

University of Nebraska - Lincoln

DigitalCommons@University of Nebraska - Lincoln

Range Beef Cow Symposium

Animal Science Department

12-9-1997

Bull Genetics: Purebreds, Composites, Full-sibs and Half-sibs

James A. Gosey

University of Nebraska-Lincoln, jim@gosey.net

Follow this and additional works at: <https://digitalcommons.unl.edu/rangebeefcowsymp>



Part of the [Animal Sciences Commons](#)

Gosey, James A., "Bull Genetics: Purebreds, Composites, Full-sibs and Half-sibs" (1997). *Range Beef Cow Symposium*. 140.

<https://digitalcommons.unl.edu/rangebeefcowsymp/140>

This Article is brought to you for free and open access by the Animal Science Department at DigitalCommons@University of Nebraska - Lincoln. It has been accepted for inclusion in Range Beef Cow Symposium by an authorized administrator of DigitalCommons@University of Nebraska - Lincoln.

Bull Genetics: Purebreds, Composites, Full-sibs and Half-sibs

Jim Gosey
Beef Cattle Breeding Specialist
University of Nebraska, Lincoln, Nebraska

INTRODUCTION

Expected Progeny Differences (EPD's) are currently calculated for a range of traits important to ranch profitability. These EPD's are mostly used for bull selection within a breed. The list of traits for which EPD's are available is certainly not complete; notable exceptions are reproduction and fitness traits plus some measure of tenderness. Across-breed EPD adjustments are available to provide a basis for comparing bulls of different breeds. EPD's for composite bulls can be calculated but are mostly confined to within herd data without the benefit of data base sharing between breeds. The perceived desire for uniformity and consistency may encourage breeders to assimilate closely related bull batteries in an effort to reduce variation. The potential impact of these various aspects of bull genetics deserves thoughtful examination. This paper will highlight some of these areas for the purpose of stimulating discussion.

IMPACT OF BULL SELECTION

Due to the greater number of potential calves sired each year by bulls compared to cows, the impact of bulls on genetic change is large. Given that a sire, contributes a sample one half of his genes to each calf and the maternal grandsire contributes another one-quarter and the maternal great-grandsire contributes another one-eighth; it can be said that sire selection controls 87 ½ percent of the genetic change in a trait over time. At least the sires used in the last three generations contribute 87 ½ percent of the genes of a particular calf crop. The formula for response to selection is:

$$\text{Response to selection (per year)} = \frac{\text{Heritability (h}^2\text{)} \times \text{Selection Differential}}{\text{Generation Interval}}$$

Heritability is the proportion of variation in a trait due to genetics or heredity. Generation Interval is the average age of parents when calves are born. Selection differential is the average superiority of selected parents in a given trait compared to the average of their contemporaries. Breeders have little or no control over heritability but do have some control of generation interval since younger bulls and females could be used to turn generations of selection faster. However, the breeder's greatest impact is through the control of the selection differential. The use of National Sire Evaluation programs to provide progeny proofs on relatively young bulls (3 to 4 years of age) and the potential use of Artificial Insemination (A.I.) allow commercial herds to dramatically change the selection differential and thus, enhance response to selection.

NATIONAL SIRE EVALUATION - EXPECTED PROGENY DIFFERENCES (EPD's)

The advent of National Sire Evaluation programs in all of the major beef breeds in the U.S. has certainly changed the nature of bull selection and marketing of those bulls. Sire Summaries are now published annually (twice each year for some breeds) and increasingly available on the Internet or via disk complete with sire search capability so that breeders can shop for bulls based on their specifications.

Although some differences do exist between breeds in the statistical model being used for their analysis, the heritability and genetic correlation traits (every breed understandably wants to use estimates from their own data) and the genetic base; nonetheless, the result is a very useful system to rank bulls within a breed for a variety of traits. Average EPD's of active sires for various breeds is presented in table 1. These averages cannot be used to compare breeds, but rather they provide a benchmark to compare bulls within a particular breed and to give breeders an indication of the genetic trend for various traits within that breed.

Table 1. Breed Average EPD's for Active Sires

Breed	BW	WW	YW	MILK
Angus	3.1	27.3	48.2	11.1
Beefmaster	0.1	3.5	6.9	2.8
Brahman	1.3	10.0	17.3	4.4
Brangus	1.5	15.7	26.9	0.4
Charolais	1.8	12.9	19.0	1.6
Gelbvieh	0.3	5.4	9.8	1.5
Hereford	4.0	30.0	52.0	9.0
Limousin	1.4	8.1	15.0	1.0
Red Angus	0.8	24.8	41.6	9.7
Salers	0.7	6.7	11.3	2.7
Shorthorn	2.3	15.8	25.3	4.1
Simmental	4.0	30.6	48.6	9.4

ACROSS BREED EPD's

Given the diversity of production environments, management systems and market targets that beef is produced in, it seems unlikely that a producer will optimize efficiency within just one breed of cattle. Bulls of different breeds can be compared with the use of adjustments as shown in table 2. This table is updated each year by Drs. Cundiff and Van Vleck and published in the Beef Improvement Federation (BIF) proceedings. These Across Breed adjustments are limited to comparisons made between breeds at the U.S. Meat Animal Research Center and are not as accurate as within-breed EPD's; however, they do represent head-to-head comparisons of 4891 progeny of 388 sires used at USMARC and can be used to provide a good guideline to commercial ranchers who desire to make comparison of bulls of different breeds based on their EPD's.

Table 2. Adjustment Factors to Add to EPD's of Twelve Different Breeds to Estimate Across Breed EPD's

Breed	BW	WW	YW	MILK
Hereford	4.7	3.7	-2.4	-6.7
Angus	0.0	0.0	0.0	0.0
Shorthorn	8.4	25.8	36.3	12.1
Brahman	15.0	32.5	-15.6	27.4
Simmental	7.4	23.0	37.1	15.1
Limousin	7.7	29.6	24.1	-3.9
Charolais	10.6	39.0	55.5	3.8
Maine-Anjou	12.4	37.7	51.0	26.3
Gelbvieh	10.0	44.4	49.0	28.4
Pinzgauer	9.1	27.0	25.9	9.7
Tarentaise	5.7	29.5	12.8	20.6
Salers	6.6	26.1	32.4	14.8

Larry V. Cundiff (402/762-417 1) or L. Dale Van Vleck (402/472-6010), USDA, ARS, Roman L. Hruska U.S. Meat Animal Research Center, P.O. Box 166, Clay Center, NE 68933.

COMPOSITE BULLS

Composite bulls won't offset poor management but they offer a tool to help solve production/management problems and optimize production for a wide range of environments.

The impact of crossbreeding through heterosis (hybrid vigor) and utilization of breed differences (complementarity) for major traits like reproduction, calf survival, maternal ability, growth, longevity and other fitness traits is powerful. The cumulative effect of crossbreeding can increase calf weight weaned per cow exposed by 20 percent.

Conventional crossbreeding programs fall short in "management ease" because: 1) Rotations tie up several breeding pastures; thus, complicating grazing management, 2) Identification by sire breed type is required for proper breeding pasture assignment and 3) There is a continual struggle with swings in breed composition as long as straight bred sires are used; thus, complicating-heifer selection and marketing of steer progeny.

Crossbreeding, along with selection against extremes, offers a method to blend desirable characteristics of several breeds in an effort to use both heterosis and complementarity while avoiding unfavorable genetic antagonisms. Composites may be the preferred tool to implement such a crossbreeding/balanced trait selection program.

BENEFITS OF USING COMPOSITE BULLS

1. Simplifies total management since only one breed type is maintained on the ranch.
2. Optimizes breed composition to match production environments and market targets.
3. Utilizes complementarity between breeds in the foundation generation and also later if specialized sire and dam line composites are used.
4. Eliminates the fluctuation in breed composition between generations.

5. Provides a sustainable method to maintain reasonable levels of heterosis.
6. Allows flexibility to tap future composites that may better target the product or fit a specific production environment.
7. Paternal heterosis in semen quality/quantity, mating capacity and longevity of crossbred bulls.

CHALLENGES TO THE USE OF COMPOSITE BULLS

1. Identification of composite seedstock sources that are adequately documented to fit a particular environment or market.
2. Overcoming conventional thinking to develop databases for composite, hybrid and F₁ cattle based on field data for major bioeconomic traits.
3. Responding to the misconception that composite sires generate more variation than purebred sires at a time when uniformity and consistency are the catch words of the beef industry.
4. Dealing with the criticism that will come for lack of EPD's or alleged low-accuracy Across Breed EPD's on composite cattle.
5. Getting beyond the "our-breed-can-do-it-all" mentality of some breeds while appreciating the need for a viable purebred seedstock segment of the industry.

MATCHING GENETICS TO RESOURCES

Table 3 presents an attempt by the Beef Improvement Federation (BIF) to characterize production environments and estimate optimum productivity within those environments. Production environments are feed availability and environmental stress. Feed availability refers to the quantity and quality of native forage and supplemental feed. Environmental stresses include heat, cold humidity, parasites, altitude, mud and disease. For each of the six traits listed in the table either a Low, Medium or High level is recommended for each production environment. For example, a typical range for low, medium and high levels of cow mature size might be 800-1000 lbs, 1000-1200 lbs and 1200-1400 lbs, respectively.

The optimum trait levels shown in Table 3 are appropriate for General Purpose type cattle, cattle that are usually used in rotational crossbreeding programs. The lower part of the table lists optimum trait levels for both the maternal and paternal sides of a terminal crossbreeding program.

Greater feed availability and lower degree of stress results in a wider optimum range of milk. Optimum range of mature size also changes with range of feed availability. Environmental stress probably only limits mature size when feed availability is low.

Cows without the ability to store energy, when feed availability is low, often do not have enough body condition to rebreed quickly. Cows that do well in low feed environments may be fat cows in high feed-low stress environments. Since lean yield and ability to store fat are antagonistic, the optimum level of leanness varies with feed availability. A lean cow may be acceptable when feed is good but with limited feed, cows need to fatten easily.

Resistance to stress is always important, especially in high stress environments. For example, heat tolerance is critical in hot, humid regions. Calving ease may become increasingly important as stress level increases or other resources (labor) decline.

Table 3. Matching Genetic Potential for Different Traits in Varying Production Environments¹

Production : Environment :							
Feed Avail-ability	Environ-mental stress ²	Milk pro-duction	Mature size	Ability to store energy ³	Adapt-ability to stress ⁴	Calving ease	Lean yield
High	Low High	M to H M	M to H L to H	L to M L to H	M H	M to H H	H M to H
Medium	Low High	M+ —	M M	M to H M	M H	M to H H	M to H M
Low	Low High	L to M L	L to M L	H H	M H	M to H H	M L to M
<u>Breed role in terminal crossbreeding systems</u>							
Maternal		L to H	L to M	M to H	M to H	H	L to M
Paternal		L to M	H	L	M to H	M	H

¹L = Low; M = Medium; H = High.

²Heat, cold, parasites, disease, mud, altitude.

³Ability to store fat and regulate energy requirements with changing (seasonal) availability of feed.

⁴Physiological tolerance to heat, cold, parasites, disease, mud, and other stresses.

Recommendations for optimum trait levels for sires and dams in terminal crossbreeding systems vary somewhat from General Purpose types. Maternal cattle generally need more adaptability, more ability to store fat and less lean yield than General Purpose types. Milk production should be about the same but size should be less to take advantage of the complimentary effects of using growthier terminal sires. Calving ease is very important. Traits emphasized in terminal types are growth rate and lean yield. Milk production and ability to store energy are not very important in terminal types. Calving ease and adaptability in Terminal types is not as critical as in maternal types but should not be ignored.

INBREEDING, LINEBREEDING AND RELATIONSHIP

The desire to increase uniformity and consistency of beef results in increased interest in any tool that could be used to reduce variation. One such tool might be the use of closely related bulls in commercial herds in order to reduce the genetic variation in calves. In order to understand these concepts, a general discussion of some basics is useful.

INBREEDING AND LINEBREEDING

Inbreeding is a system of mating in which offspring are produced by parents that are more closely related than the average of the population from which they came. The genetic effect of inbreeding is to make more pairs of genes in the population homozygous regardless of the kind of gene action involved. Linebreeding is a special form of inbreeding but unlike inbreeding, linebreeding keeps the relationship high to a particular ancestor in the pedigree.

CALCULATING INBREEDING COEFFICIENTS

The formula for calculating inbreeding coefficients is as follows:

$$F_x = \frac{1}{2} \sum \left[\left(\frac{1}{2} \right)^n (1 + F_a) \right]$$

where

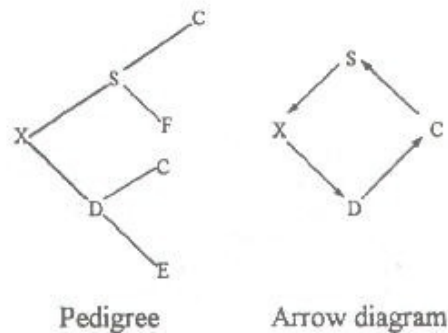
F_x refers to the inbreeding coefficient of individual X ,
 \sum is the Greek symbol meaning to sum or add all paths,
 n is the power to which one-half must be raised, depending upon the number of arrows connecting the *sire* and *dam* through the common ancestor,
 F_a is the inbreeding coefficient of the common ancestor

If the common ancestor is not inbred, the formula to use in calculating the inbreeding coefficient becomes:

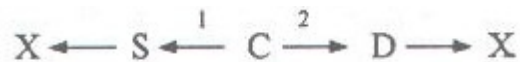
$$F_x = \frac{1}{2} \sum \left[\left(\frac{1}{2} \right)^n \right]$$

HALF-SIB MATINGS

The following pedigree and arrow diagram show a full-sib mating, the sire and the dam of individual X having had the same sire (©). The only common ancestor in this pedigree is individual C , because he appears in the pedigree of both the sire and the dam of individual X . The arrow diagram shows that there is only one pathway from C to X through the sire and only one



through the dam. This pathway may now be straightened out for illustrative purposes, and it becomes



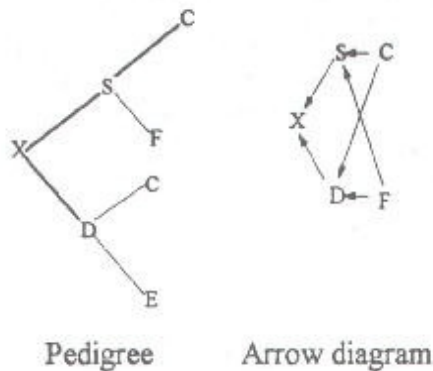
We now number the arrows running from the sire (*S*) through the common ancestor (©) to the dam (*D*). We do not count the arrows running from individual *X* to the sire and dam. The number of arrows connecting the sire and dam with the common ancestor is two, and this is the *n* in the formula. Our calculation of the inbreeding coefficient now proceeds by letting

$$F_x = \frac{1}{2} \left(\frac{1}{2} \right)^2, \text{ or } \frac{1}{2} (0.25), \text{ or } 0.125.$$

The inbreeding coefficient of individual *X*, then, is 0.125, and this can be expressed as 12.5 percent.

FULL-SIB MATINGS

The method for calculating the inbreeding coefficient for a full-sib mating is very similar to that described for half-sib matings, except that an additional path and common ancestor are involved. The following pedigree-and-arrow diagram illustrates how calculations are made for such a mating:



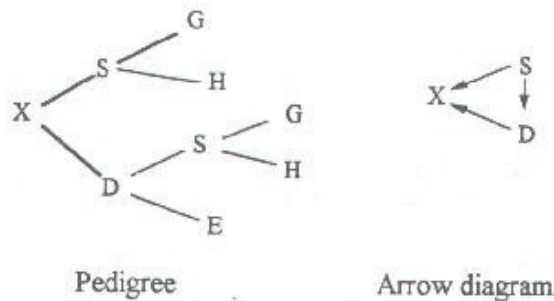
The two pathways are

X ← S ← ¹ C → ² D → X	$X = (1/2)^2 = 0.25$
X ← S ← ¹ F → ² D → X	$X = (1/2)^2 = 0.25$
<div style="display: flex; justify-content: space-between; width: 100%;"> Total 0.50 </div>	

The inbreeding coefficient of individual X is one-half of the sum of these two paths, or $F_x = \frac{1}{2} (0.50) = 0.250$, or 25 per cent inbreeding. Note that in this pedigree there are two common ancestors (G and F). We calculate the figure for all pathways, which totals two in this pedigree, from the common ancestors, and then sum all paths, as indicates. Then, when all are added, we take one-half of the total to get the inbreeding coefficient.

SIRE X DAUGHTER MATINGS

The inbreeding coefficient is calculated for parent X offspring matings in the same manner as for half and full sibs with only slight variations. The following is a pedigree of an individual from a mating of a sire to his own daughter. The inbreeding coefficient from such a mating is 0.25, providing the sire himself is not inbred.



The pathway is

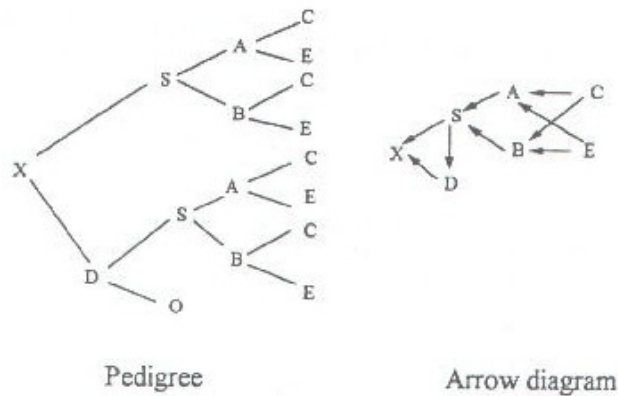
$$X \leftarrow S \xleftarrow{1} D \rightarrow X = (1/2)^1 = 0.50$$

Thus, $F_x = \frac{1}{2} (0.50)$, or 0.25, or 25 percent inbreeding.

Inbreeding coefficients for dam x son matings are calculated in a similar manner, except the arrow diagrams run from the dam as the common ancestor.

SIRE X DAUGHTER MATING WITH THE SIRE INBRED

The following pedigree is one in which a sire x daughter mating is made, but the sire himself is inbred. The first step in calculating the inbreeding coefficient for such an individual is to complete the arrow diagram as shown.



The first common ancestor in this pedigree, is individual *S*, which is the sire of individuals *X* and *D*. First calculate the inbreeding coefficient of individual *S* or the sire, as was done in the previous example for full-brother x full-sister matings. After this is done, for each path going from individual *S* to individual *D*, which is just one in this case, we multiply the path by $(1 + F_a)$, or one plus the inbreeding coefficient of individual *S*.

The calculation of the inbreeding coefficient for individual *S* is as follows:

S	←	A	← ¹	C	→ ²	B	→	S	= (1/2) ² = 0.250
S	←	A	← ¹	E	→ ²	B	→	S	= (1/2) ² = 0.250
Total								0.500	

The inbreeding coefficient of individual *S*, or F_s , would be $\frac{1}{2}$ (0.500), or 0.250, or 25 percent. We now proceed to calculate the inbreeding coefficient (F_x) of individual *X*. Only one pathway is involved, and this is

$$X \leftarrow S \xleftarrow{1} D \rightarrow X = (1/2)^1, \text{ or } 0.50.$$

Since individual *S*, which is the common ancestor, is inbred, we must use the complete formula as given earlier. The computations then are $F_x = \frac{1}{2} [0.50(1.25)] = \frac{1}{2} (0.625)$, or 0.3125. Thus, individual *X* is 31.25 percent inbred.

COEFFICIENTS OF RELATIONSHIP

The coefficient of relationship between two individuals is an expression of the probability that they possess duplicate genes, because of their common line of descent, over and above those found in the base population. It is evident that an increase in inbreeding causes the relationship of individuals within an inbred line to increase. On the other hand, it is possible for two different

inbred lines to be inbred the same amount but still not be related. For example, individuals in an Angus line might be inbred 25 percent and in a Hereford line a similar amount. They do not have duplicate genes in common because of common descent, although they do possess some of the same genes because they belong to the same species.

RELATIONSHIP COEFFICIENTS BETWEEN COLLATERAL RELATIVES

Methods of calculating relationships are very similar to those used for calculating inbreeding coefficients, and arrow diagrams are of value in this respect. The formula is as follows:

$$R_{xy} = \frac{\sum [(1/2)^n (1+F_a)]}{\sqrt{(1+F_x)(1+F_y)}}$$

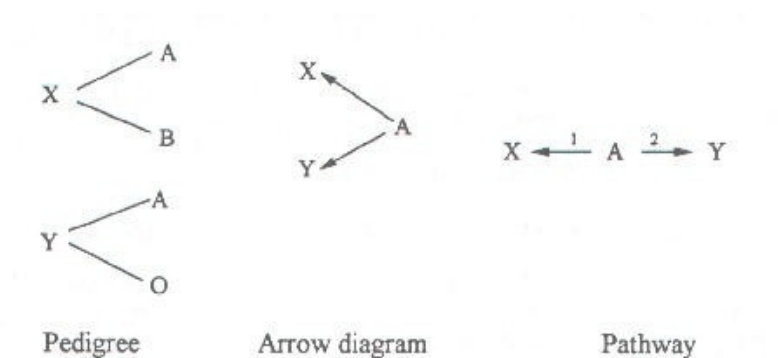
where

- R_{xy} is the relationship coefficient between animals X and Y ,
- Σ is the Greek symbol meaning to sum or add,
- n is the number of arrows connecting individual X and Y through the common ancestor for each path,
- F_x is the inbreeding coefficient of animal X ,
- F_y is the inbreeding coefficient of animal Y ,
- F_a is the inbreeding coefficient of the common ancestor.

If individuals X and Y and their common ancestor are not inbred, the formula becomes:

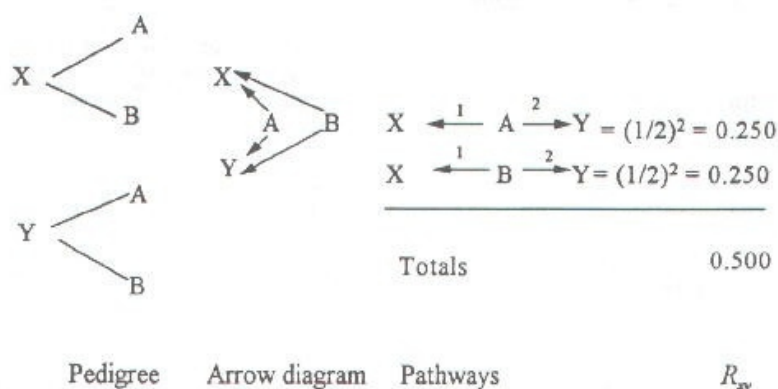
$$R_{xy} = \Sigma [(1/2)^n].$$

The following is an example in which the relationship coefficient between half brothers and half sisters is calculated. In this example, we shall let individual X be the male and individual Y the female. Since none of the individuals involved are inbred, we can use the simple form of the formula for calculating the relationship coefficient.



The relationship coefficient between individuals X and Y , or R_{xy} , is $(\frac{1}{2})^2$, or 0.250. This means that these two individuals are related by about 25 percent, or they probably have an increase in this percentage of duplicate genes over that found in the base population.

The calculation of the relationship coefficient between full brothers and sisters is similar to the above example, except that there are two common ancestors in such a case, and there are two pathways of gene flow. The calculation of the coefficient of relationship is as follows:



The relationship coefficient for individual X and Y in this example is 0.50.

USE OF RELATED BULLS IN COMMERCIAL HERDS

At first thought, the idea of using related bulls in a commercial herd would seem to make good common sense; however, using related bulls will likely have far less impact than most ranchers might believe. Table 4 shows the genetic relationship of various bull groups and the resulting genetic variation shared within the bull battery. Phenotypic variation is a combination of genetic and environmental variation; thus, the heritability of the trait is important. Traits low environment. Table 4 includes unrelated bulls of the same breed being used for comparison because all cattle in a breed are somewhat related even if it is distant. Also for comparison is a scenario where one sire is used, perhaps via A.I. to sire the whole calf crop. Using the intermediate level of heritability = 40 percent, we see the relatively low impact of a full-brother bull battery on increasing genetic likeness.

Table 5 carries this comparison one step further to look at the potential impact on the phenotypic variation in calf crops sired by the various bull batteries. Again at the heritability of 40 percent, the impact of full-brothers, for example, on reducing variation is minimal (5 percent). Using one sire would be twice as effective (10 percent) as using a full-brother battery of bulls.

Table 6 examines an important but often ignored point about the genetic relationship being an "average" estimate. Depending on the number of gene pairs that affect the trait of interest, the standard deviation (amount of variation around the mean) tells us that, for example, not all full brothers share "exactly" 50 percent of their genes.

Table 4. Effect of Relationship on Variation in a Bull Battery

Bull Battery Relationship	Average Genetic Relationship	Percent Genetic Variation Shared Within the Bull Battery		
		*h ² =.20	h ² =.40	h ² =.60
Unrelated, Same Breed	.05	1	2	3
Half-Brothers	.25	5	10	15
³ / ₄ Brothers	.37	7	15	22
Full-Brothers	.50	10	20	30
One Sire	1.00	20	40	60

*h²=heritability of trait

Table 5. Effect of Bull Relationship on Calf Crop Variation

Bull Battery Relationship	Percent Reduction in Calf Crop Phenotypic Variation due to Bull Relationship		
	*h ² =.20	h ² =.40	h ² =.60
Unrelated, Same Breed	4	4	1
Half-Brothers	1	2	4
³ / ₄ -Brothers	2	4	6
Full-Brothers	3	5	8
One Sire	5	10	15

h²=heritability of trait

Table 6. Effect of Number of Gene Pairs on Standard Deviation of Genetic Relationship

Relationship	Average Genetic Relationship	Percent Standard Deviation of Genetic Relationship with Various Number of Gene Pairs			
		Gene Pairs = 9	25	49	81
Half-Brothers	.25	8	5	3.5	3
³ / ₄ -Brothers	.37	12	7	5	4
Full-Brothers	.50	17	10	7	5.5

Given 25 gene pairs affecting a trait, table 7 shows the amount of variation that would be expected in genetic relationship. Again using full-brothers as examples, we see that 68 percent (± 1 standard deviation) of such full-brothers would have a true genetic relationship between 40 percent and 60 percent. Also, smaller numbers of bulls would be even farther to the extreme ends of the normal distribution (Bell curve). Thus, while full-brothers have a genetic relationship

which "averages" 50 percent, there will be a small number which will share substantially more 80 percent) and others substantially less (20 percent) of a genetic relationship.

Table 7. Deviation from Average Genetic Relationship with 25 Gene Pairs

Relationship	Avg. Genetic Relationship	<u>Range in Genetic Relationship at 1, 2, or 3 Std Deviation</u>		
		± 1 Std Dev. (68%)	± 2 Std Dev. (95%)	± 3 Std Dev. (99%)
Half-Brothers	.25	20-30	15-35	10-40
¾-Brothers	.37	30-44	23-51	16-58
Full-Brothers	.50	40-60	30-70	20-80

A dramatic example of two full-brothers that likely have a low genetic relationship is presented in table 8.

Table 8. *Comparison of EPD's of Two Full-Sib Angus Bulls

Trait	TC Rancher		TC Stockman	
Birth wt.	-.4	(.99)	8.6	(.99)
Wean wt.	20	(.99)	42	(.99)
Milk	14	(.99)	9	(.99)
Yearling wt.	42	(.98)	82	(.99)
Marbling	+.48	(.63)	.17	(.25)
Scrotal Circ.	.23	(.99)	.93	(.99)

*Accuracies in parenthesis.

Table 9 is an example of variation that exists within half-sibs; in this case, all 66 sons of the Angus bull, Scotch Cap.

Table 9. EPD's for the Angus Bull, Scotch Cap and 66 Sons

Trait	Scotch Cap EPD's		<u>Range of Son's EPD's</u>	
			Low	High
Birth wt.	5.9	(.99)	.5	9.4
Wean wt.	35	(.99)	12	56
Milk	8	(.99)	2	24
Yearling wt.	68	(.99)	38	101
Marbling	+.43	(.97)	-.12	+.79
Scrotal Circ.	-.27	(.99)	-.53	+.78

If a rancher had used all 66 sons of Scotch Cap, on average, the result would have been predicted by Scotch Cap's EPD's but, like all bulls, Scotch Cap sires a distribution of individuals.

Seems to me the lesson to take home from all of this is that progeny proofs are still needed and that seedstock herds need to continue to use a mixture of "proven" sires and young sires. Commercial herds should pay particular attention to buying bulls that meet their specification regardless of their relationship and perhaps be wary of paying a premium for closely related bulls.