CAN BEEF CATTLE BREEDING SATISFY CUSTOMER DEMANDS IN THE 21ST CENTURY?

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INTRODUCTION

As animal breeders, we are engaged in the noble pursuit of developing science-based technologies which will result in genetic improvement of livestock production. In the recent past, it has become apparent that in many cases the amount of information available is much greater than the true practicing breeder can ably apply. There is a detectable sense of information overload amongst industry breeders, with no end in sight. While the perspective of this presentation will come from the experience of the United States beef cattle industry, one could easily substitute the other livestock commodities, in a global perspective, and retain many of the same conclusions. It is the hope of the authors that it will stimulate the scientific community to feel some sense of urgency regarding the need for engagement in not only research, but policy making and industry educational endeavors as well. The objectives of this presentation are to: 1) Provide an overview of how to match a producer and production system to a specific industry target; 2) Discuss current and future tools needed for proper genetic decision-making, and 3) Provide some perspective on how the beef cattle industry can go about increasing "quality and consistency" while maintaining balances in efficiency and profitability.

WHERE SHOULD WE BE PLACING EMPHASIS IN GENETIC IMPROVEMENT?

All changes in a commercial cow-calf operation must be evaluated in terms of their effect on profitability of the whole enterprise. Given the problem that profitability is often, in the short-term, very affected by external market conditions, Dickerson (1970) advocated that these changes be evaluated on the basis of economic efficiency measured as the ratio of input costs per unit of output product value. When one operates under this philosophy, cost of production becomes very important relative to desired increases in product value mentioned above as industry goals. Furthermore, it is imperative to remember that many of these desired ends are often antagonistically related, meaning that we must be careful to keep the "big picture" in perspective.

For example, traditionally we have thought that in relative economic terms, reproductive efficiency is roughly twice as important as growth performance which is approximately five times as important as carcass merit (Melton *et al.* 1979). A few years ago, a reanalysis of the importance of these three types of traits under a more current, value-based type of marketing system was completed. Under this more current marketing system, the former 10 reproduction: 5 growth: 1 product ratio was now closer to 2 reproduction: 1 growth: 1 product (Melton, 1995). A more recent evaluation of these economic weights has been presented from the American Gelbvieh Association's Gelbvieh Alliance marketing program (Figure 1). After some 110,000 feedlot cattle had gone through their program, the estimated relative importance of these three trait categories was approximately 4:2:1 (Schiefelbein, 1998). There are several things about these relative economic values that are very important. First, under the general assumptions used in their derivation, these results indicate that

while we have paid a lot of attention to growth of calves in the past, that will not suffice in the future. In most cases, the problems are in the other two categories: reproductive efficiency because it has been so difficult to genetically change, and carcass merit because we simply have not paid much attention to this area.
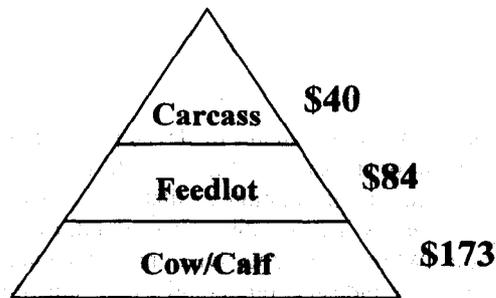

Figure 1. Relative Importance of Trait Categories (Schiefelbein, 1998).

Secondly, one should not fall prone to the common error of assuming that these economic weights are universally true. They are applicable to one particular system and environment but may be quite different if the system is changed. One of the universal strengths that makes the beef industry unique is that it uses God-given resources from the land which cannot be more efficiently utilized by other production systems. Cattle harvest energy from sunlight, soil, and water that is then converted to a higher quality form of protein. They do this from a set of natural resources that cannot be "farmed" any other way. The problem is that those resources exist under such a wide array of ecosystems that we are challenged to come up with one management system that will work for all environments (Hohenboken, 1988). Herein also lies our genetic dilemma when we try to build the best beast to harvest and harness that energy from the environment.

Thirdly, we also often tend to over-generalize in the beef industry when talking about "THE TARGET". As Dell Allen of Excel, Inc. has stated, there a several different target markets in the beef industry (Allen, 1987). The first question that a commercial breeder must ask before addressing anything else genetically, is "Which target am I going to aim my production resources toward?". As marketing of cattle in alliance and grid programs has escalated over the past 24 months in the U.S., it has become clear that there are major targets in "lean beef", "high-quality beef", and "export beef" trade. There are certainly other smaller specialty markets as well. The market may change over time in relation to premiums and discounts for "leanness" versus "quality". However, a given producer must decide *before the genetic decisions are made* on a well-defined target that is comfortable. Given the current plethora of alliance marketing programs, one must become educated on where he/she fits and then set their target based on that marketing program. *Only then can one truly go about determining the relative importance of these traits.*

WHAT SHOULD BE IN A COMMERCIAL BREEDER'S WANT AD?
In 1987, the beef cattle symposium program at the annual meeting of the American Society of Animal Science was entitled "Bovine Nirvana". In that program, Rick Bourdon and Bill Hohenboken discussed different perspectives on how one might describe the "ideal" cow (Bourdon 1988; Hohenboken 1988). As they both stated in their remarks, this beast does not really exist, primarily due to the reasons already described earlier in this paper. However, we do know that it is possible to provide some general guidelines for the specifications we would look for in performance criteria in the beef cattle production system.

Bob Taylor, a recently deceased colleague and friend in the beef cattle management systems area, had great foresight in realizing the need to look at "balanced" performance of cattle long before it was popular. A number of years ago, he developed a simple analogy to illustrate the importance of this philosophy to his beef production students. He said that what commercial producers should do is develop a "want ad" for the type of bulls and females they use in their system. This want ad should then be what is used by the seedstock industry to develop "specification seedstock" to address the needs of the commercial production sector of the industry. While this is a very simple approach, in concept, one is left to wonder just how often it has been applied. Taylor's generalized want ad, shown in table 1, provides an excellent overview of the challenge a breeder has to mount in order to "hit the overall" target.

Table 1. Production and marketing specifications for beef cattle

Trait	Optimum Range[a]	Industry Target[b]
Reproduction		
Age at Puberty (mos)	12-16	14
Scrotal Circumference (cm)	32-40	36
Reproductive Tract Score (14 mos)	4-5	5
Weight at Puberty (kg)		
Heifers	270-360	320
Bulls	400-500	450
Age at First Calving (mos)	23-25	24
Birth Weight		
Calves from Cows (kg)	35-45	39
Calves from Heifers (kg)	27-36	32
Body Condition Score (BCS, 1-9)	4-6	5
Postpartum Interval (d)	55-95	75
Calving Interval (d)	365-390	365
Calving Season (d)	45-90	65
Calf Crop Weaned (% cows exposed)	80-95	85
Cow Longevity (yr of age)	9-15	12
Growth		
Mature Cow Weight (kg at BCS 5)	400-600	500
Weaning Weight (kg; steer @ 7 mos)	200-275	240

Yearling Weight (kg; steer @ 365 d)		
Grazed and / or backgrounded	275-365	320
Weaning to Feedlot	400-500	450
Feedlot Gain (kg / d)	1.1-1.6	1.4
Feedlot Feed Efficiency (steer)	5-7[c]	6[c]
Days on feed (high energy ration)	60-120	90
Carcass		
Carcass Weight (kg)	275-365	320
Quality Grade	Select[a] to Choice[b]	Choice
USDA Yield Grade	1.5-3.5	2.5
Fat Thickness (mm)	2.5-15.2	7.5
Ribeye Area (cm^2)	71-97	84
Palatability (% fat in retail cuts)	3-7	5
Warner-Bratzler Shear Force (kg)	Below 3.65	Below 3.65
Muscle to Bone (kg muscle to kg bone)	3.5-4.5	4.0
Lean Yield / Day Age (kg)		
Weaned Steer to Feedlot	0.35-0.45	0.40
Grazed Yearling Steer to Lot	0.20-0.30	0.25
Frame Score		
Steers	4-6	5
Cows	4-6	5
Bulls – Maternal	4-6	5
Terminal	5-7	6

(Adapted from Taylor and Field, 1999).
[a]Range will include most commercial beef operations where an optimum combination
of productivity and profitability is desired.
[b]Target gives central focus applicable to many commercial beef operations. Deviation
from this target and optimum range is dependent on market, economic, and environmental
conditions in specific commercial beef operations.
[c]High-energy ration, kg feed per kg gain.

IS IT POSSIBLE TO GENETICALLY IMPROVE COW ADAPTABILITY AND CARCASS ACCEPTABILITY?

Within Population Selection. Fortunately, collective research results over the past 50 years have clearly shown that genetic variation exists both between and within breeds for many of the important measures of performance in beef cattle production. Table 2 provides a summary of the average levels of heritability for a variety of reproductive, growth and carcass traits as provided in an exhaustive analysis of the research literature by Koots *et al* (1994a). In general, selection within breed populations is quite effective for carcass traits, moderately effective for growth related traits, and much slower for reproductive efficiency related traits.

Table 2.   Levels of Heritability (h²) of Beef Cattle Performance Traits

Trait	Number of Studies[a]	Weighted Mean h² [b]
Reproduction		
Age at First Calving (Direct)	7	6
Age at First Calving (Maternal)	1	19
Calving Date	7	8
Calving Interval (Cows)	3	1
Calving Interval (Heifers)	7	6
Calving Ease (Direct)	19	10
Calving Ease (Maternal)	11	9
Calving Rate	9	17
Scrotal Circumference	25	48
Heifer Conception Rate (Direct)	9	5
Heifer Conception Rate (Maternal)	1	2
Cow Conception Rate (Direct)	21	17
Cow Conception Rate (Maternal)	1	2
Growth		
Birth Weight (Direct)	167	31
Birth Weight (Maternal)	34	14
Weaning Weight (Direct)	234	24
Weaning Weight (Maternal)	38	13
Yearling Weight (Direct)	147	33
Yearling Weight (Maternal)	6	6
Mature Cow Weight	24	50
Feed Efficiency	25	32
Feed Intake	21	34
Relative Growth Rate	12	22
Carcass		
Backfat Thickness	26	44
Ribeye Area	16	42
Slaughter Weight	52	41
Carcass Weight	19	23
Dressing Percentage	13	39
Cutability	12	47
Lean:Bone Ratio	4	63
Marbling Score[c]	12	38
Warner-Bratzler Shear Force	12	29
Sensory Panel Tenderness	3	13
Yearling Frame Score	27	61

(Adapted from Koots *et al.*, 1994a and Green, 1999).
[a]Number of research studies represented.
[b]Average heritability of trait, weighted by number of observations in studies. Expressed as a percentage.
[c]Recent review of Marston *et al* (1999) reported average of 43% heritability for marbling.
[d]All traits are expressed on an age constant basis where applicable.

Until recently, we have believed that there was limited opportunity to genetically improve fertility via direct selection within breeds. While indicator traits of fertility and age at puberty, such as

scrotal circumference, have proven to be quite useful and heritable (Brinks *et al.* 1996), they have not been shown to be highly genetically correlated to fertility measured as pregnancy success. Because fertility measures are binary traits (ie they are observed as either pregnant or not pregnant), it is quite difficult to use phenotypic information to determine genetic differences (eg. two females may both get pregnant but may differ widely in their true genetic potential for fertility). This results in traditional analytical methods not being adequate to separate these genetic differences and thus, we have always stated that the heritability of these traits is quite low (see table 2). More appropriate statistical methodology called "threshold modelling" allows appropriate analysis of these types of traits on an underlying continuous probability scale. One of the first applications this approach was to define a new trait called "stayability" that has been adopted by the Red Angus Association of America and is now in the process of being implemented by several other breeds (Snelling *et al.* 1995). This estimated breeding value is a genetic prediction of the probability of females still being in the herd at a breakeven age of six years given that they were selected as replacements. This measure combines performance differences in fertility, growth, and survivability/adaptability of these females.

In the direct fertility area, an analysis of heifer pregnancy records from the Hereford herd at the Bell Ranch in New Mexico has recently been completed (Evans *et al.* 1996). In that study, the researchers determined that heifer pregnancy was indeed more heritable than previously thought (14%). Furthermore, when the relationship of heifer pregnancy with yearling bull scrotal circumference was estimated, a non-linear relationship (ie the bulls with low SC EBV had low HP EBV, moderate SC EBV had the highest HP EBV and highest SC EBV had lower HP EBV) was revealed. A second study conducted a similar analysis using historical data from the Colorado State University Beef Improvement Center Angus population at Saratoga, WY (Doyle *et al.* 1996). These researchers reported a heritability level for heifer pregnancy of 19%, corroborating the result of Evans *et al* (1996). These two studies indicate that it is feasible to produce genetic predictions to enable direct genetic improvement in reproductive rate. The only obstacle is getting breed association national cattle evaluation performance databases to adopt a "whole-herd reporting" format that is necessary to allow computation of these types of EBV (Golden *et al.* 1996). While this is only a start on the whole reproductive efficiency complex, it is a 200% improvement over current genetic capabilities in this important area.

Between Population Selection. Larry Cundiff and co-workers at the U.S. Meat Animal Research Center have conducted the most extensive genetic evaluation of breeds in the world over the past 30 years in the Germ Plasm Evaluation (GPE) program at the U. S. Meat Animal Research Center. The design for this project (table 3) has allowed for the evaluation of a widely diverse set of breeds, as shown grouped by biological type in table 4 (Cundiff and Gregory 1999). From the collective results of this effort, they have reported that the magnitude of genetic variability between breeds is roughly equivalent to that within breeds (table 5) for most performance traits. While this infers that genetic improvement is possible through proper breed selection implemented in designed crossbreeding programs (ie breed complementarity), it also points out that no one breed excels in all characteristics simultaneously, along with a great degree of overlap between various breeds.

Table 3. Sire breeds used in the germ plasm evaluation program (Cundiff and Gregory 1999)

Cycle I (1970-72)	Cycle II (1973-74)	Cycle III (1975-76)	Cycle IV (1986-90)	Cycle V (1992-94)
F_1 crosses from Hereford or Angus dams (Phase 2)[a]				
Hereford	Hereford	Hereford	Hereford	Hereford
Angus	Angus	Angus	Angus	Angus
Jersey	Red Poll	Brahman	Longhorn	Tuli
S. Devon	Braunvieh	Sahiwal	Salers	Boran
Limousin	Gelbvieh	Pinzgauer	Galloway	Belgian Blue
Simmental	Maine Anjou	Tarentaise	Nellore	Brahman
Charolais	Chianina		Shorthorn	Piedmontese
			Piedmontese	
			Charolais	
			Gelbvieh	
			Pinzgauer	
3-way crosses out of F1 dams (Phase 3)				
Hereford	Hereford			
Angus	Angus			
Brahman	Brangus			
Devon	Santa Gertrudis			
Holstein				

[a]In Cycle V, composite MARC III (1/4 Angus, 1/4 Hereford, 1/4 Pinzgauer and _ Red Poll) cows are also included.

[b]Hereford and Angus sires used in Cycle IV included 10 Hereford sires born from 1963 to 1969 and 14 Angus sires born from 1968 to 1970 used as reference sires in Cycles I, II, III and IV to produce reciprocal cross Hereford X Angus (HA_o) progeny, and 32 Hereford sires born from 1982 to 1985 and 28 Angus sires born from 1983 to 1985 used to produce reciprocal cross Hereford x Angus by a current sample of sires (HA_c) in Cycles IV and as reference sires in Cycle V.

Table 4. Breeds evaluated in USDA-ARS germ plasm evaluation program grouped into biological type (Cundiff and Gregory 1999)

Breed Group	Growth Rate / Mature size	Lean to fat ratio	Age at puberty	Milk Production
Jersey (J)	X	X	X	XXXXX
Longhorn (Lh)	X	XXX	XXX	XX
Hereford-Angus (HAx)	XXX	XX	XXX	XX
Red Poll (R)	XX	XX	XX	XXX
Devon (D)	XX	XX	XXX	XX
Shorthorn (Sh)	XXX	XX	XXX	XXX
Galloway (Gw)	XX	XXX	XXX	XX
South Devon (Sd)	XXX	XXX	XX	XXX
Tarentaise (T)	XXX	XXX	XX	XXX
Pinzgauer (P)	XXX	XXX	XX	XXX
Brangus (Bg)	XXX	XX	XXXX	XX
Santa Gert. (Sg)	XXX	XX	XXXX	XX
Sahiwal (Sw)	XX	XXX	XXXXX	XXX
Brahman (Bm)	XXXX	XXX	XXXXX	XXX
Nellore (N)	XXXX	XXX	XXXXX	XXX
Braunvieh (B)	XXXX	XXXX	XX	XXXX
Gelbvieh (G)	XXXX	XXXX	XX	XXXX
Holstein (Ho)	XXXX	XXXX	XX	XXXXX
Simmental (S)	XXXXX	XXXX	XXX	XXXX
Maine Anjou (M)	XXXXX	XXXX	XXX	XXX
Salers (Sa)	XXXXX	XXXX	XXX	XXX
Piedmontese (Pm)	XXX	XXXXXX	XX	XX
Limousin (L)	XXX	XXXXX	XXXX	X
Charolais (C)	XXXXX	XXXXX	XXXX	X
Chianina (Ci)	XXXXX	XXXXX	XXXX	X

[a]Increasing number of X's indicate relatively higher values.

Table 5. Relativity of variation within and between breeds for various performance criteria

Trait	Number of Additive Genetic Standard Deviations
Age at Puberty (d)	8.5
Slaughter Weight (450 d) -	8.0
Retail Product Weight (450 d)	8.2
Retail Product % (450 d)	6.6
Marbling Score (450 d)	6.1
Warner-Bratzler Shear Force (kg)	5.1

Adapted from Cundiff and Gregory (1999).
[a]Assumption is made here that within a breed approximately six genetic standard deviations of variation exist in any trait.

The GPE program, along with other studies, has also shown that many genetic antagonisms exist in beef production systems. Koots *et al* (1994b) summarized published estimates of genetic and phenotypic correlations between a number of traits of interest (table 6). These estimates clearly reveal general genetic antagonisms between growth rate and calving ease, growth rate and mature cow size, maternal characteristics and cutability, and carcass quality and cutability. Additionally, the review of these authors pointed out how many genetic relationships between traits of economic importance are poorly understood. A prime example of the sparseness of information is the lack of any understanding of the relationship between measures of tenderness and other perfomance criteria.

Table 6. Weighted mean literature estimates of genetic correlations between various performance traits[a]

Traitsb	Phenotypic Correlation	Genetic Correlation
Calving Ease / Birth Weight	-0.28	-0.74
Birth Wt / Feed Efficiency	-0.12	-0.46
Yearling Wt / Feed Efficiency	-0.46	-0.60
Feed Intake / Feed Efficiency	---	0.71
Wean Maternal / Feed Intake	---	0.80
Scrotal Circumference / Feed Efficiency	0.12	0.61
Birth Wt / Weaning Wt	0.46	0.50
Birth Wt / Yearling Wt	0.38	0.55
Weaning Wt / Yearling Wt	0.71	0.81
Weaning Wt / Mature Wt	0.45	0.57
Weaning Wt / Slaughter Wt	0.65	0.79
Yearling Wt / Slaughter Wt	0.65	0.56
Yearling Wt / Scrotal Circumference	0.36	0.39
Backfat / Feed Intake	0.29	0.44
Backfat / Scrotal Circumference	0.27	0.78
Carcass Wt / Birth Wt	0.41	0.60
Carcass Wt / Yearling Wt	0.85	0.91
Cutability / Yearling Wt	0.85	0.87
Marbling / Yearling Wt	0.14	-0.33
Marbling / Feed Intake	0.24	0.90
Marbling / Cutability	-0.25	0.35
Ribeye Area / Weaning Wt	0.23	0.49
Ribeye Area / Yearling Wt	0.35	0.51
Ribeye Area / Slaughter Weight	0.33	0.43
Ribeye Area / Cutability	0.33	0.45
Ribeye Area / Marbling	0.06	-0.21
Tenderness / Marbling	????	????
Tenderness / Cutability	????	????

[a]Estimates shown are taken from Koots *et al* (1994b) and represent the weighted mean of available literature estimates.

[b]Traits represented are expressed on an age constant basis where appropriate and represent direct genetic effects.

The most troubling genetic antagonism we must consider when attempting to genetically improve product quality and consistency concerns the relationship between carcass attributes and measures of reproductive efficiency. There is generally a lack of this type of information in the research literature. The best existing data relating actual carcass measures to reproductive traits comes from a study by MacNeil *et al* (1984) at the U. S. Meat Animal Research Center. Table 7 provides a

summary of that information and indicates antagonistic relationships between selection to increase retail product weight and age at puberty, services required to settle a cow and mature size. When one considers these estimates in concert with the experiences of the swine industry with pale, soft, and exudative pork (PSE), a definite red flag is raised.

Table 7. Genetic Correlations Between Measures of Carcass Merit and Reproductive Efficiency (MacNeil *et al.* 1984)

Female Trait	Postweaning Gain (kg)	Carcass Weight (kg)	Fat Trim (kg)	Retail Product (kg)
Age at Puberty (d)	.16	.17	-.29	.30
Wt at Puberty (kg)	.07	.07	-.31	.08
Services/conception	1.33	.61	.21	.28
Gestation Length (d)	-.10	.03	-.07	.13
Calving Difficulty	-.60	-.31	-.31	-.02
Birth Weight (kg)	.34	.37	-.07	.30
Mature Weight (kg)	.07	.21	-.09	.25

Unfortunately, even though there have been numerous attempts to make one believe otherwise, these antagonisms leave no doubt that no one breed allows breeders to have their cake and eat it, too! Bourdon (1994) used the analogy of "sensible beef stew" to describe the effectiveness of utilizing designed mating systems to "mix and match" strengths and weaknesses of breeds to meet specifications for balanced performance. This fact has been further supported in the analysis of the American Gelbvieh Alliance results where a ratio of 50% British to 50% Continental European breeding appears optimal to hit market targets (Schiefelbein 1998). Cundiff *et al* (1994) additionally pointed out the need for alteration of breed inputs in sub-tropical environments to include either some Bos indicus or heat tolerant Bos taurus germ plasm.

HETEROSIS... THE FINAL PIECE IF THE PUZZLE

Fortunately, nature has provided a significant amount of heterosis observed in the reproductive efficiency and maternal trait complex to allow breeders to overcome the obstacles of direct selection for fertility and cow adaptability mentioned earlier. Heterosis levels of 20 to 25% are achievable in pounds of calf weaned per cow exposed to breeding using systems which exploit a terminal sire breed mated to crossbred females of unrelated breeds (table 8; Cundiff and Gregory 1999). This amount varies according to the breeds used in the crossing system because heterosis is directly proportional to the difference in gene frequencies affecting the traits between the breeds used in the cross. This is the basis for the success of the *Bos indicus x Bos taurus* crosses in the sub-tropical zones where these females express phenomenal heterosis in maternal and reproductive performance.

Unfortunately, in the chase to utilize this "free-lunch" heterosis gift, as has too often been the case in animal breeding, there has been too much emphasis on "maximize" and not enough emphasis on "optimize". When we recall what was mentioned before about evaluating the effects of change on cost per unit of output product value, there is an optimum amount of everything we do, even reproductive performance. Beyond that optimum it costs more to achieve than benefits received in return. This is an important concept to keep in check.

Table 8. Heterosis effects in crosses of *Bos Taurus x Bos Taurus* breeds and in crosses of *Bos Indicus x Bos Taurus* breeds from diallel crossing experiments[a]

Trait	N	*Bos taurus x Bos taurus* Units	%	N	*Bos indicus x Bos taurus* Units	%
		Crossbred calves (individual heterosis)				
Calving rate, %	11	3.2	4.4			
Survival to weaning, %	16	1.4	1.9			
Birth weight, kg	16	0.8	2.4	4	3.3	11.1
Weaning weight, kg	16	7.4	3.9	10	21.7	12.6
Postweaning ADG, kg/d	19	.034	2.6	6	.116	16.2
Yearling weight, kg	27	13.2	3.8			
Cutability, %	24	-.3	-.6			
Quality grade, 1/3 grade	24	.12	---	6	.3	---
		Crossbred cows (maternal heterosis)				
Calving rate, %	13	3.5	3.7	7	9.9	13.4
Survival to weaning	13	.8	1.5	7	4.7	5.1
Birth weight, kg	13	0.7	1.8	6	1.9	5.8
Weaning weight, kg	13	8.2	3.9	12	31.1	16.0
Longevity, yrs	3	1.36	16.2			
Lifetime production						
No. Calves	3	.97	17.0			
Cumulative weaning weight	3	272	25.3			

[a]Estimates are from experiments contributing to North Central Regional Project NC-1(Iowa, Indiana, Missouri, Ohio, USDA-ARS and Nebraska), Southern Regional Project S-10 (Virginia, Florida, Louisiana, Texas, SDA- ARS and Louisiana, USDA-ARS and Florida) as reported by Cundiff and Gregory (1999).

SO, HOW DO WE GENETICALLY MANAGE TO SIMULTANEOUSLY IMPROVE END-PRODUCT PERFORMANCE AND LOWER COST OF PRODUCTION?

Given that there are literally hundreds (thousands may be even more appropriate) of feed resource and climatic environments used in cattle production, yet end-product performance must fit within specification targets, what do we do? Animal breeders have unanimously stated over the past several generations of cattle production that we must achieve this balance by using breed complementarity and heterosis in very carefully designed crossbreeding programs. This must be a several step process to work successfully. First, the proper breeds must be chosen for matching maternal performance of the cow herd to a given production environment. Secondly, the proper lines from within those breeds must be selected to properly hit those environmental targets while also meeting minimum acceptable performance in end-product characteristics. Then a terminal sire breed must be selected to bring necessary performance for growth and end-product performance to the system. Furthermore, the sires selected from within the terminal breed (or breeds) chosen, must have documented performance for growth and carcass traits (ie EBV) in addition to the sires selected for maternal replacements having documented EBV for reproductive and functional soundness.

There are several different types of crossbreeding programs available to producers. These have been discussed in detail in the past (Bourdon 1994; Kress 1994; Cundiff and Gregory 1999). There are certainly advantages and disadvantages to each of them. Unfortunately, a number of the product inconsistency problems our industry is experiencing today are from misuse and abuse of these systems. It has not usually been the choice of the particular crossbreeding program that has gotten

breeders into trouble as much as the inability to properly design, implement and then stay the course in a crossbreeding program. Many programs have been doomed from the start because they were not properly thought out, while yet others have failed because a new breed has come along that tempts the curiosity too much. Furthermore, there are still many breed and tradition loyalties which run rampant which often get in the way of breeding program objectivity. These facts, coupled with the wild chase for extra growth and extra heterosis have resulted in what some have called the "mongrelization" of the U.S. beef cow herd.

IS THERE ANY WAY TO REDUCE CROSSBREEDING VARIATION?

Cundiff and Gregory (1999) presented an excellent summary of the effectiveness of various crossbreeding systems in terms of heterosis utilization, use of breed complementarity, and consistency of production in 1994. In that presentation, the most effective system at doing all three things simultaneously, along with being the easiest to manage effectively, was composite breeding. The theory behind composites has been amply proven by the Germ Plasm Utilization Project at the U.S. Meat Animal Research Center under the leadership and guidance of Keith Gregory. The published summary (Gregory *et al.* 1995) of that work proves that composite breeding offers a usable solution to many of the problems we are discussing here. Heterosis utilization is high, breed percentages are fixed and do not vary between generations, and breed differences can be utilized to match breed strengths and weaknesses to the production and marketing environment. The ability to overcome genetic antagonisms and still retain high levels heterosis in maternal performance is unmatched by any of the other designed systems. Furthermore, once the composite is formed, the breeding system is much simpler to manage than any of the others.

Detractors of the composite approach have argued that composite mating systems will increase rather than decrease variability of production due to increased levels of heterozygosity. USDA-ARS work has shown that there is not a significant increase in the variability observed in the composite lines as compared to the purebreds (table 9). Furthermore, compared to other mating systems such as rotational crosses and rota-terminal systems, the inter-generational variation is eliminated (figure 2). These same detractors of composites have argued that we cannot afford to give up the consistency that purebreeds have worked so hard to develop through their history. They do forget, however, that those purebreeds with their consistency have to be the foundation for the composite lines. Just like there is no one breed that offers everything, the beef cattle industry will not be able to develop only one maternal line composite. While that may work better for the poultry and swine industries, it will not work for the beef industry. Therefore, the challenge is for the purebred breeds to find where they will fit into various composite lines as they develop.
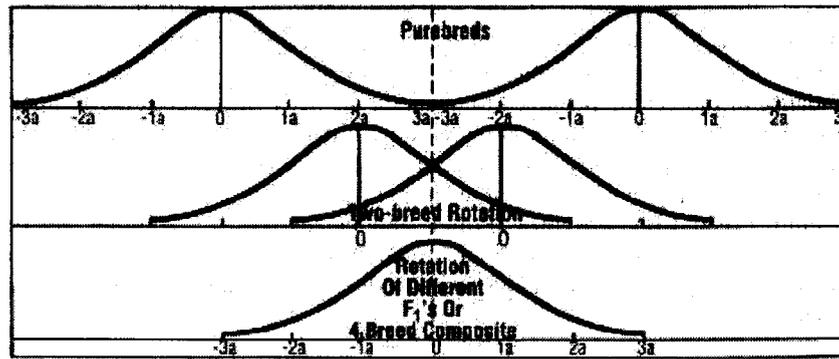
Figure 2. Variation Resulting From Various Mating Systems (Cundiff and Gregory 1994).

Table 9. Genetic Standard Deviations (s_g) and Phenotypic Coefficients of Variation (CV) for Purebreds and Composites (Castrate Males)

Trait	Purebreds		Composites	
	s_g	CV	s_g	CV
200-d weight, kg	13.3	.10	14.2	.11
Slaughter weight, kg	21.7	.08	28.7	.08
Carcass weight, kg	12.4	.08	17.9	.09
12th rib fat, mm	1.3	.48	2.0	.44
Retail product, %	2.2	.04	2.3	.06
Carcass lean weight, kg	8.1	.08	10.7	.09
Carcass fat weight, kg	8.6	.18	6.3	.19
Carcass bone weight, kg	2.8	.08	2.1	.10
Longissimus muscle fat, %	.6	.27	1.0	.29
Shear force, kg	.18	.22	0.59	.21

(Cundiff and Gregory 1999 and Gregory *et al.* 1995)

Reactions to the idea of composite breeding have been very interesting to watch. There have been some purebred breeds which have realized that they need to find where they can provide useful germ plasm for the formation of these composites. There have been other breeds who have denounced the very idea of such an approach, rather than asking the question of where they, too, can fit. There seems to be the mentality that the purebred breeds will disappear from existence because of composites. How can this be true? If one really analyzes the situation, the most likely scenario is for MATERNAL line composites to be developed by geo-climatic zone which will then be terminal sire mated to produce market offspring. Many of the breeders who are embracing and implementing the composite idea are doing so because they intend to produce replacement females and sire seedstock for the maternal side while at the same time selling purebred or F1 terminal sires.

There are, however, also a few negatives to the composite approach. One is that in order to develop a composite line, it needs to be done from a relatively large base to avoid inbreeding. The typically used number is to have 400 to 500 females in the breeding population. Then there has to be intentional avoidance of inbreeding practiced to maintain the heterosis level in the composite line. A second negative is that genetic evaluation is much more difficult, ie EBV are not readily available, nor as accurate, for most composites as compared to purebreeds. We are just beginning to see some movement in the U.S. to address this problem through such efforts as the American Simmental Association's multi-breed EBV program (Pollak and Quaas 1998). Another negative is that composite breeding still cannot overcome poor breeding decisions. A composite made from the wrong breeds and the wrong lines within those breeds still is a bad product. It has to be carefully and meticulously done.

HOW ARE WE COMING WITH CARCASS EBV?

So, even if many problems can be remedied with designed breeding programs, breeders still must be able to accurately select the best animals. If we do not have the information for end product breeding value, then how do we select the right terminal sire? For example, there is little doubt that the Brahman crossbred female is hard to outperform in the Gulf Coast region of the U.S. and the sub-topical / tropical regions of Australia. However, we also know that we need to find a way to make sure that the Brahman sire lines used in that cross do not present the wrong type of end-product specs (particularly for tenderness; Sherbeck et al. 1995a,b; Crouse et al. 1989). If we do not have genetic predictions available for these carcass traits, we are doing no better than shooting in the dark.

If there is such a need for carcass EBV and the genetic bases of these traits is relatively high, why are they not widely available? Even though there have been several factors which have contributed to this problem in the U.S., fortunately we are finally in the midst of seeing them resolved. The largest hindrance to collecting carcass information has been that until recently we have had to solely rely on progeny data. This type of information requires time, expense and labor to collect and also requires cooperation in the packing plant for accurate individual identification of carcasses. The combination of these factors has resulted in somewhat limited amounts of progeny data being placed into breed performance databases in the past. In the U.S., the American Angus Association has had the most concerted effort in designed progeny testing of sires. Approximately 50% of their currently published sires have carcass information (2,772 of 5,527 with published EBV (Angus 1998)). While this proves the difficulty of obtaining progeny data for carcass traits, it also emphasizes that useful carcass information can be obtained for a meaningful percentage of the breed. Several other breed programs are attempting to build databases (table 10).

Table 10. Current U.S. National Cattle Evaluation Programs – Carcass Merit (as of 1 Jan 99)

Breed	Total Sires	Total Published Sires	Sires with Carcass Data	Sires with Carcass EBV	Traits Evaluated[a]	Ultrasound Accepted?
Angus	95,995	5,527	1,944	2,772	1,2,3,4,5	Yes
Beefmaster	10,756	401	180	Not Released	2,3,4	Yes
Brangus	8,999	982	150	Not Released	2,3,4	Yes
Charolais	21,453	1,650	27	0	2,3,4,5	Yes
Gelbvieh	5,173	1,800	363	219	1,2,3,4	Evaluating
Hereford	94,221	4,261	4,986	1,010	2,3,4	Yes
Maine-Anjou	1,240	348	55	0	1,2,3,4	Evaluating
Red Angus	16,910	1,145	829	293	2,3,4	No
Salers	10,827	657	N/a	85	1,2,3,4	No
Shorthorn	11,788	862	565	115	1,2,3,4	No
Simmental	80,804	2,804		372	1,4,5	Yes

[a]Traits: 1=Carcass Weight, 2=Ribeye Area, 3=Fat Thickness, 4=Marbling, 5=% Retail Cuts.

The second hindrance has been the lack of ability to determine true carcass value differences on live, yearling seedstock cattle to circumvent the need for progeny data. Real-time ultrasound imaging technology has been pursued over the past ten years as the primary means to obtain these live animal measures and now appears to be entering the adoption mode. A national consortium of U.S. universities worked together during the early 1990s in a project which had as one of its three objectives "to determine the efficacy of using real-time ultrasound imaging to measure body composition and carcass merit traits in beef cattle" (Bertrand *et al.* 1994; Green *et al.* 1994; Wilson *et al.* 1994). The conclusions drawn from a compilation of this and other research indicate: 1) assessment of retail yield amount or percentage on the basis of 12th rib fat thickness (FT) and 12th rib ribeye area (REA) is slightly less effective using ultrasonic measures on the live slaughter animal as compared to direct measures on the carcass postmortem (Hamlin *et al.* 1995; Herring *et al.* 1994; Perkins *et al.* 1992b); 2) FT is a better predictor of cutability than is REA in the current cattle population (Hamlin et *al.*, 1995; Herring *et al.* 1994), although not so of retail product weight, 3) ultrasonic measures of these retail yield indicators appear to be under a moderate degree of genetic control (weighted average h2 of 0.37 for FT and 0.26 for REA (Hassen *et al.* 1999; Shepard *et al.* 1996; Evans *et al.* 1995; Robinson *et al.* 1993; Johnson *et al.* 1993; Duello *et al.* 1993; Arnold *et al.* 1991; Turner *et al.* 1990; Lamb *et al.* 1990; deRose *et al.* 1988), 4) genetic correlation estimates between ultrasonic predictors of carcass merit and other economically important traits are sparse but indicate some antagonism between REA and mature size (Shepard *et al.* 1996; Johnson *et al.* 1993), 5) prediction of intramuscular fatness and palatability traits is more difficult using ultrasound, although high and acceptable levels of accuracy have been achieved in the past few years (Brethour 1998; Crouch, personal communication; Wilson *et al.* 1995), and 6) data to estimate relationships between ultrasonic measures in yearling bulls and slaughter steer carcass retail yield and palatability have been more limiting (Crouch, personal communication; Kriese 1996; Diles *et al.* 1996a,b; Wilson *et al.* 1995; Evans *et al.* 1995; Steinkamp, 1995; Schalles *et al.* 1992).

This last issue has been the hardest one to resolve in recommending the adoption of ultrasound-generated carcass data for breed improvement programs. As data addressing this issue have been

accumulated over the past five years, the conclusions of various researchers have not all agreed. However, as more data have been analyzed in some larger breed databases, the conclusions have become more clearly in favor of the use of real-time ultrasound. Data from the Brangus (Kriese 1996) and Angus (Crouch, personal communication) breeds have indicated high correlations between ultrasound and actual progeny carcass data for sires where both types of information have been collected. These conclusions have lead to the recent adoption of policy to accept ultrasound data by several breed associations, including Angus, Hereford, Simmental, Brangus, and Gelbvieh (table 10), with more associations to follow suit in the next few years. Coupled with actual carcass progeny data, use of real-time ultrasound data should allow great acceleration to occur in the percentage of active sires with carcass EBV for most breeds. For example, the American Angus Association amassed enough ultrasound data in the first 9 months after adoption to increase the size of its carcass record database by almost 50% (Crouch, personal communication).

DO WE HAVE ALL OF THE NECESSARY INFORMATION TO GENETICALLY ADDRESS CARCASS ACCEPTABILITY?

The only area that may be a little tough (no pun intended) is genetic evaluation of overall meat quality, particularly tenderness. The reason that this is a major issue for the beef industry to confront is that we have estimates that one in five of the steaks produced in the current industry are tougher than desired (Morgan *et al.* 1991). No industry can afford this kind of defect rate!

There have been numerous debates in the U.S. over the last few years regarding how marbling can, or cannot, be used to address the meat quality and tenderness issue. This same discussion has also been occurring in Australia as you have begun to implement eating quality assurance grading standards (George 1999). The collective U.S. experience indicates that while it would be nice to rely on marbling and USDA Quality Grade to be the "insurance policy" for palatability, it is simply not good enough. As shown graphically in figure 3, while the probability of getting an unpalatable steak does significantly reduce when going from Standard up through Choice and Prime grades, there is so much overlap in palatability amongst the grades that today it is possible to have steaks from carcasses of Prime and Standard grades that will be equally palatable (Smith *et al.* 1987).

Increasing emphasis is being placed on marbling in breeding programs at the current time, largely due to the marketing success of the Certified Angus Beef program (Marston *et al.* 1999). Increasing selection intensity for marbling appears to be short-sighted, however, for several reasons: 1) marbling is, at best, an insurance policy for eating satisfaction of beef; 2) marbling only explains 10 to 15% of the variation in overall palatability of cooked beef product; and 3) just as in any other trait, there are genetic antagonisms with marbling which must be carefully managed (recall the discussion of cutability and marbling earlier in this paper). However, without a more direct, accurate system for assessing true palatability differences, breeders are responding to increased consumer demand for quality and consistency using marbling as their selection criterion since it is the only tool available to them. As long as this selection occurs in a balanced, multiple trait configuration it should net small, yet positive, gains over time (Marston *et al.* 1999).
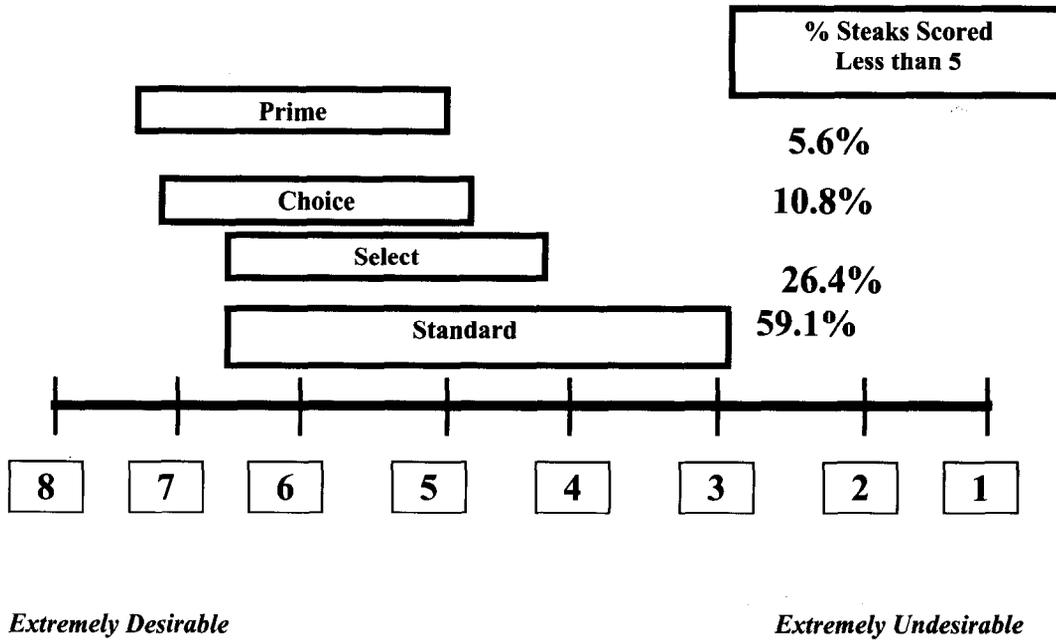
% Steaks Scored
Less than 5

Prime

5.6%

Choice

10.8%

Select

26.4%

Standard **59.1%**

| 8 | 7 | 6 | 5 | 4 | 3 | 2 | 1 |

Extremely Desirable   *Extremely Undesirable*

Figure 3. Relationship Between Palatability and USDA Quality Grade (Smith *et al.* 1987).

WHAT ABOUT TENDERNESS?

It seems like there has been more discussion about beef tenderness in the past five years than in all of the previous century. As reviewed by Tatum (1999), beef is perceived to currently have a toughness problem, particularly in relation to cattle of *Bos indicus* descent (O'Connor *et al.* 1998; Sherbeck *et al.* 1995). There are two ways to handle this problem; tenderize the product post-mortem and/or genetically fix it. We know that postmortem aging, electrical stimulation, and calcium chloride injection post-mortem can be used to reduce toughness problems (Tatum *et al.* 1997). We also know that tenderness, assessed as Warner-Bratzler shear force of loin or rib steaks at a 14 d aging endpoint is heritable ($h2 = 0.38$) and variable (Wulf *et al.* 1996). Although calpastatin, a primary inhibitor of muscle proteolysis post-mortem, appeared to offer a useful selection criterion in early research targeting genetic improvement in tenderness (Wulf *et al.* 1996; Koohmaraie *et al.* 1995), genetic polymorphisms in the calpastatin gene have not proved practically usable (Lonergan *et al.* 1995; Green *et al.* 1996a,b; Green *et al.* 1994). However, application of best management practices post-mortem results in a toughness rate that is still unacceptable, with the only long-term remedy through genetic selection (Tatum, 1999). Collectively, this means that breeders must position themselves on the tenderness issue by collecting objective progeny tenderness data (measured as Warner-Bratzler shear force).

This challenge has been taken very seriously by commodity group leaders in the U.S. and abroad. In 1998, an extensive genetic evaluation project for carcass merit was approved for funding by a

consortium of 16 U.S. beef cattle breed associations and the national beef checkoff (Green *et al.* 1998). The 42 month study, referred to as the National Carcass Merit Project, was initiated in June of 1998 and will collect complete carcass data (including ribeye shear force) from 11,000 progeny of sires from these breeds. Each breed is testing a minimum of ten of their most widely used sires with a minimum of 50 progeny each. Additional sires will be tested with fewer progeny in a majority of the breeds. The objectives of the project include estimation of EBV for shear force and sensory panel assessments of tenderness (as well as all other carcass traits) and an economic analysis of the costs and benefits associated with this type of information. As the planning for this project developed, a particular focal point of the effort became an evaluation of a set of previously identified and promising 11 DNA marker tests for carcass merit. Since DNA technology has been portrayed at times to be the savior of the beef industry, more discussion of this area is warranted.

DNA TO THE RESCUE ...

A number of developments over the past ten years have led to some DNA testing beginning to be made available to industry. Since we have been discussing tenderness and carcass merit traits at length, it might be helpful to show what is happening in this area as an example.

As pointed out previously, the beef cattle industry in the United States has been attempting to improve consumer demand for beef products by improving carcass merit of the cattle population. In particular, the need has been identified to increase the marbling potential of domestic grain-fed U.S. beef. In response to these needs, a beef checkoff funded project was initiated at the Angleton research station of Texas A&M University to identify genes, referred to as "quantitative trait loci" (QTLs), affecting variation in marbling ability (Taylor *et al.* 1996). The project was started in 1990 and required the development of resource families that would be expected to be highly heterozygous for gene loci affecting this trait as well as other measures of carcass merit. Based upon previous research, the scientists chose a design that utilized Brahman X Angus crosses to develop these families due to their divergent performance relative to marbling (Angus high, Brahman low). They first produced reciprocal F1 crosses between these two breeds. These first crosses were then used to produce full sib families of backcrosses to either Angus or Brahman through multiple ovulation and embryo transfer. A total of 42 full sib families were produced representing 16 sires and 19 dams. Life history data on 613 head of progeny were collected in this project (Taylor *et al.* 1997).

In analyses conducted in this project, the research team identified a number of possible QTL for several traits including five genes which appear to affect marbling, and an additional seven genes that influence either tenderness as assessed by Warner-Bratzler shear force or sensory taste panel. Additionally, the project has allowed identification of five QTL effects on ribeye area and 5 QTL for dressing percentage. One QTL effect that was detected in the project seemed to influence postweaning growth independent of birth weight variation, a very favorable gene effect. This QTL maps to the same chromosome (bovine chromosome 2) that had been identified to contain the gene causing double-muscling, the so-called myostatin gene (Grobet *et al.* 1997).

Several things are evident from the experience and results of this project. First, it is clear that these resource families take a great deal of time to develop and collect information from. It is a slow, expensive, and laborious process. Secondly, the reverse genetics approach (ie designing the families

to allow detection of differences after the fact), is fairly powerful for detecting these effects, but will likely only yield linked markers in chromosomal regions containing large QTL effects. The researchers still must positionally clone and sequence these gene loci before they can determine the genetic cause of these differences and have more direct genotype tests. This positional cloning requires much finer mapping in order to elucidate the gene of interest. Thirdly, because of patenting/licensing of any DNA tests that develop from this type of research, much vagueness is observed in reporting of research results. Instead of knowing the map locations of the QTL effects presented above, the research group can only say that have identified effects rather than elucidating where those are located and in what linkage groups. Unfortunately this slows down overall progress in the field but is a fact of life in any form of current day biotechnology. Fourthly, because the reverse genetics approach hopes to identify markers to be used in a marker-assisted selection approach, the linkage relationships identified from a particular set of families may not hold up in other populations due to the phase of the linkage relationship. In other words, the markers linked to QTL effects identified in this particular project may not be useful in other families or breed populations. For example, perhaps the effects being found are breed-specific alleles that we already see in measuring differences between breeds, yet are not segregating within those other breeds (ie they are fixed). This last issue can possibly result in the direct application of QTL detected through this approach being difficult to apply beyond the resource population of study.

This research provides an excellent example of the process the animal industries will face to make usable technology from this approach. Given that it is unknown how useful the markers identified in that project will be across other families and breeds, a second step must be taken. This is where the National Carcass Merit Project mentioned earlier will play a major role. The project has several objectives, one being to validate the DNA markers identified by the Texas A&M project across the major U.S. beef breeds. The project is designed to collect complete carcass data, including Warner-Bratzler shear force, on 50 progeny from each of 10 widely used reference sires in each of the 16 breeds. Additionally, sensory panel evaluation will be performed on steaks from approximately 3,000 of these progeny. By going through this effort, the question will quickly be answered about whether these markers will be useful in a wide array of germ plasm. Additionally, it is hoped that the researchers will at the same time be able to move closer to positionally cloning the actual QTLs being "marked". The breeds and numbers of progeny participating in the project are shown in table 11.

Table 11. Distribution of progeny across breeds in the national carcass genetic merit project (Green *et al.* 1998)

Breed	# DNA Sires @ 50 hd each	# Addl. EBV Sires @ 25 hd each	Total # Sires
Angus	10	20	30
Beefmaster	10	5	15
Brahman	10	5	15
Brangus	10	0	10
Braunvieh	10	0	10
Charolais	10	9	19
Gelbvieh	10	7	17
Hereford	10	23	33
Limousin	10	15	25
Maine-Anjou	10	5	15
Red Angus	10	10	20
Salers	10	0	10
Shorthorn	10	5	15
Simmental	10	15	25
Simbrah	10	5	15
South Devon	10	0	10
Total # Sires	**160**	**124**	**284**
Total # Progeny	**8,000**	**3,100**	**11,100**

*EBV sires are to calculate EBV only (no DNA analyses will be performed).

It is interesting to note that there seems to be some redundancy in efforts occurring around the world in this area of technology development. One could easily take the Texas A&M and U.S. national project experience described above and change the names to CRC for Meat Quality and CSIRO Australia and have a very parallel story to tell over the same time period. The same could be done for the University of Saskatchewan and Ag. Canada. In the opinion of the author, more cooperation and less competitiveness ih this area might do all of our industries a lot of good. Unfortunately, that does not appear to be the lay of the land for the future.

WHAT OTHER QTL HAVE BEEN FOUND ??

There are a number of QTL effects that have now been identified through research work at several locations. In addition to the work described above, associations have been reported for myostatin (Georges *et al.* 1998); growth traits (Beever *et al.* 1992); and carcass attributes, including tenderness (Keele *et al.* 1999; Stone *et al.* 1999; Green *et al.* 1996a,b). Additionally, associations have been reported with the ryanodine receptor gene with the pale, soft and exudative meat quality problem (Milan *et al.* 1996), markers associated with growth and fatness traits (Andersson *et al.* 1994; Archibald *et al.* 1994), and the estrogen receptor gene with litter size (Rothschild *et al.* 1998) in swine; the callipyge gene with double-muscling in sheep (Cockett *et al.* 1994, 1997; Freking *et al.* 1999); the bovine leukocyte adhesion deficiency condition in Holstein dairy cattle and other markers related to milk production traits (Dentine, 1995; Georges *et al.* 1995); and the hyper-parakalemic periodic paralysis condition in American Quarter Horses (Spier *et al.* 1993). It is not a coincidence that many of these associations are with single-gene, simply inherited traits. We are likely to see much of the benefit of DNA marker, or direct gene, testing on these types of qualitative traits.

More recently, mapping efforts have been initiated using complex study populations to identify large QTL effects for traits previously untouchable in genetic improvement programs. The two most exciting of these are both located in Nebraska. The first is a project being led by Daniel Pomp and Merlyn Nielsen at the University of Nebraska where they are using lines of mice which have been selected divergently for heat production. Heat loss can be used to estimate maintenance energy requirements of an animal through direct calorimetry. The Nebraska project was initiated in the early 1980s to determine if genetic variation existed for maintenance requirements using this approach. They have been successful in changing the heat production between high and low lines by 50% of the average. Earlier this year, this group reported that in a QTL search of an F2 intercross of lines of these mice, they were able to identify two major QTL affecting heat production, with another two putative QTL (Moody *et al.* 1998). This is exciting in that it indicates that it may be possible through marker-assisted selection approaches to identify animals with improved feed efficiency, perhaps our most difficult economic trait to measure.

A second major QTL effort is underway at the USDA-ARS Meat Animal Research Center. In one aspect of that effort, researchers are attempting to utilize the twinning population where selection has been applied over several generations for twinning rate, to detect QTL for ovulation rate and embryo survival. Initial results in that project have been very promising, with at least one major QTL already identified in the early part of the project (Kappes and Cundiff, pers. comm.)

The resulting QTL that are identified through the ongoing searches of the developing bovine gene map are likely to be most beneficial for those traits that are difficult and expensive to measure, as detailed above. We can expect the following categories of traits to benefit the most from marker-assisted selection (in order of greatest to least degree of benefit): disease resistance and immunocompetence, carcass quality and palatability attributes, fertility and reproductive efficiency, maintenance requirements (ie energetic efficiency), carcass quantity and yield, milk production and maternal ability, and growth performance. This ranking is due to a combination of considerations including: 1) the relative difficulty in collecting performance data, 2) the relative magnitude of the heritability and phenotypic variation observed in the traits, 3) the current existing amount of performance information available, and 4) when performance data becomes available in the life-cycle of the cow herd, (collected at birth, weaning, yearling, maturity?). Most of the rankings above then become self-explanatory.

To be realistic, however, we must realize that QTL will not serve as magic, silver bullets. As long as we are relying on markers, rather than the QTL themselves, we are still only crudely defining the genotypes across the larger beef cattle population. Once QTL are finely mapped and direct tests are available, then the accuracy of selection will be markedly improved.

While marker-assisted selection is a popular new phrase in academic animal breeding circles, what we are more likely to see needed is what could be called "marker-assisted optimum selection". What this means is that markers identifying QTL of large effect can be used to add to EBV for the same trait. This will result in optimal use of information from both the molecular and phenotypic performance levels. In other words, marker-assisted selection or EBV singularly are not great, but

together they markedly increase the accuracy of genetic evaluation. It is important for the breeder to put these last two paragraphs firmly into perspective.

BUT HOW DOES ONE PRACTICE BALANCED TRAIT SELECTION WHEN THERE ARE SO MANY IMPORTANT TRAITS?...

One of the areas being currently debated by some of the thought leaders in the academic beef cattle breeding community would really help producers in this regard. The ideas being batted around relate to how to best combine information on several traits into "selection indexes" for specified breeding objectives. These ideas have been around a long time (since Jay Lush and Lanoy Hazel at Iowa State first proposed them in 1943), but have really become applicable and important as we have developed genetic information on more and more traits in the past ten years. For example, suppose one is looking for a maternal-line bull to produce females for a given production and marketing environment, then these indexes of traits weighted according to their relative amounts of heritable variation, relationships with other traits, and relative economic importance could be very valuable tools.

The dairy and swine industries have already produced indexes for use in their national genetic evaluation programs and I will not be surprised if the beef industry sees rapid development of the same in the next few years. In our case, however, the indexes will need to be somewhat "customized" for a given type of production scenario, similar to the discussion earlier in this paper about the importance of defining and sticking to a particular market target for a producer before deciding what to do genetically. Fortunately, we are seeing tools developed to help in this area such as the recently released Decision Evaluator for the Cattle Industry (DECI) model developed by USDA scientists at the U.S. Meat Animal Research Center (Bourdon 1998; Jenkins and Williams 1999). This simulation model is an attempt to provide a tool that will allow a producer to provide a base-line picture of his/her production system so that lots of "what if" questions can be asked. This is a critical area where a great deal of research and development is needed.

IMPLICATIONS

The following are unavoidable conclusions from experiences over the past 30 years:

1) Beef is losing market share relative to poultry and pork.
2) A large portion of the reason for lost market share is due to higher costs of production. Reproductive efficiency and other aspects of maternal performance in the environment cannot be sacrificed.
3) We can genetically alter cattle for end-product performance.
4) The most feasible way to approach the end-product non-conformance problem genetically is to use properly designed and implemented crossing systems which match maternal production to environmental feed resources with sire selection based on growth and carcass performance.
5) The benefits of heterosis on overall performance of a cow herd (upwards of 25% improvement in weight of calf weaned per cow exposed) cannot be ignored.

6) Proper terminal sire selection for growth and carcass performance is unachievable in the absence of end-product EBV and proper maternal sire selection for reproductive and maternal performance is unachievable in the absence of appropriate EBV.
7) Single-trait selection has never been and will never be a wise breeding philosophy.

Given these conclusions, we have several possible approaches to be successful in *achieving both cow adaptability and carcass acceptability.* Each of these has merit, and therefore, should be attempted. In priority order, they are:

1) Immediately demand that end-product performance data be gathered and utilized in national cattle evaluation programs. This must be done by amassing the necessary progeny data (either carcass or ultrasound) for lean yield and objectively measured meat quality attributes. Additionally, we must implement whole-herd reporting formats for breed performance data collection to enable calculation of EBV for fertility and longevity-related traits.
2) Educational plans should be developed, by geo-climatic region, for matching of breed resources to environments. Breeders must more willingly evaluate the alternative of using "composite" breeding program where they are applicable. Breeds need to be working today to determine where their germ plasm fits into the composite puzzle which is inevitably going to become a reality.
4) We must develop a high-integrity system of identification on every animal produced in the beef production system. We must then be willing to use this system to provide information feedback and true value discovery / pricing.
5) We must use all available resources to identify new DNA-based technologies to assist in making genetic improvement in problematic traits (eg. Maintenance energy cost, disease resistance).
6) Seedstock suppliers must adopt the philosophy of being a *full service genetic provider* to their clientele.

Several of these items are much more politically difficult to achieve than others which are physically more challenging. The political may, or may not, ever happen. This entirely depends on whether groups and people within the industry are committed to the good of the whole industry or the good of their portion of the industry. The physical challenges, however, are ones over which scientists and breeders have direct control. We can make those happen with the right resources directed in the right directions (eg. carcass EBV, individual animal ID and feedback, and whole-herd reporting). What happens if every commercial bull-buyer starts demanding reproductive / fertility and end-product EBV specifications before he/she will buy a bull? What happens if a feedlotter requires an electronic ID (or better yet a DNA bar code) on every incoming feeder or yearling before they will purchase and/or feed them? What happens if, on the basis of that identification, the industry provides direct pricing (with information feedback) on every animal? What happens if seedstock suppliers develop systems to analyze the needs of their customers followed by production of specification seedstock rather than producing first and then trying to find customers? What happens if animal breeding scientists take a more active role in education and technology adoption? The entire beef industry would universally benefit in the long term!

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