine Anjou. Limousin fit the

goals and likes of the Symens Brothers the best and the purebred operation was born. Through A.I. and embryo transplant, as well as purchasing fullblood Limousin sires and cows, the herd was expanded rapidly. Bulls were sold private treaty until 1981 when the first production sale was held.

From 1975 to 1993, Symens Brothers marketed fat cattle under a Limousin Lean Label and also sold beef directly off the farm. Presently most of the fed cattle are contracted with Laura's Lean Beef under a natural, lean label. Carcass data is returned and each animal is priced according to its lean beef yield.

The operation leases 1,900 acres of pasture for grazing and raises all the feed for the feedlot and winter cow feed.

The next generation is represented by Irwin's son, Brad, and Paul's son, Warren. They, along with one full-time employee are also supported by the operation.

The North American Limousin Foundation is proud to nominate Symens Brothers Limousin.

Touchstone Angus

Brad and Cathy James, Wyoming

The American Heritage Dictionary defines a Touchstone as: 1. A hard black stone, such as jasper or basalt, formerly used to test the purity of gold or silver by comparing the streak left on the stone by one of these metals with that of a standard alloy. 2. An excellent quality or example that is used to test the excellence or genuineness of others.

The program was named Touchstone Angus to symbolize the pure strain of Emulous cattle that the program began with. Touchstone Angus has been in operation for over 10 years beginning in Elizabeth, Colorado, in 1993 and relocated to Lusk, Wyoming in 1999. The registered Angus cow herd calves in the spring and numbers around 170 linebred Emulous cows. Annual sales are held in Lusk each spring to market registered bulls and females.

A significant part of the program is a branded beef product began in 1994 called Touchstone Angus Natural Beef. It is a "Natural" product from grain fattened Touchstone bred steers. Selling natural beef built a link directly to the consumer that greatly influences breeding priorities and philosophies.

The Wyoming Beef Cattle Improvement Association is proud to nominate Touchstone Angus.

Triple U Ranch

Craig and Elaine Utesch, Iowa

Triple U Ranch is located in the northeast corner of Woodbury and the southwest corner of Cherokee counties in the rolling hills of northwest Iowa. Craig Utesch is one of three brothers who are the third generation of Utesches to farm this land. His grandfather purchased the original farm in 1944 and fed cattle with Craig's father, William (Bill), in the 1950's. Bill and his wife, Mary, purchased the farm from Bill's father's estate in 1960, and together they farmed and raised their family – Craig, brothers Brad and Kirk, and sister Cathy.

Today, Triple U Ranch encompasses some 3,200 acres owned by the family members and rented back to the farming operation. Of these acres, approximately 1,000 acres are pasture or timbered pasture and 2,200 acres are row cropped.

Triple U Ranch is a combination of three enterprises - a 250 head cow-calf herd, a 3,000 head one-time capacity feedlot, and a 2,200 acre row crop operation. Each of the brothers manages a specific area: Craig manages the cow/calf operation, Brad manages the feedlot, and Kirk manages the row crops. This has allowed each to specialize their knowledge of their area of management. Family meetings which include the spouses and Craig's mother, Mary, keep all family members up to date on the major management decisions of the family farming business.

In 1977, Craig purchased some rougher land and decided to begin a cow herd, originally purchasing about 40 crossbred cows. In 1978, he began production testing the herd and keeping his own replacements. He originally developed three separate herds – a purebred Simmental herd stressing black genetics, purebred Gelbvieh herd, and a commercial herd to capitalize on the crossbred genetics they were able to create for the feedlot.

Craig's first venture into the seedstock business came in the spring of 1981 when he sold his first production tested bull at the Iowa Beef Improvement Association sale in Storm Lake. This first bull was a brown Simmental which sold for $900. In the twenty-three years since, Utesch and his family have continued to market seedstock through the Iowa Beef Improvement Association, the Iowa Cattlemen's Bull and Heifer Test program, the Iowa Beef Expo, at local livestock auctions, and by private treaty sales from the ranch.

The seedstock breeding herd currently consists of 29 registered Angus cows, 15 registered Gelbvieh cows, 117 registered purebred Simmental cows, and 43 registered percentage Simmental cows. The commercial herd consists of 45 cows, predominantly Angus-Simmental crossbreds. Triple U heifers begin calving February 15, with the cows starting on March 15. Calving will finish up by May 15 each spring.

The Iowa Simmental Association is proud to nominate Triple U Ranch.

Commercial Producer Honor Roll of Excellence

Chan Cooper ..... MT 1972
Alfred B Cobb, Jr. ..... MT 1972
Lyle Eivens ..... IA 1972
Broadbent Brothers ..... KY 1972
Jess Kilgote ..... MT 1972
Clifford Ouse ..... MN 1973
Pat Wilson ..... FL 1973
John Glaus ..... SD 1973
Sig Peterson ..... ND 1973
Max Kiner ..... WA 1973
Donald Schott ..... MT 1973
Stephen Garst ..... IA 1973
J.K. Sexton ..... CA 1973
Elmer Maddox ..... OK 1973
Marshall McGregor ..... MO 1974
Dave Matti ..... MT 1974
Lloyd DeBruycker ..... MT 1974
Gene Rambo ..... CA 1974
Jim Wolf ..... NE 1974
Henry Gardiner ..... KS 1974
Johnson Brothers ..... SD 1974
John Blankers ..... MN 1975
Paul Burdett ..... MT 1975
Oscar Burroughs ..... CA 1975
John R. Dahl ..... ND 1975
Eugene Duckworth ..... MO 1975
Gene Gates ..... KS 1975
V.A. Hills ..... KS 1975
Robert D. Keefer ..... MT 1975
Kenneth E. Leistritz ..... E 1975
Ron Baker ..... OR 1976
Dick Boyle ..... ID 1976
James Hackworth ..... MO 1976
John Hilgendorf ..... MN 1976
Kahau Ranch ..... HI 1976
Milton Mallery ..... CA 1976
Robert Rawson ..... IA 1976
William A. Stegner ..... ND 1976
U.S. Range Exp. Stat. ..... MT 1976
Maynard Crees ..... KS 1977
Ray Franz ..... MT 1977
Forrest H. Ireland ..... SD 1977
John A. Jameson ..... IL 1977
Leo Knoblauch ..... MN 1977
Jack Pierce ..... ID 1977
Mary & Stephen Garst ..... IA 1977
Todd Osteross ..... ND 1978
Charles M. Jarecki ..... MT 1978
Jimmy G McDonnal ..... NC 1978
Victor Arnaud ..... MO 1978
Ron & Malcom McGregor ..... IA 1978
Otto Uhrig ..... NE 1978
Arnold Wyffels ..... MN 1978
Bert Hawkins ..... OR 1978
Mose Tucker ..... AL 1978
Dean Haddock ..... KS 1978
Myron Hoeckl ..... ND 1979
Harold & Wesley Arnold ..... SD 1979
Ralph Neill ..... IA 1979
Morris Kuschel ..... MN 1979
Bert Hawkins ..... OR 1979
Dick Coon ..... WA 1979
Jerry Northcutt ..... MO 1979
Steve McDonnell ..... MT 1979
Doug Vandermyde ..... IL 1979
Norman, Denton & Calvin Thompson ..... SD 1979
Jess Kilgore ..... MT 1980
Robert & Lloyd Simon ..... IL 1980
Lee Eaton ..... MT 1980
Leo & Eddie Grubl ..... SD 1980
Roger Winn, Jr. ..... VA 1980
Gordon McLean ..... ND 1980
Ed Disterhaupt ..... MN 1980
Thad Snow ..... CAN 1980
Oren & Jerry Raburn ..... OR 1980
Bill Lee ..... KS 1980
Paul Moyer ..... MO 1980
G.W. Campbell ..... IL 1981
J.J. Feldmann ..... IA 1981
Henry Gardiner ..... KS 1981
Dan L. Weppler ..... MT 1981
Harvey P. Wehri ..... ND 1981
Dannie O'Connell ..... SD 1981
Wesley & Harold Arnold ..... SD 1981
Jim Russell & Rick Turner ..... MO 1981
Oren & Jerry Raburn ..... OR 1981
Orin Lamport ..... SD 1981
Leonard Wulf ..... MN 1981
Wm. H. Romersberter ..... IL 1982
Milton Krueger ..... MO 1982
Carl Odegard ..... MT 1982
Marvin & Donald Stoker ..... IA 1982
Sam Hands ..... KS 1982
Larry Campbel ..... KY 1982
Earl Schmidt ..... MN 1982
Raymond Josephson ..... ND 1982
Clarence Reutter ..... SD 1982
Leonard Bergen ..... CAN 1982
Kent Brunner ..... KS 1983
Tom Chrystal ..... IA 1983
John Freltag ..... WI 1983
Eddie Hamilton ..... KY 1983
Bill Jones ..... MT 1983
Harry & Rick Kline ..... IL 1983
Charlie Kopp ..... OR 1983
Duwayne Olson ..... SD 1983
Ralph Pederson ..... SD 1983
Ernest & Helen Schaller ..... MO 1983
Al Smith ..... VA 1983
John Spencer ..... CA 1983
Bud Wishard ..... MN 1983
Bob & Sharon Beck ..... OR 1984
Leonard Fawcett ..... SD 1984
Fred & Lee Kummerfeld ..... WY 1984
Norman Coyner & Sons ..... VA 1984
Franklyn Esser ..... MO 1984
Edgar Lewis ..... MT 1984
Boyd Mahrt ..... CA 1984
Neil Moffat ..... CAN 1984
William H. Moss, Jr. ..... GA 1984
Dennis P. Solvie ..... MN 1984
Robert P. Stewart ..... KS 1984
Charlie Stokes ..... NC 1984
Milton Wendland ..... AL 1984
Bob & Sheri Schmidt ..... MN 1985
Delmer & Joyce Nelson ..... IL 1985
Harley Brockel ..... SD 1985
Kent Brunner ..... KS 1985
Glenn Havery ..... OR 1985
John Maino ..... CA 1985
Ernie Reeves ..... VA 1985
John R. Rouse ..... WY 1985
George & Thelma Boucher ..... CAN 1985
Kenneth Bentz ..... OR 1986
Gary Johnson ..... KS 1986
Ralph G. Lovelady ..... AL 1986
Ramon H. Oliver ..... KY 1986
Kay Richarson ..... FL 1986
Mr. & Mrs. Clyde Watts ..... NC 1986
David & Bev Lischka ..... CAN 1986
Dennis & Nancy Daly ..... WY 1986
Carl & Fran Dobitz ..... SD 1986
Charles Fariss ..... VA 1986
David Forster ..... CA 1986
Danny Geersen ..... SD 1986
Oscar Bradford ..... AL 1987
R.J. Mawer ..... CAN 1987
Rodney G. Oliphant ..... KS 1987
David Reed ..... OR 1987
Jerry Adamson ..... NE 1987
Gene Adams ..... GA 1987
Hugh & Pauline Maize ..... SD 1987
P.T. McIntire & Sons ..... VA 1987
Frank Disterhaupt ..... MN 1987
Mac, Don & Joe Griffith ..... GA 1988
Jerry Adamson ..... NE 1988
Ken, Wayne, & Bruce Gardiner ..... CAN 1988
C.L. Cook ..... MO 1988
C.J. & D.A. McGee ..... IL 1988
William E. White ..... KY 1988
Frederick M. Mallory ..... CA 1988
Stevenson Family ..... OR 1988
Gary Johnson ..... KS 1988
John McDaniel ..... AL 1988
William Stegner ..... ND 1988
Lee Eaton ..... MT 1988
Larry D. Cundall ..... WY 1988
Dick & Phyllis Henze ..... MN 1988
Jerry Adamson ..... NE 1989
J.W. Aylor ..... VA 1989
Jerry Bailey ..... ND 1989
James G. Guyton ..... WY 1989

Kent Koostra ..... KY 1989
Ralph G. Lovelady ..... AL 1989
Thomas McAvory, Jr, ... GA 1989
Bill Salton ..... IA 1989
Lauren & Mel Schuman ..... CA 1989
Jim Tesher ..... ND 1989
Joe Thielen ..... KS 1989
Eugene & Ylene Williams .... MO 1989
Phillip, Patty, & Greg Bartz . MO 1990
John C. Chrisman ..... WY 1990
Les Herbst ..... KY 1990
Jon C. Ferguson ..... KS 1990
Mike & Dianna Hooper ..... OR 1990
James & Joan McKinlay ..... CAN .. 1990
Gilbert Meyer ..... SD 1990
DuWayne Olson ..... SD 1990
Raymond R. Peugh ..... IL 1990
Lewis T. Pratt ..... VA 1990
Ken & Wendy Sweetland ..... CAN .. 1990
Swen R. Swenson Cattle ..... TX 1990
Robert A Nixon and Sons ..... VA 1991
Murray A. Greaves ..... CAN .. 1991
James Hauff ..... ND 1991
J.R. Anderson ..... WI 1991
Ed & Rich Blair ..... SD 1991
Reuben & Connee Quinn ..... SD 1991
Dave & Sandy Umbarger ..... OR 1991
James A. Theeck ..... TX 1991
Ken Stielow ..... KS 1991
John E. Hanson, Jr. ..... CA 1991
Charles & Clyde Henderson . MO 1991
Russ Green ..... WY 1991
Bollman Farms ..... IL 1991
Craig Utesch ..... IA 1991
Mark Barenthsen ..... ND 1991
Rary Boyd ..... AL 1992
Charles Daniel ..... MO 1992
Jed Dillard ..... FL 1992
John & Ingrid Fairhead ..... NE 1992
Dale J. Fischer ..... IA 1992
E. Allen Grimes Family ..... ND 1992
Kopp Family ..... OR 1992
Harold, Barbara, & Jeff Marshall ..... PA 1992
Clinton E. Martin & Sons ..... VA 1992
Loyd & Pat Mitchell ..... CAN .. 1992
William Van Tassel ..... CAN .. 1992
James A. Theeck ..... TX 1992
Aquilla M. Ward ..... WV 1992
Albert Wiggins ..... KS 1992
Ron Wiltshire ..... CAN .. 1992
Andy Bailey ..... WY 1993
Leroy Beiterspacher ..... SD 1993
Glenn Valbaugh ..... WY 1993
Oscho Deal ..... NC 1993
Jed Dillard ..... FL 1993
Art Farley ..... IL 1993
Jon Ferguson ..... KS 1993
Walter Hunsuker ..... CA 1993
Nola & Steve Kielboeker ..... MO 1993
Jim Maier ..... SD 1993
Bil & Jim Martin ..... WV 1993
Ian & Adam McKillop ..... ON 1993
George & Robert Pingetzer ... WY 1993
Timothy D. Sufphin ..... VA 1993
James A. Theeck ..... TX 1993
Gene Thiry ..... MB 1993
Fran & Beth Dobitz ..... SD 1994
Bruce Hall ..... SD 1994
Lamar Ivey ..... AL 1994
Gordon Mau ..... IA 1994
Randy Mills ..... KS 1994
W.W. Oliver ..... VA 1994
Clint Reed ..... WY 1994
Stan Sears ..... CA 1994
Walter Carlee ..... AL 1995
Nicholas Lee Carter ..... KY 1995
Charles C. Clark, Jr. ..... VA 1995
Greg & Mary Cunningham ... WY 1995
Robert & Cindy Hine ..... SD 1995
Walter, Jr. & Evidean Major . KY 1995
Delhert Ohnemus ..... IA 1995
Henry Stone ..... CA 1995
Joe Thielen ..... KS 1995
Jack Turnell ..... WY 1995
Tom Woodard ..... TX 1995
Jerry & Linda Bailey ..... ND 1996
Kory M. Bierle ..... SD 1996
Mavis Dummermuth ..... IA 1996
Terry Stuard Forst ..... OK 1996
Don W. Freeman ..... AL 1996
Lois & Frank Herbst ..... WY 1996
Mr. & Mrs. George A. Horkan, Jr. ..... VA 1996
David Howard ..... IL 1996
Virgil & Mary Jo Huseman ... KS 1996
Q.S. Leonard ..... NC 1996
Ken & Rosemary Mitchell .... CAN ... 1996
James, Sr., Jerry, & James Petlik ..... SD 1996
Ken Risler ..... WI 1996
Merlin Anderson ..... KS 1997
Joe C. Bailey ..... NC 1997
William R. "Bill" Brockett .... VA 1997
Howard McAdams, Sr. & Howard McAdams, Jr. .. NC 1997
Rob Orchard ..... WY 1997
David Petty ..... IA 1997
Rosemary Rounds & Marc & Pam Scarborough ..... SD 1997
Morey & Pat Van Hoecke ..... MN 1997
Randy and Judy Mills ..... KS 1998
Mike & Priscille Kasten ..... MO 1998
Amana Farms, Inc. ..... IA 1998
Terry & Dianne Crisp ..... AB 1998
Jim & Carol Faulstich ..... SD 1998
James Gordon Fitzhugh ..... WY 1998
John B. Mitchell ..... VA 1998
Holzapfel Family ..... CA 1998
Mike Kitley ..... IL 1998
Wallace & Donald Schilke .... ND 1998
Doug & Ann Deane & Patricia R. Spearman ..... CO 1998
Glenn Baumann ..... ND 1999
Bill Boston ..... IL 1999
C-J-R Christensen Ranches ... WY 1999
Ken Fear, Jr. ..... WY 1999
Giles Family ..... KS 1999
Burt Guerrieri ..... CO 1999
Karlen Family ..... SD 1999
Deseret Ranches of Alberta ... CAN ... 1999
Nick & Mary Klintworth ..... ND 1999
MW Hereford Ranch ..... NE 1999
Mossy Creek Farm ..... VA 1999
Iris, Bill & Linda Lipscomb .. AL 1999
Amana Farms, Inc. ..... IA 2000
Tony Boothe ..... AL 2000
Glenn Clabaugh ..... WY 2000
Connie, John & Terri Griffith ..... KS 2000
Frank B. Labato ..... CO 2000
Rober & Sharon Lamont & Doug & Shawn Lamont . SD 2000
Bill & Claudia Tucker ..... VA 2000
Wayne & Chip Unsicker ..... IL 2000
Billy H. Bolding ..... AL 2001
Mike & Tom Endress ..... IL 2001
Henry & Hank Maxey ..... VA 2001
Paul McKie ..... KS 2001
3-R Ranch ..... CO 2002
Agri-Services Division, OklahomaDepartment of Corrections ..... OK 2002
Alpine Farms & Walter Nelson ..... VA 2002
Amana Farms ..... IA 2002
Griffith Seedstock & Griffith Family ..... KS 2002
Indian Knoll Cattle Co./ Bliler Family ..... IL 2002
Miles Land & Livestock & Price Family ..... WY 2002
Shovel Dot Ranch ..... NE 2002
Torbert Farms ..... AL 2002
White Farms ..... IA 2002
Voyles Farms ..... IN 2002
Clear Creek Cattle Company . WY 2003
Crider Salers ..... ND 2003
Mike Goldwasser ..... VA 2003
Patterson Ranch ..... CO 2003
W.S. Roberts & Sons ..... IN 2003
Shriver Farms ..... OH 2003
Stroud Farms ..... AL 2003
Tailgate Ranch Company ..... KS 2003

Commercial Producer of the Year

Chan Cooper	MT	1972
Pat Wilson	FL	1973
Lloyd Nygard	ND	1974
Gene Gates	KS	1975
Ron Blake	OR	1976
Steve & Mary Garst	IA	1977
Mose Tucker	AL	1978
Bert Hawkins	OR	1979
Jess Kilgore	MT	1980
Henry Gardiner	KS	1981
Sam Hands	KS	1982
Al Smith	VA	1983
Bob & Sharon Beck	OR	1984
Glenn Harvey	OR	1985
Charles Fariss	VA	1986
Rodney G. Oliphant	KS	1987
Gary Johnson	KS	1988
Jerry Adamson	NE	1989
Mike & Diana Hopper	OR	1990
Dave & Sandy Umbarger	OR	1991
Kopp Family	OR	1992
Jon Ferguson	KS	1993
Fran & Beth Dobitz	SD	1994
Joe & Susan Thielen	KS	1995
Virgil & Mary Jo Huseman	KS	1996
Merlin & Bonnie Anderson	KS	1997
Randy & Judy Mills	KS	1998
Mike & Priscilla Kasten	MO	1998
Giles Ranch	KS	1999
Mossy Creek Farm	VA	1999
Bill Tucker	VA	2000
Maxey Farms	TX	2001
Griffith Seedstock	KS	2002
Tailgate Ranch	KS	2003

Tailgate Ranch Receives 2003 BIF Commercial Producer of the Year Award

Tailgate Ranch is a commercial cow-calf operation consisting of about 1,500 acres of cool-season grass and legume pastures, 390 acres of brome hay meadows, and 60 acres of alfalfa. Tailgate was formed in 1962 by Paul McKie. The ranch is located at Tonganoxie, Kansas, about 30 minutes west of Kansas City.

The ranch currently consists of about 280 females, including 80 replacement heifers, in our spring-calving herd and 120 cows in the fall-calving herd. The main focus for the last seven years has been developing and breeding high-quality replacement females following a strict culling regime in order to build a superior maternal cow herd. Feedlot and carcass data have been collected to help improve feed efficiency and product quality.

Bred heifers begin calving February 10 and finish within 45 days. Heifers are synchronized and artificially inseminated (AI) once, then exposed to proven, easy-calving Angus and Red Angus bulls used for cleanup. Spring cows, consisting mostly of Red Angus or Angus crosses, calve March 1 through April 15.

Calves are vaccinated prior to weaning, then weaned September 20 and put on growing ration and pasture until steers are either sold or sent to a feedlot. Heifers continue developing on pasture for the AI breeding program. Fall-calving cows, mostly straight Angus, calve September 1 to October 15. Fall calves are generally creep-fed 60-80 days, weaned at 150 days of age, preconditioned and sold as grass cattle. Angus, Red Angus, and Red Angus x Simmental bulls are used on the spring herd. Angus, Red Angus and Braunvieh bulls are used on fall cows.

2004 BIF Commercial Producer Award Nominees

Burkhalter Cattle

Gordon & Nina Burkhalter and Patt Burkhalter, Alabama

Burkhatler Cattle is a family farm located near Clanton in the central region of Alabama. Gordon and his wife, Nina, manage an Angus and Simmental cross cow herd of 105 mature cows, 20 bred heifers, and also a herd of 20 purebred Angus cows, which are used to produce F-1 Simmental-Angus females. This operation is maintained on 500 acres, and an additional 80 acres is utilized for hay production, both for the farm and as supplemental income. The Burkhalters have operated at this location for the past 22 years and began to collect performance records in 1992. This led to a great increase in their average weaning weights from 438 lbs in 1993 to 603 lbs for the past two years.

Gordon serves as president of the Central Alabama Feeder Calf Marketing Association, where he markets his performance based feeder steers each year in August. An additional herd of 52 cows are leased to two local producers in order to produce a full 50,000 lbs truckload lot of steers each year. Replacement heifers, both open and bred, and bred cows are marketed each year in Alabama BCIA sales to increase the average value by $125 per head over market. Burkhalter Cattle is also utilizing carcass ultrasound technology to evaluate their replacement heifers for percent intramuscular fat and ribeye area, and also reproductive ultrasound to determine heifers bred in the first 60 days of the breeding season to retain in the herd as the most fertile females.

The Alabama Beef Cattle Improvement Association is proud to nominate Burkhalter Cattle.

Doler Farm

Wayne and L.W. Doler, Mississippi

Wayne Doler's grandfather moved to Calhoun County, Mississippi in 1928 bringing a cow with him. There have been cattle on the Doler Farm ever since. Along with his grandfather, Wayne's father, L.W. Doler, bought up land as it became available. The cow herd had an Angus and Hereford base up through the 1960's. In the 1970's, the Dolers increased the Charolais influence in the herd. During the 1980's, the Doler herd used Beefmaster and Simbrah bulls on the cowherd.

Adapting to changing marketing environments, the Dolers shifted the breeding composition of the herd to an Angus base in the 1990's and continue this breeding program with a 300-head cow herd today. The calving season runs from September 15 to January 15 to most efficiently utilize forage and feed resources and match production to optimal market windows. Wayne and L.W. have also cooperated with neighbors in row crop production by sharing labor resources. The Doler operation is a family business that takes pride in producing a consistent, quality product, adopting cost-effective production practices, and operating without using borrowed capital. Wayne and L.W. Doler are working towards producing a more efficient animal and better quality beef by keeping up with the latest in beef and forage production technology, addressing the needs of their customers, and continuously adapting their operation to improve profitability and sustainability.

The Mississippi Beef Cattle Improvement Association is proud to nominate Doler Farm.

LU Ranch

Mike Healy, Debbie Hammons, and Cathy Healy, Wyoming

The LU Ranch, originally known as the L.U. Sheep Company, lies between Thermopolis and Meeteetse, Wyoming. It runs from a seven inch precipitation desert just above 5,000 feet in elevation to a rugged 12 inch precipitation, mountain foothill area that ranges from 7,000 feet on the valley floors up to 8,500 feet on the valley peaks. It was incorporated in 1899 by a Scotsman named Dave Dickie. My grandfather bought controlling interest in it in the mid-1930's upon Dickie's death.

The ranch ran both sheep and Angus cattle until 1984 when the last of the sheep were sold. It was in 1996 when the decision to crossbred was made. The bull battery was changed to Saler for several years followed by gradual replacement with Angus based composite bulls. The composites have been strongly influenced by Gelbvieh and Saler and, more recently, Simmental.

The size of the operation is, of course, influenced by its low precipitation. It is nearly 150,000 acres with 80% being publicly owned. On this large expanse, we run a 1,500 head mother cow operation. That's right, 100 acres to the cow. Our calving season is broken into two time periods: February 10th through March 25th for the two-year-olds and April 1st through mid-May for the older cows.

Hay is grown on two farms. They are 160 and 240 acres in size. The fields are typically long and narrow and are flood irrigated with diverted water from the creeks they lie beside. Both farms are located at about 5,500 feet in elevation.

The Wyoming Beef Cattle Improvement Association is proud to nominate the LU Ranch.

Namminga Angus

Dennis and Maxine Namminga, Mark and Kelly Namminga, South Dakota

Namminga Angus is a diversified farming/ranching operation located in southeastern South Dakota in the

Missouri River breaks. The original farm/ranch was homesteaded in 1873. This five-generation operation has been raising Black Angus cattle, and the crops needed to supply feedstuffs, for over 100 years. Dennis and Maxine Namminga, their son, Mark, his wife, Kelly, and children, Riley and Kristen are owner/operators.

Two hundred Angus cows start calving in mid-March. Replacement heifers are synchronized, and AI'd to calve one heat cycle before the cows. Young cows are AI'd for 30 days before being turned out with clean-up bulls. Steer and heifer calves not kept as replacements are put on feed and sold on high quality, value-based marketing grids. Birth, weaning, and yearling weights are taken. Complete carcass data has been collected for ten years.

Native grass pastures (1,300 acres) provide grazing during the summer and fall, while corn stalks serve as a low cost forage source until calving in the spring. Supplementation with alfalfa hay usually starts 60 to 90 days prior to calving, depending on weather conditions. Corn, soybeans, alfalfa, tame and native grass hay are grown on 1,000 acres of both irrigated and non-irrigated farmland.

The South Dakota Cattlemen's Association is proud to nominate Namminga Angus.

Nellwood Farms

Chap and Hal Cromley, Georgia

The Cromley family came to Bulloch County, Georgia from South Carolina in the mid 1800's. Our children are the sixth generation to be raised here. Presently, row crops, cattle and timber provide a livelihood for our families. Approximately 2,000 acres are in production.

Cattle have always been a mainstay of our farm. The majority of our pastureland is land not suited for cultivation. Pasture upgrade is an ongoing process as new varieties of grass become available. Limit-grazing of winter annuals is the backbone of our winter feeding program.

Crossbreeding has always been a key to maximizing production, primarily focusing on maternal traits and growth. Angus, Gelbvieh and Hereford are the breeds used for the last ten years.

Certain disciplines are followed closely. Bulls are turned out from January until mid-March for a 75 day breeding season. Yearling bulls are bred to heifers. Replacement heifers are saved from the top producers in the herd. Replacement heifers are freeze-branded, dewormed, and vaccinated for lepto-vibro each fall before being bred in January. All calves to be sold meet the terms and conditions to be in the August sale of the Southeast GA Cattle Marketing Association. We work closely with our veterinarian and follow his recommendations.

Since 1975, females not successfully weaning a calf have been sold. This is necessary because of our need to maintain optimal stocking efficiency. Many replacement heifers are sold to neighboring producers as replacements. Production efficiency and optimal resource utilization provide the focus for our operation.

The Georgia Cattlemen's Association is proud to nominate Nellwood Farms.

Olsen Ranches, Inc.

The Arthur Olsen Family, Nebraska

The promise of plentiful land brought Lars Olsen to Banner County in the western Panhandle of Nebraska in 1885. The Olsen family has raised Hereford cattle and farmed in Banner County ever since. Four generations later, the operation Lars founded, now known as Olsen Ranches, Inc., is managed by Lars's grandson, Arthur Olsen, and his great-grandson, Douglas Olsen.

Today, the progressive Olsen operation focuses on its commercial cow-calf herd, with 750 cows comprised primarily of Hereford genetics with crossbreeding of Red Angus genetics. Located in a region that receives approximately 14" of moisture annually, Olsen Ranches has 11,000 acres of native range and 5,500 acres of tillable ground (both dryland and irrigated) on which they raise wheat, corn, alfalfa, millet, peas, barley and small grain hay. The Olsens also offer custom backgrounding and AI services for an increasing number of customers.

The Olsens are very involved in programs designed to improve Hereford genetics and grow the market for Hereford beef. The Olsens are one of the key Hereford breeders participating in the American Hereford Association's National Reference Sire Program (NRSP) and the National Cattlemen's Beef Association tenderness project, as well as in the international study sponsored by the American Hereford Association to standardize Hereford breed EPDs between the United States, Canada and Australia.

The Olsens believe in the strength of the Hereford breed and have a passion for promoting the beef industry. Most especially, the Olsens have a deep appreciation for the blessing of the rural lifestyle they enjoy and the incredible opportunity they have to be involved in this business.

The American Hereford Association is proud to nominate Olsen Ranches, Inc.

Prather Ranch (Ralphs Ranches Inc.)

Ralphs and Rickert Families, Jim and Mary Rickert, California

The 15,000 acre Prather Ranch is a vertically integrated cattle business that operates in four far northern California counties. The ranch was founded in the 1870's and was acquired by Walter Ralphs (former president of Ralphs Supermarket) in 1964.

The ranch operates a "closed herd" of 1,350 English crossbred cows. The cow herd is about 20% straight Angus and 20% straight Hereford with approximately 60% of the

herd black baldy cows. The cows are run with 60% spring calving near Macdoel, California, in our "natural beef" program. The remaining 40% are fall calvers and are "certified organic". The organic herd is maintained separately, summering in the Fall River Valley of northeastern California and winters in the northern Sacramento Valley. This facilitates the unique marketing programs that the Prather Ranch has established.

This "closed herd" concept is based on the need to maximize biosecurity. Prather Ranch supplies bovine raw materials to various pharmaceutical companies and as a requirement, extensive record-keeping and Standard Operating Procedures are in place. On the female side, the herd was closed in 1975. Since 1990, the herd has been bred by artificial insemination or ranch raised pick-up bulls. The ranch has implemented and participates in a young sire progeny testing program, known as Gen-Scan, by working with purebred breeders and the American Hereford and American Angus Associations.

In 1996, the ranch built a USDA inspected on-site slaughter house and meat processing facility. The ranch direct markets both natural and organic dry-aged beef in southern Oregon and northern California.

The University of California – Agriculture and Natural Resources Cooperative Extension, Siskiyou County, California, is proud to nominate Prather Ranch.

Blair Porteus and Sons

Blair, Brent and Knox Proteus, Ohio

The farm is located four miles south of Coshocton, Ohio, on State Route 83 in the rolling hills of East Central Ohio. Currently, there are three generations of our family working this diversified beef, grain and forage operation. Blair Porteus, the eldest generation, started his cow herd at the present location in 1941. His two sons, Brent and Knox, both returned to the family farm upon graduation from college in the last 1970s and early 1980s, and are now being joined by Brent's daughters, Amy and Beth.

The cows are an Angus based commercial herd of approximately 245 head that is rotationally grazed on 450 acres of managed pasture. In addition to the cattle, corn and soybeans are grown on 1,100 acres of river bottom and sloping ground located between the rolling pasture lands and there is another 200 acres in alfalfa hay raised on the farm.

Our goal is to position the beef enterprise to provide a significant positive net return to the farm by utilizing forage resources to their maximum advantage. In order to accomplish that goal, we expect to wean a calf from each cow exposed during the breeding season that will go on to produce a carcass that can be marketed on a high quality grade based grid.

In 1973, we built a slated floor 200 head feedlot barn on the arm. The heifers not chosen as replacements and all steer calves are fed on a corn silage and high moisture corn based ration on the farm until harvest. Over the years, most of the cattle produced on the farm have been sold to Moyer Packing and Taylor Packing, targeting a high quality end product.

The Ohio Cattlemen's Association is proud to nominate Blair Porteus and Sons.

Rx Ranch

Dr. Larry & Kristy Letner, Missouri

Rx Ranch is a 1,400 head commercial cow/calf operation located in north central Missouri. The Ranch has been in operation since 1983 with the focus on a common sense approach to utilizing grazing practices, and applying scientific knowledge to herd health. Rx Ranch is owned and operated by Dr. Larry Letner, his wife Kristy, and their children, Lindsay, Will and Jake.

As a veterinarian, the importance of herd health, quality assurance and management practices are not just something that is discussed with clients, but put into practice on Rx Ranch. The base cow herd is predominately black/black white face western origin cows with a spring calving season only. The cattle are utilized as a field trial herd for the practices that are advocated through the veterinary clinic. By "practicing what you preach" the cattle and general practices speak for themselves and the return customers and data provide the statistical information.

The use of Weink registered Charolais bulls has brought the genetic predictability to the commercial cow. These bulls have been able to provide uniformity and a performance in both the weaned calf and yearling product. A terminal cross operation, Rx Ranch is concerned with the ability for that calf to be a profitable quality product for both producer and consumer.

This strictly grazing operation with no creep feeding utilizes the concept that the cows and bulls have to do their own work. The cow has to take care of herself and take care of her calf and the bull has to be able to maintain condition and breeding with grazing only. The Weink Charolais bull has been instrumental in this concept. These bulls have the ability to maintain their soundness, condition, and breeding ability with grazing only. These bulls are selected with high maternal EPD scores that correlate directly to easy fleshing.

The American International Charolais Association is proud to nominate Rx Ranch.

Schuette Farms

Cliff Schuette, Illinois

Schuette Farms is a family operation consisting of approximately 767 acres of row crops and 200 acres of permanent pasture. Cliff Schuette took over the family farm in 1996 and began immediately to transform the cash grain farm to a year round commercial beef operation.

Cliff, his wife Christy, son, Evan, and stepson, Andy, run the family farm operation. Converting marginal cropland into pastures with a rotational grazing program has expanded the beef cattle operation. High tensile fence has been installed, along with permanent water systems in most pastures. This includes some new Max Q fescue to improve pasture quality and animal performance.

The Schuette farm consists of a 150 cow/calf operation with both a spring and fall calving herd. Both cow herds are on a year round management grazing program. Both herds are on a 60 day calving season. In drought years, an early weaning program is used to help reduce feed costs and stress on cows. An early weaning program is used for all steer calves, and 25% of the bottom heifers in the herd. Calves are weaned between 45 and 60 days of age, and weigh between 180 and 400 pounds. All first calf heifers are early weaned so they will breed back in 60 days and continue to develop normal growth. A cross breeding program consists of Angus and Simmental.

All steer calves and bottom 25% of the herd calf crop are fed out on the farm and marketed through six local grocery chains. Carcass data is obtained on all calves.

The Illinois Beef Association is proud to nominate Schuette Farms

Valdez Ranches

Virgil A. and Eleanor Valdez, Colorado

Our operation is located in the San Luis Valley, La Jara, Colorado. In 1958, I was attending Adams State College and with one semester left, the sudden death of my Father required me to quit school and take are of the farm and ranch operation.

In 1960 we were married. Our ranch only had 50 cows and were summered on the Ranch. In 1962 to 1965, we built our herd to 320 head. Now we summer all our cattle in New Mexico on the Carson National Forest. We graze fall and part of the winter and spring on the B.L.M. We calve here at the ranch and go back on B.L.M. and National Forest Land. Due to the drought this year, we have no B.L.M. fall pasture and decided to rent pasture in La Junta, Colorado. The cattle will be there from October 25, 2003 to June 6, 2004.

We started with Herefords in 1960. In 1963, we bought Limousin mixed with Herefords. We have worked on our cattle herd to get a good weaning weight of about 600#. Today, we have grown from 520# steers to 620#. The breed today is Red Angus, Black Angus, Limousin and Gelbvieh. Our bulls come from Vonforell Ranch in Wheatland, Wyoming. Other breeders are Seedstock Plus and Hunt Limousin Ranch in Elizabeth, Colorado.

One of our major projects as stewards of the land was to install four and a half miles of pipe line to water the cattle on the B.L.M. This has proved to be a big asset to our operation.

San Luis Valley Cattlemen's Association is proud to nominate Valdez Ranches.

Wickstrum Farms, Inc.

Larry and Sharon Wickstrum, Kansas

Since 1934, the Wickstrum family has raised cattle and farmed on the northern edge of the Kansas Flint Hills near Manhattan. Operating with Larry's father and brother through the 1970's, the operation has evolved into a diversified cow-calf, cattle feeding, farming and custom harvesting business. In 1987, Larry and Sharon Wickstrum formed Wickstrum Farms, Inc., the family-owned corporation that exists today. Sons, Todd, an engineer in Texas, and Troy, an accountant in Manhattan, assist in management decisions, whether it be cattle, machinery or land issues. In the last 25 years, the operation has expanded to include native grass and tillable land, both owned and leased. Ninety percent of this land is native and brome grass, with the remainder in tillable land. The recent acquisition of a ranch some 125 miles south of the headquarters operation will allow the Wickstrums to diversify their grazing opportunities. The location of this ranch allows access to earlier season grasses, plus the ability to better manage against late summer drought.

With 1,200 straight Angus cows, the Wickstrums calve about 250-270 heifers each year in calving facilities beginning in late January. Heifers are artificially inseminated (AI) to low-birth-weight Angus sires. All females are left to graze pastures or stockfields until early December. If snow cover develops, supplemental feed of wheat midds and hay is fed.

Calves are weaned in September with steers being placed on rations of corn, wheat midds, corn gluten, alfalfa, mixed hays and silage. Being only six months of age, these calves are progressed through a series of rations to allow them to grow. The calves are marketed in April or May on a quality grid.

Heifers are sorted with the top end being kept for replacements, the second group sold to repeat buyers for herd development, and the third group fed in their feedlot. They are fed a slightly higher roughage ration to attain growth with less fat retention. Other feeder calves are wintered and finished in the feedlot and purchased from ranchers or cattle auctions.

The diversified farming operation complements the cattle production. Grain and hay produced on the farm are fed through the family's feedlot, which markets approximately 2,800 head annually, or used to supplement the cowherd. In addition, the family operates a custom harvesting business. Beginning in June, the Wickstrums, plus a crew of four or five South African employees, travel through Oklahoma, Kansas and Colorado harvesting wheat. They make the loop again in the fall to harvest silage, returning home in October to harvest fall crops and prepare for fall calving.

Although they operate a very diversified agricultural operation, the Wickstrums' main goal is to develop high-quality Angus cattle for today's selective consumer, while maintaining a profitable business.

The Kansas Livestock Association is proud to nominate Wickstrum Farms, Inc.

Ambassador Award Recipients

Warren Kester	Beef Magazine	MN	1986
Chester Peterson	Simmental Shield	KS	1987
Fred Knop	Drovers Journal	KS	1988
Forrest Bassford	Western Livestock Journal	CO	1989
Robert C. DeBaca	The Ideal Beef Memo	IA	1990
Dick Crow	Western Livestock Journal	CO	1991
J. T. "Johnny" Jenkins	Livestock Breeder Journal	GA	1993
Hayes Walker, III	America's Beef Cattleman	KS	1994
Nita Effertz	Beef Today	ID	1995
Ed Bible	Hereford World	MO	1996
Bill Miller	Beef Today	KS	1997
Keith Evans	American Angus Association	MO	1998
Shauna Rose Hermel	Angus Journal & Beef Magazine	MO	1999
Wes Ishmael	Clear Point Communications	TX	2000
Greg Hendersen	Drovers	KS	2001
Joe Roybal	Beef Magazine	MN	2002
Troy Marshall	Seedstock Digest	CO	2003

2003 BIF Beef Ambassador Award

Marshall Named BIF Ambassador

The Beef Improvement Federation (BIF) honored Troy Marshall with the Ambassador Award at the 35th Annual Meeting and Research Symposium in Lexington, Kentucky, on May 30, 2003. The prestigious honor is given to a member of the media each year for their efforts in helping cattle producers understand cattle performance testing and genetic prediction tools.

Troy grew up in Wheatland, Wyoming, and obtained an Equine Science/Animal Science degree from Colorado State University where he competed on both the livestock and World Champion Horse Judging teams. Following college, he worked as a Market Analyst for Cattle-Fax covering different regions of the country.

Troy also worked as Director of Commercial Marketing for two breed associations. These positions were some of the first to provide direct links tying breed associations to the commercial cow-calf industry.

Troy's idea for *The Seedstock Digest* started when he was working towards a Master's degree in the Beef Industry Leadership Program at Colorado State University. Troy published his first issue of *The Seedstock Digest* in July 2000. Troy is a visionary with a great grasp for all segments of the industry. He used this background and recognized a need for a "no nonsense" publication to provide cattle producers with key information in a concise and accurate format. He also saw the need for a publication that took a more in-depth look at key issues written by someone who truly understands the economics and challenges of the different industry segments in a factual, unbiased manner.

Troy has served as an editor for the weekly e-mail newsletter "The Cow/Calf Weekly" published by *BEEF* magazine, another highly respected industry publication. His writing has gained great respect, with articles reprinted in over 20 different publications. Several breed associations for whom he serves on a consulting basis have utilized his insight and expertise.

Troy takes science-based beef cattle materials and transfers this technology to producers. BIF is proud to have a strong friend and leader in their mix, as is Troy Marshall.

Nevertheless, Troy considers himself a beef producer first and foremost. That is what makes his perspective so unique. He runs an Angus and hybrid seedstock operation with his wife, Lorna, in Burlington, Colorado, along with their children, Wyatt, 6, Justis, 4, and Wynn, 3.

Pioneer Award Recipients

Jay L. Lush	IA	1973
John H. Knox	NM	1974
Ray Woodward	ABS	1974
Fred Wilson	MT	1974
Charles E. Bell, Jr.	USDA	1974
Reuben Albaugh	CA	1974
Paul Pattengale	CO	1974
Glenn Butts	PRT	1975
Keith Gregory	MARC	1975
Braford Knapp, Jr.	USDA	1975
Forrest Bassford	WIJ	1976
Doyl Chambers	LA	1976
Mrs. Waldo Emerson Forbes	WY	1976
C. Curtis Mast	VA	1976
Dr. H. H. Stonaker	CO	1977
Ralph Bogart	OR	1977
Henry Holsman	SD	1977
Marvin Koger	FL	1977
John Lasley	FL	1977
W. L. McCormick	GA	1977
Paul Orcutt	MT	1977
J. P. Smith	PRT	1977
James B. Lingle	WYE	1978
R. Henry Mathiessen	VA	1978
Bob Priode	VA	1978
Robert Koch	MARC	1979
Mr. & Mrs. Carl Roubicek	AZ	1979
Joseph J. Urick	USDA	1979
Bryon L. Southwell	GA	1980
Richard T. "Scotty" Clark	USDA	1980
F. R. "Ferry" Carpenter	CO	1981
Clyde Reed	OK	1981
Milton England	TX	1981
L. A. Moddox	TX	1981
Charles Pratt	OK	1981
Otha Grimes	OK	1981
Mr. & Mrs. Percy Powers	TX	1982
Gordon Dickerson	NE	1982
Jim Elings	CA	1983
Jim Sanders	NV	1983
Ben Kettle	CO	1983
Carroll O. Schoonover	WY	1983
W. Dean Frischknecht	OR	1983
Bill Graham	GA	1984
Max Hammond	FL	1984
Thomas J. Marlowe	VA	1984
Mick Crandell	SD	1985
Mel Kirkiede	ND	1985
Charles R. Henderson	NY	1986
Everett J. Warwick	USDA	1986
Glenn Burrows	NM	1987
Carlton Corbin	OK	1987
Murray Corbin	OK	1987
Max Deets	KS	1987
George F. & Mattie Ellis	NM	1988
A. F. "Frankie" Flint	NM	1988
Christian A. Dinkle	SD	1988
Roy Beeby	OK	1989
Will Butts	TN	1989
John W. Massey	MO	1989
Donn & Sylvia Mitchell	CAN	1990
Hoon Song	CAN	1990
Jim Wilton	CAN	1990
Bill Long	TX	1991
Bill Turner	TX	1991
Frank Baker	AR	1992
Ron Baker	OR	1992
Bill Borror	CA	1992
Walter Rowden	AR	1992
James W. "Pete" Patterson	ND	1993
Hayes Gregory	NC	1993
James D. Bennett	VA	1993
O'Dell G. Daniel	GA	1993
M. K. "Curly" Cook	GA	1993
Dixon Hubbard	USDA	1993
Richard Willham	IA	1993
Dr. Robert C. DeBaca	IA	1994
Tom Chrystal	IA	1994
Roy A. Wallace	OH	1994
James S. Brinks	CO	1995
Robert E. Taylor	CO	1995
A. L. "Ike" Eller	VA	1996
Glynn Debter	AL	1996
Larry V. Cundiff	NE	1997
Henry Gardiner	KS	1997
Jim Leachman	MT	1997
John Crouch	MO	1998
Bob Dickinson	KS	1998
Douglas MacKenzie Fraser	AB	1998
Joseph Graham	VA	1999
John Pollak	NY	1999
Richard Quaas	NY	1999
Robert R. Schalles	KS	2000
J. David Nichols	IA	2000
Harlan Ritchie	MI	2000
Larry Benyshek	GA	2001
Minnie Lou Bradley	TX	2001
Tom Cartwright	TX	2001
H. H. "Hop" Dickenson	MO	2002
Martin & Mary Jorgensen	SD	2002
L. Dale Van Vleck	NE	2002
H.H. "Hop" Dickenson	MO	2003
Martin and Mary Jorgenson	SD	2003
L. Dale Van Vleck	NE	2003

2003 BIF Pioneer Awards

George Chiga Receives BIF Pioneer Award

The Beef Improvement Federation (BIF) honored George Chiga with the Pioneer Award at the 35th Annual Meeting and Research Symposium in Lexington, Kentucky, on May 30, 2003. The award recognizes individuals who have made lasting contributions to the improvement of beef cattle.

George C. Chiga of Tulsa, Oklahoma, was selected to receive the Beef Improvement Federation Pioneer Award. George represents a true American success story, and embodies one of the true pioneers in our industry's performance movement.

George's parents emigrated from Hungary to Saskatchewan, Canada where George was born in 1913. George grew up on the family homestead, but to ease the financial burden on the family, he left home at an early age to make a living on his own as best he could. His many jobs included cleaning bricks piecemeal, cutting ice, working on the highway, cooking in mining camps, and serving as a bouncer.

While working in Flin Flon, Manitoba during the height of the depression, George developed an interest in boxing and wrestling; an interest that would lead to higher education and new opportunities. George represented Canada as a heavyweight wrestler in the 1936 Olympics hosted in Germany where his talents were recognized and he was offered a spot on the Oklahoma State University wrestling team.

Although economics had prohibited George from completing the tenth grade, he attended Oklahoma State University where he played football and wrestled, and was honored as a Phi Kappa Phi student. During this time George met Vernice, who would become his wife, business partner and office manager in the years to come. He graduated with a degree in Animal Science with a deep interest in genetics and animal breeding. Enrolling in graduate school for a Master's degree he completed his thesis project on the inbreeding and outbreeding of swine. From this work George became a disciple of line and inbreeding which characterized his breeding philosophy throughout his career.

To gain U.S. citizenship, George volunteered for the service during World War II. After the war he returned to Oklahoma and taught Agriculture at Guthrie, Oklahoma, to World War II veterans under the G.I. Bill of Rights. During this time, George enrolled at the Oklahoma City Law School, passed the bar and began to practice law throughout his professional lifetime.

Both George and Vernice dreamed of owning cows, and in 1949 they selected Red Angus in which to invest because: 1) Angus was an already established breed with known strengths and weakness; and 2) he could afford the red cattle since they were barred from registry at the American Angus Association. By 1954, they had collected 17 cows, and from this humble beginning, George's operation grew to the point that he controlled the marketing and breeding of over 1,000 cows. Many people believe this was the first use of cooperators, as we know it today.

The Red Angus Association of America's formation meeting was held in 1954. At the meeting, George and Waldo Forbes worked for three days and nights to develop the rules and regulations that would result in the industry's first breed performance program. Other innovations included mandatory reporting of weaning weights, the first to collect yearling weights, open A.I., and barring of nurse cows. At this meeting Waldo was elected President and George Vice President. George assumed the Presidency in 1956 upon the untimely death of Waldo and served in this position until 1960.

George explained, "The establishment of Red Angus was more than an accumulation of numbers. It was dreaming about a new approach – performance testing was a part of Red Angus from its inception." To put this in perspective, "The first Red Angus registry certificate had a place on it for recording adjusted weaning weights – a full two years before PRI (Performance Registry International) was organized and adopted the 205 day adjustments used today." Wasting no time, Red Angus adopted the 205 day standard one week after the PRI meeting. George explained, "Progressiveness was the key character of the Red Angus breed... This initial progressive spirit has survived and expanded."

George's impact on Red Angus and the early performance movement are incalculable. In the Red Angus breed, 95 percent of today's cattle descend from George's "Chiefline" breeding. Above all George is an individualist who stuck with, promoted and expanded the use of performance testing during the time when people looked upon them as "just a bunch of harmless screwballs."

Perhaps George's life is best summed up by Robert de Baca's book Courageous Cattlemen when he explained, "Chiga is an entrepreneur. He capitalized on his opportunities. He rose above the limitations that were his given the economics of the times and family means into which he was born. He succeeded while doing the things at which others were failing. He knew how to be a friend. And he believes strongly in society's giving a helping hand to other survivors who have a right and a desire to share in the American dream."

Burke Healey (1932-2002) Receives BIF Pioneer Award

The Beef Improvement Federation (BIF) posthumously honored Burke Healey as a recipient of the Pioneer Award at the 35th Annual Convention in Lexington, Kentucky, on May 30, 2003. The award recognizes individuals who have made lasting contributions to the improvement of beef cattle.

Burke Healey's name has always been synonymous with being a leader, a visionary, and an advocate of the beef industry. Burke possessed a great dedication to cattle production and he pursued the success of the industry as well as the success of his own herd with a passion.

Burke was a cattle producer with his wife, Tina, and five children at the Southern Cross Ranch in Davis, Oklahoma. The original ranch, the Flying L, was co-owned with his brother Skip until 1988. After 1988, the ranch was divided into two ranches, the Flying L and Southern Cross. The Southern Cross is a 3,500-acre Hereford cattle operation appropriately called "Hereford Heaven" near the Arbuckle mountains. The Healey's operation is regarded as one of the premier Hereford herds in North America and a cornerstone for performance programs with beef cattle.

Early in life, Burke attended Duke University to study business, and he later completed his education at Oklahoma State University with a degree in Animal Husbandry in 1955. Burke has been recognized on several occasions for his contributions to Oklahoma State University, and he was honored as an OSU Graduate of Distinction in 1980. Burke was a member of the Oklahoma State University Board of Regents from 1963 to 1975, serving as chairman for four years. In 2001, he was recognized by Oklahoma State University as the Distinguished Agriculture Alumnus.

Burke was a respected member of the beef industry and he served the industry well at local, state, and national levels. Burke once said "the most effective way to cope with change was to help create it". As leaders in the industry, Burke Healey and his family were active members of many organizations such as Oklahoma Beef Cattle Improvement Association, Oklahoma Beef Incorporated, American Hereford Association, and National Cattlemen's Beef Association. He actively participated in several committees for the National Cattlemen's Beef Association, Cattlemen's Beef Promotion and Research Board, Beef Industry Council, American Hereford Association, and numerous others. He has been an integral part of the Beef Improvement Federation's evolution in multiple roles with the most distinguished as President in 1996 to 1997.

As a leader in the performance movement, Burke made many contributions especially in the area of linear measurements and adoption of frame scores. Burke was quoted as saying, "From the first day we started our operation, our goal was not to be breed multipliers, but rather breed improvers". Burke always maintained a strong presence in the performance movement ranging from recording weights to gene mapping.

The contributions made by Burke and the Healey family have been recognized in many ways. Bob deBaca's book, "Courageous Cattlemen," has recognized Burke Healey as one of 50 cattlemen and researchers who most influenced the performance movement in U.S. beef production. In 1994, Burke was named the Trailblazer of the year by *BEEF* Magazine. The Beef Improvement Federation honored Burke in 1998 with the Continuing Service award. H.H. Hop Dickenson, former Executive Vice President of the American Hereford Association said, "Burke Healey has not only been a performance advocate, but made it a policy to understand what each step of research application meant. He is essentially a combination of cattlemen and a scientist. And he has a grasp of worldwide research on a new technology before he puts it into place in their operation."

Burke Healey passed away on October 14, 2002 at his home in Davis, Oklahoma.

Keith Zoellner Receives BIF Pioneer Award

The Beef Improvement Federation (BIF) honored Dr. Keith Zoellner with the Pioneer Award at the 35th Annual Meeting and Research Symposium in Lexington, Kentucky on May 30, 2003. The award recognizes individuals who have made lasting contributions to the improvement of beef cattle.

Dr. Keith Zoellner was born in Groton, South Dakota, where he grew up on a purebred Angus and crop farm. He was married in 1958 to Arlys Johnson and they have a daughter, Dr. Lori Zoellner, who is on the faculty at the University of Washington.

Dr. Keith Zoellner received a B.S. in Animal Husbandry from South Dakota State University in 1953. After spending two years in the U.S. Army Veterinary Corps, he entered graduate school at South Dakota State University where he earned a M.S. in Animal Breeding in 1957. Dr. Zoellner then joined the Animal Husbandry Extension Staff at the University of Nebraska. He left in 1959 to pursue a Ph.D. in Animal Breeding from the University of Missouri, where he graduated in 1962. Dr. Zoellner then joined the Animal Husbandry Extension Department at Kansas State University.

During his 34 years of service to the Animal Sciences and Industry Department at Kansas State University, Dr. Zoellner was an innovator and educator who brought many significant contributions and changes to the beef cattle industry. New statewide educational programs for beef cattle breeding and management as related to reproduction, performance testing, growth and profitability, with emphasis on both purebred and commercial cowherds were organized and held under Dr. Zoellner's outstanding leadership.

Dr. Zoellner was instrumental in establishing and leading the first Kansas Bull Test. It proved so successful that a second Bull Test was established to serve another geographical area of the state. These bull tests served as models to other states in setting up their programs. Pioneering the way, several Steer Futurities, Purebred Seminars, and for the first time a 4-H State Beef Conference were held. New influential programs were set-up for on-farm performance testing, sire selection and evaluation, cowherd conditions, crossbreeding programs, parasite control, and up-to-date cattle management technologies.

Dr. Zoellner is a consultant to Perkins Blue Sky Farms, a purebred operation, staring in 1974. He also worked with the Calvey Ranches in Nicaragua in 1984 with their purebred operation. He did consulting for the Missouri Coordinating Board for Higher Education and the American Hereford Association Genetic Review Committee. He served on the Farmers Hybrid Cattle Breeding Muskogee, Oklahoma, review committee. He served on the screening committee for the Northeast Kansas Hereford Association for many years.

Dr. Zoellner was the Kansas representative to the Beef Improvement Federation from its beginning until his retirement. He served as Chairman of the BIF Bull Test Committee and was the author of the BIF Feeder Calf Performance Program. He served on many committees including the Show and Exhibits Committee, Carcass Data Committee, Growth and Efficiency Committee, Annual Meeting Committee, Awards Committee, Central Test Committee, plus several others. Dr. Zoellner has authored many publications and papers.

Upon Dr. Zoellner's retirement in 1996, a plaque was given to him by the Kansas Bull Test which read as follows: "In special recognition of Keith Zoellner who devoted outstanding service, dedication, and foresight to the Kansas Bull Test Program for improvement of the beef industry." Dr. Zoellner is now Professor Emeritus at Kansas State University.

Continuing Service Award Recipients

Clarence Burch	OK	1972
F. R. Carpenter	CO	1973
E. J. Warwick	DC	1973
Robert DeBaca	IA	1973
Frank H. Baker	OK	1974
D. D. Bennett	OR	1974
Richard Willham	IA	1974
Larry V. Cundiff	NE	1975
Dixon D. Hubbard	DC	1975
J. David Nichols	IA	1975
A. L. Eller, Jr.	VA	1976
Ray Meyer	SD	1976
Don Vaniman	MT	1977
Lloyd Schmitt	MT	1977
Martin Jorgensen	SD	1978
James S. Brinks	CO	1978
Paul D. Miller	WI	1978
C. K. Allen	MO	1979
William Durfey	NAAB	1979
Glenn Butts	PRI	1980
Jim Gosey	NE	1980
Mark Keffeler	SD	1981
J. D. Mankin	ID	1982
Art Linton	MT	1983
James Bennett	VA	1984
M. K. Cook	GA	1984
Craig Ludwig	MO	1984
Jim Glenn	IBIA	1985
Dick Spader	MO	1985
Roy Wallace	OH	1985
Larry Benyshek	GA	1986
Ken W. Ellis	CA	1986
Earl Peterson	MT	1986
Bill Borror	CA	1987
Daryl Strohbehn	IA	1987
Jim Gibb	MO	1987
Bruce Howard	CAN	1988
Roger McCraw	NC	1989
Robert Dickinson	KS	1990
John Crouch	MO	1991
Jack Chase	WY	1992
Leonard Wulf	MN	1992
Henry W. Webster	SC	1993
Robert McGuire	AL	1993
Charles McPeake	GA	1993
Bruce E. Cunningham	MT	1994
Loren Jackson	TX	1994
Marvin D. Nichols	IA	1994
Steve Radakovich	IA	1994
Dr. Doyle Wilson	IA	1994
Paul Bennett	VA	1995
Pat Goggins	MT	1995
Brian Pogue	CAN	1995
Harlan D. Ritchie	MI	1996
Doug L. Hixon	WY	1996
Glenn Brinkman	TX	1997
Russell Danielson	ND	1997
Gene Rouse	IA	1997
Keith Bertrand	GA	1998
Richard Gilbert	TX	1998
Burke Healey	OK	1998
Bruce Golden	CO	1999
John Hough	GA	1999
Gary Johnson	KS	1999
Norman Vincil	VA	1999
Ron Bolze	KS	2000
Jed Dillard	FL	2000
William Altenburg	CO	2001
Kent Andersen	CO	2001
Don Boggs	SD	2001
S. R. Evans, Jr.	MS	2002
Galen Fink	KS	2002
Bill Hohenboken	VA	2002
Dr. Connee Quinn	NE	2003
Dr. Ronnie Silcox	GA	2003
Ronnie Green	MD	2003
Sherry Doubet	CO	2003

2003 Continuing Service Awards

Sherry Doubet
Receives BIF Continuing Service Award

Sherry Doubet was raised on a diversified ranching operation in Lodgegrass, Montana, where her family, Jim and Mary Brown raise 1250 head of beef cows, including purebred Salers, Hereford and South Devons along with a large commercial herd. The family also farms a large wheat acreage in addition to alfalfa. Growing up she was active in 4-H and the American Junior Hereford Association. She was elected to the American Junior Hereford Association Board of Directors in 1985 and was elected as Secretary in 1986 and went on to serve as President in 1987. While on the board, Sherry helped organize the Australian Junior Hereford Exchange.

Sherry attended Colorado State University where she was an active member of Block and Bridle, Alpha Zeta and the CSU Livestock Judging Team. She received her Bachelor of Science degree from CSU in 1988. After a 6-month tour of Australia as a participant in the Junior Hereford Exchange, she began working for the American Salers Association in 1989 as the Director of Communications. She served in that capacity for 4 1/2 years before taking over as the Director of Advertising and Registrations in 1994. Sherry became the American Salers Association Executive Vice President in 1996 and has been in this capacity for the last 7 years. During her time at the Salers association, she has seen the implementation of EPDs for carcass traits, scrotal circumference, and the traits of docility and stayability and she continues to stress the importance of performance measurements in beef production.

Sherry has served on various committees in the National Cattlemen's Beef Association. She served as a BIF board member for 2 terms. She is currently the International Salers Federation secretary and is President of the US Beef Breeds Council.

Sherry is also kept busy, along with her husband Jim, raising three young boys, Curtis (11), Cody (9) and Justin (3). She enjoys her time back on the family ranch whenever time allows. She counts the annual trek to artificially inseminate heifers each year as a highlight where the implementation of performance records and EPDs play a key role in sire selection. As a member of the Brown family, Sherry enjoys the distinction of being part of the longest continuous participating family in one of the most successful performance bull tests in North America, Midland Bull Test, having participated since 1966.

Ronnie Green
Receives BIF Continuing Service Award

The Beef Improvement Federation (BIF) honored Dr. Ronnie Green with the continuing Service Award at the 35th Annual Meeting and Research Symposium in Lexington, Kentucky on May 30, 2003.

Ronnie Green grew up raising Angus and crossbred cattle with his family on their farm near Fincastle, Virginia. There he developed passions for learning, hard work, persistence and continuous improvement. His service to others started at an early age with his leadership and involvement in 4-H & FFA. He received his degrees from Virginia Tech, Colorado State & The University of Nebraska. He and Jane, his loving wife of 17 years, are blessed with 4 wonderful children.

The influence of his major professor, Dr. Gordon Dickerson who was honored at BIF last year, had a lasting impact on Ronnie's life. Ronnie has that same passion for teaching and doing work that is practical and applicable to the industry. Ronnie also has tremendous dedication to his family and his Christian faith, continuously, yet lovingly encouraging those around him to enjoy the same. He has helped lay a strong foundation in the lives of so many students and friends. Ronnie has been and continues to be a man of strong character who is not afraid to ask the tough questions, or go against the mainstream crowd in order to do what is right.

Ronnie served as a professor of animal breeding and genetics at Texas Tech University for 7 years and performed some of the early work in developing carcass EPDs from Ultrasound data. He also helped develop the genetic plan for the Hotlander composite line of cattle. He then served 4 years as a professor and scientist at Colorado State University. There he became a leader in DNA research and technology for beef cattle, striving to bring industry application to a very complex science. While in academia Ronnie received numerous awards for his research, teaching, advising and service, while publishing 210 professional referred journals, abstracts and technical reports. He also served as advisor to numerous university organizations, National President of Block & Bridle and instigated the Collegiate Livestock Leaders Institute.

Following his passion of bringing industry application to science and technology, Ronnie left the University system to join the staff of Future Beef Operations where he served as Director of Genetics and later as Vice President of Cattle Operations. As a man of integrity, Ronnie was selected and served as the man to close down the struggling company, maintaining his commitment to his employees, co-workers and all involved, until the very end. Currently Ronnie serves as the National Program Leader of Food Animal Production

for the Agriculture Research Service, United States Department of Agriculture.

Ronnie continuously serves the beef industry on numerous committees for BIF, NCBA, ASAS, ARS and has been a featured speaker at more than 120 major livestock functions in the past 10 years. He has served on the BIF Board of Directors since 1995 and has been a speaker on the program numerous times. Continuing service in all aspects of life truly describes our friend, Ronnie Green. BIF is pleased and honored to recognize Ronnie Green's continuous contributions to the beef industry by presenting him with the BIF Continuing Service Award.

Connee Quinn Receives BIF Continuing Service Award

The Beef Improvement Federation (BIF) honored Dr. Connee Quinn with the Continuing Service Award at the 35th Annual Meeting and Research Symposium in Lexington, Kentucky, on May 30, 2003.

Connee Quinn has a lifelong involvement in and passion for ranching and the beef cattle business. Raised on a ranch near Chadron, Nebraska, Connee and husband Reuben, currently operate Quinn Cow Company along with niece Wendy and her husband, Tony George. The Quinn ranch is a commercial cow-calf enterprise utilizing mostly leased land on the Pine Ridge Indian Reservation in southwestern South Dakota. Connee received her B.S. and M.S. degrees from Chadron State College in science education. After teaching high school science for four years, she earned a PhD in animal science from Colorado State University, specializing in animal nutrition. Connee taught vocational agriculture in Mission, South Dakota, and developed an award winning high school curriculum on native range grasses as recognized by the Soil Conservation Service.

Since receiving her Ph.D., Connee has been employed by Elanco Animal Health as a sales representative working in western South Dakota, northeastern Wyoming and the Nebraska Panhandle. On behalf of Elanco, Connee calls on cow-calf producers and feedlot operators in the area.

The Quinn's have been recognized as the South Dakota Commercial Producers of the Year by the South Dakota Beef Improvement Council and were nominated for the BIF Commercial Producer of the Year in 1990. Connee received a prestigious award from the University of Nebraska for Outstanding Contributions to Agriculture in Western Nebraska also in 1990. In 1991 she was awarded one of the five "Prime Promoter" awards from the South Dakota Beef Industry Council for her outstanding educational efforts on behalf of ranchers and feedlot operators. Connee serves as chairman of the NCBA's IRM Calf Information Task Force. This task force has the charge to determine what information is important to the cow/calf producers customer and how that information can be most efficiently transferred. She also served on the NCBA's Industry Planning Group. She is currently involved is several Integrated Resource Management (IRM) committees at both the state and national level as well as serving on the IRM Advisory Board. Connee is immediate past-president of the Beef Improvement Federation (BIF) and served three years on the BIF board.

Connee has made numerous high-energy, challenging presentations to rancher, feedlot, veterinary and other beef industry groups. Her passion for the practical side of ranching and appreciation of the science of the beef business give Connee a unique credability that few can match. Connee Quinn's tireless travels and efforts on behalf of the beef industry are truly commendable. Her continuing sevice on behalf of the beef industry is truly a labor of love.

Ronnie Silcox Receives BIF Continuing Service Award

The Beef Improvement Federation (BIF) honored Dr. Ronnie Silcox with the Continuing Service Award at the 35th Annual Meeting and Research Symposium in Lexington, Kentucky, on May 30, 2003.

Dr. Silcox was born in 1955 in Goodway, Alabama, and grew up on a cotton, soybean, and cattle farm. He received his B.S. in Agricultural Education (1977) and M.S. in Animal Science from Auburn University (1980). After completing his Ph.D. at Iowa State University in 1985, he accepted the position of Extension Beef Cattle Specialist at The University of Georgia.

During his extension efforts at The University of Georgia, Dr. Silcox coordinates the junior livestock program in the Animal Science Department, develops adult outreach programs in beef cattle genetics, and coordinates the State Beef Quality Assurance program. His current appointment is 80% Extension, and 20% Teaching, which includes teaching Beef Cattle Production and faculty advisement to the UGA Block & Bridle Club and the UGA Cattlemen's Association. Silcox has been a national leader and contributor to National 4-H Livestock Contest Committees. He was recognized in 1997 by the National Association of County Agricultural Agents with the highly respected Distinguished Service Award. In 2001, he received the Outstanding Extension Faculty Award from The University of Georgia Gamma Sigma Delta Society.

Dr. Silcox has provided unending service to BIF throughout his career. His assignments included coordinating the Central Test Committee (secretary, 1986-1992; chair 1992-1996), Eastern Regional Secretary (1991-1999), and the extensive responsibilities of BIF Executive Director from 2000-2002. He was actively involved in two revisions of the BIF Guidelines for Uniform Beef Improvement Programs, along with leadership responsibilities in the Awards Committee, Scholarship

Committee, and Fact Sheet development and Editorial efforts.

The BIF is fortunate to have Ronnie Silcox as part of its history. Along with his formal BIF responsibilities, he has always been willing to provide service and dedication to all BIF leadership, membership, and educational activities.

Dr. Silcox and his wife, Terry, have been married 21 years, and have two sons, Christopher and Patrick.

Edited by Cody Wright, Extension Beef Specialist, and Betty Knutsen, Information Assistant

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