# Guidelines

## For Uniform Beef Improvement Programs

*Eighth Edition*

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*Guidelines* is a publication of the Beef Improvement Federation, Ronnie Silcox, Executive Director, Animal & Dairy Science Department, The University of Georgia, Athens, GA 30602.

www.beefimprovement.org

# CONTRIBUTORS

## Editor

William D. Hohenboken, Virginia Tech

## Chapter 1, Introduction

Ronnie Silcox, University of Georgia

## Chapter 2, Breeding Herd Evaluation

Bill Bowman, American Angus Association
Bruce Golden, Colorado State University
Lowell Gould, Red Angus Association of America
* Robert Hough, Red Angus Association of America
Kenda Ponder, Red Angus Association of America
Robert E. Williams, American International Charolais Association

## Chapter 3, Animal Evaluation

Denny Crews, Agriculture & Agri-Food Canada
Michael Dikeman, Kansas State University
* Sally L. Dolezal, Dolezal Enterprises
Twig W. Marston, Kansas State University
Larry W. Olson, Clemson University
Joe C. Paschal, Texas A&M University
Gene Rouse, Iowa State University
Bob Weaber, American Simmental Association
Robert E. Williams, American International Charolais Association
Doyle E. Wilson, Iowa State University

## Chapter 4, Biotechnology

Sue DeNise, Celera AgGen
Bridger Feuz, Celera AgGen
* Ronnie D. Green, Future Beef Operations
Tom Holm, Celera AgGen

**Chapter 5, National Cattle Evaluation**

Keith Bertrand, University of Georgia
* Larry Cundiff, Agricultural Research Service, USDA
Bruce Golden, Colorado State University
Stephen D. Kachman, University of Nebraska
Richard Quaas, Cornell University
Dale Van Vleck, University of Nebraska
Robert E. Williams, American International Charolais Association

**Chapter 6, Utilization**

* Darrh Bullock, University of Kentucky
Mark Enns, Colorado State University
Lowell Gould, Red Angus Association of America
Mike MacNeil, Agricultural Research Service, USDA
Gary P. Rupp, University of Nebraska

**Glossary**

John Hough, EPD International
* Ronnie Silcox, University of Georgia

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* Chapter Coordinator

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# CHAPTER 1 - INTRODUCTION

The Beef Improvement Federation was formed on February 1, 1968 to standardize programs and methodologies and to create greater awareness, acceptance and usage of beef cattle performance concepts. The purposes of BIF as expressed in its by-laws are:

Uniformity – To work for establishment of accurate and uniform procedures for measuring, recording and assessing data concerning the performance of beef cattle which may be used by participant organizations.

Development – To assist member organizations and/or their affiliates in developing their individual beef improvement and quality management programs consistent with the needs of their members and the common goals of such generally accepted record keeping programs.

Cooperation – To develop cooperation among all segments of the beef industry in the compilation and utilization of performance records to improve efficiency, profitability and sustainability of beef production.

Education – To encourage the Federation's member organizations to develop educational programs emphasizing the use and interpretation of performance data and quality management programs in improving the efficiency, profitability and sustainability of beef production.

Confidence – To develop the increased confidence of the beef industry in the economic potential available from performance measurement and assessment.

BIF is a federation comprised of member organizations that include:

Provincial, state and national beef cattle improvement associations and other organizations that sponsor beef cattle improvement.

Breed associations in the United States and Canada that are involved in performance programs.

Other organizations involved in beef improvement such as the National Cattlemen's Beef Association, National Association of Animal Breeders, and artificial insemination organizations.

Associate memberships are available to individuals or agencies interested in beef cattle performance.

The eighth edition of *Uniform Guidelines for Beef Improvement Programs* represents a legacy of work that spans over thirty-five years of cooperation among the various segments of the beef cattle industry. The first edition of *Guidelines* was published in

1970 and it was revised in 1972, 1976, 1981, 1986, 1990 and 1996. Committees established by the BIF Board of Directors develop recommendations based on scientific research results and industry experience. Through the years *Guidelines* has evolved as new information has become available. Contributing authors have updated, revised or added sections in this edition based on BIF committee recommendations.

*Guidelines* is published primarily to assist member organization in the development and operation of performance programs for their members. The objectives of this publication are to outline standard procedures for measuring, recording and using beef cattle performance data and to facilitate greater uniformity in terminology and methodology in the beef industry. BIF shows no preference for, or discrimination against, any breed of cattle or industry organization.

*Guidelines* contains recommended procedures. BIF does not mandate or dictate that any organization follow all or any of these recommendations. There are situations where individual organizations can develop procedures that are more suitable for their members. For example, this publication contains BIF's weaning weight adjustment factors. Most associations, while adopting the BIF standard adjustment ages of 205 and 365, have used their extensive databases to develop adjustment procedures that are more appropriate for the specific breed. It is not the purpose of BIF to recommend one standard program for all segments of the industry or to discourage the development of better procedures when specific data are available.

*Guidelines* contains standard procedures based on research and industry experience. This publication is a valuable tool for use in designing and conducting beef cattle performance programs. Procedures outlined in this publication are used widely in the beef industry. Member organization are encouraged to use these standard procedures in all cases where they are appropriate. Use of these standards by an organization makes communication with members of other organizations and other industry segments easier and more accurate. Improving the accuracy of measuring, recording, evaluating and communicating should be the goal of any performance program.

# CHAPTER 2- BREEDING HERD EVALUATION

Efficient reproduction is necessary to profitable and efficient beef cattle production. Management and environment significantly affect male and female reproductive performance, but genetics also is important. Because reproductive traits generally are considered lowly heritable, little emphasis has traditionally been placed on them in genetic improvement programs. However, with the development of appropriate analytical methods that account for the unique properties of categorical traits, the industry now is able to produce useful genetic predictions for some reproductive traits. These advances highlight the need to develop reporting procedures that facilitate the collection of reproductive data.

Using inventory based methods of Whole Herd Reporting, breeders are encouraged to record male and female reproductive performance in their herds. This information can be used to monitor overall reproductive performance, identify genetic, environmental, and management areas in which to concentrate improvement efforts, assist in selection and culling decisions, and generate data for producing genetic predictions for reproductive traits.

## Beef Identification Systems

Unique identification (ID) of cattle within the nation's beef herd is required for accurate genetic evaluation and subsequent improvement by selection. In Appendix 2.1, a uniform coding system for identifying bull semen is described, and in Appendix 2.2, an international system assigning letters to calf birth years is presented. Both were developed by the National Association of Animal Breeders.

Two key elements in an identification system are 1) a premises ID to uniquely identify an operation or producer and 2) an individual identification for each animal on a premises.

Historically, a premises ID has been used to identify the participating rancher. This is commonly a member code that is assigned by a breed association in order that the member may conduct business with the association. A premises ID could further be used to identify location, management group, and contemporary group information.

The identification of individual animals within a particular ranch has several benefits. In seedstock production, the documentation of identity matched to a unique registration number that is tied to a pedigree is an essential component of merchandizing. Individual animal identification also is essential to ownership issues and effective management and documentation of data for performance recording and evaluation.

Individual ID on a registered animal is currently handled by utilizing a unique registration number assigned by a breed association, tied to a within-herd ID number administered

by the breeder. Traditionally, the within-herd number is a permanent number attached to the animal in the form of a tattoo or a brand. These numbers (tattoos or brands) may be unique to that ranch of origin, but duplicates may occur from operation to operation. Though not a foolproof system, when tied with other tools such as blood typing and DNA analysis, breeders have confidence in this identification method.

Technological advances will allow for new methods of identifying animals, especially as hardware cost decreases and infrastructure is developed. Radio frequency devices (e.g., tags and implants), biometric identification (e.g., retinal imaging), and DNA technologies all are receiving increased interest as a significant segment of identification programs. These technologies will allow for an efficient interface with electronic data transfer.

Today, a tremendous amount of interest is developing in a national identification system for all beef cattle. Basically all that is needed is to utilize the unique animal number recorded in an identified production unit. This would be a useful resource in issues including animal health and disease surveillance programs, building consumer confidence in food safety, enhancing international trade, increasing the efficiency of performance recording and national cattle evaluation, and finally for process and source verification associated with premium branded programs, alliances, and cooperatives. In the future, individual animal identification at the ranch of origin may become a necessary element of market accessibility for the commercial beef cattle producer.

BIF encourages data exchange and interfacing among data management and software companies. However, this raises many issues concerning the ownership and rights to use of the data. Reasonable data security is necessary and should be guaranteed before data are entered into a system. Written rules governing the sharing and transfer of information from one party to another should be agreed upon in advance between owners and others interested in the genetic improvement of beef cattle.

**Whole Herd Reporting**

Historically, many beef breed genetic evaluations were based on progeny weaned and/or registered and did not require that data be recorded from females that failed to reproduce or whose progeny were not registered. By contrast, inventory based Whole Herd Reporting (WHR) requires collection of annual production and performance records on all cattle within a herd.

The objective of WHR is to accumulate reproductive and performance data on all animals in a breed. It does not, however, seek to control which animals will be registered. That remains a decision of individual breeders. With WHR, performance records (or disposal codes) are required on all calves produced by each breeder, but whether any or all of those calves receive registration papers is the breeder's decision.

The following procedures and definitions are recommended for an efficient and effective inventory based Whole Herd Reporting system:

**Heifer exposure inventory.** To collect reproductive data on potential replacement heifers, a yearling heifer exposure inventory must be produced. This inventory would typically be sent in May for spring born heifers and in November for fall born heifers. On the inventory, producers should indicate breeding season start and end dates, individual exposure status, management group, and disposal information. Differences among management groups in post-yearling feeding, management, or mating practices should be recorded.

**Breeding herd inventory.** An annual inventory will be sent from the breed association to the breeder in December or early January for spring calving herds (January 1st – June 30th) and in June for fall calving herds (July 1st – December 31st). Breeders will identify those animals to be removed from inventory, add new animals of breeding age not found on the inventory report (e.g., new purchases), and return the completed inventory report to the breed association national office. These inventories will list all animals the breeder will be collecting production data on for the next 12 months.

The two-inventory system described above is recommended over single inventory systems that encompass both calving seasons. To identify which cattle will be expected to calve in the coming year, the two-inventory times, spring and fall, allow breeding inventories to be determined when cows are at the same relative stage of production – regardless of calving season. The inventory times, December to early January for spring calving and June for fall calving, are desirable because they follow weaning and pregnancy testing but precede the peak of the calving season. This allows both reproduction and production to be tracked in a uniform manner.

Breeders must complete and report herd inventories to the association on a set schedule. The objective is to record performance data from the entire herd. Therefore, the fee assessment structure must encourage complete and unbiased reporting of data. Charging assessment fees and/or penalties for non-reporting of data may differ from one association to the next. With inventory based WHR, consideration should be given to an inventory-based fee assessment system because: 1) it removes all financial disincentives to submitting complete production and performance data; 2) it encourages producers to maintain an accurate active inventory; and 3) it promotes the registration and transfer of seedstock destined for use in commercial production.

**Performance record requirements.** During each 12-month period, one of the following must be recorded for each cow on inventory:

- A calf record, including a disposal code for calves that die before weaning.
- A disposal code for the cow.
- A reason code for the cow's failure to produce a calf (e.g., open, embryo transfer program, moved to the next calving season).

Any cow on inventory will be inactivated unless one of these three items is reported. To ensure complete reporting, a reactivation fee should be required for reinstatement. It is recommended that the reinstatement fee be of sufficient magnitude to discourage selective reporting resulting from producers taking cows on and off breeding herd inventories. No reactivation fee should be imposed for bulls.

**No progeny report.** Prior to inactivation, breed associations should send producers a "no progeny" report listing all cows that have not met reporting requirements. This would allow the producer to complete reporting on any cattle that might have been missed.

**Sample annual schedule for Whole Herd Reporting.**

| Spring calving | Description | Fall calving |
|---|---|---|
| Dec. or Jan. 1 | Association sends out preliminary herd inventory. | June 1 |
| February | Member returns the inventory to the Association with all changes. | July |
| March 15 | Association sends “No Progeny Report” on females missing WHR requirements. | August 15 |
| April 15 | “No Progeny Report” due back to Association. | September 15 |
| May | Association runs inactivation program. | October |
| July | Association bills for annual WHR assessments based on herd inventory. | December |
| May 15 | Association sends preliminary inventory for heifer exposure information. | November 15 |
| August 1 | Association sends pre-listed weaning worksheets. | March 1 |
| August 15 | Member returns heifer exposure inventory with all exposure and disposal information. | February 15 |
| November | WHR assessment must be paid in full. | May |

**Data to be recorded on individual cows.**

Breeding dates. Record dates of artificial insemination services or of observed natural matings. For pasture matings, record natural service exposure dates (start and end of breeding season).

Pregnancy status. Prior to determining a breeding herd inventory for the coming year, cows should be pregnancy tested by trained personnel.

Calving date. Each calf's birth date is also its dam's date of calving. As a trait of the cow, this date may be used to calculate gestation length, days to rebreeding, and calving interval.

Calving difficulty or ease. Record with the following scores:

1 – No difficulty, no assistance
2 – Minor difficulty, some assistance
3 – Major difficulty, usually mechanical assistance
4 – Caesarian section or other surgery
5 – Abnormal presentation

From these data, expected progeny differences for calving ease-direct and calving ease-maternal can be calculated. Scores of 5 should be excluded from such evaluations, because abnormal presentations do not appear to be heritable either as a trait of the calf or of the dam.

Disposal codes: Birth to weaning.

1 – Stillborn/full term
2 – Died at birth - defect
3 – Died at birth - other
4 – Born alive, died before weaning - disease
5 – Born alive, died before weaning - other

Disposal codes: Weaning to two years of age.

10 – Died after weaning – disease
11 – Died after weaning – other
12 – Culled – feet and legs
13 – Culled – performance
14 – Culled – temperament
15 – Sold exposed – open
16 – Sold exposed – pregnant

Disposal codes: Mature cows and bulls.

30 – Sold – certificate not transferred (if seedstock)
31 – Culled – teat and udder
32 – Culled – feet and legs
33 – Culled – reproduction
34 – Culled – productivity/progeny performance

35 – Culled – temperament
36 – Culled – age
37 – Died – age
38 – Alive but not active in herd inventory (bulls only)

Reason codes. Reason codes should be utilized to document why a cow did not raise a natural calf.

50 – Open – missed calving opportunity
51 – ET program – donor dam
52 – ET program – recipient dam
53 – Moved to next calving season
54 – Aborted / premature

The following additional traits may be important in some breeds and circumstances:

Gestation length. The number of days between known breeding date (conception) and subsequent calving date. Cows with longer gestation periods have a shorter post-calving interval in which to conceive, if they are to stay on a yearly calving schedule.

Calving interval. The number of days between the most recent and the second-most-recent calving. Cows with consistently long calving intervals may fail to rebreed under fixed breeding season management. Evaluating the average calving interval in a herd may help the breeder identify areas for management improvement.

Lifetime average calving interval is calculated as the number of days between first and last calving divided by the number of calvings. It is a useful indicator of herd reproductive performance.

Cow weight. Each cow should be weighed at least once each year. Most breeders choose to weigh their cows at weaning time, thus fixing stage of production when the weights are collected. Body weight is an indicator of nutrient requirements and cost of production.

Cow body condition score. A cow's current body condition is determined by her maintenance requirement, her past nutrient intake, and her past production. Current body condition influences subsequent growth, reproduction, milk production, and life span. The relationships between body condition and these economically important traits brought about interest in a subjective scoring system for estimating cow condition.

Body condition scores are numerical values that reflect fatness or condition of the beef cow. Scores are subjectively assigned, ranging from 1 = Severely emaciated to 9 = Very obese. Body condition scoring is generally done by visual appraisal, but palpation of the animal's condition may be beneficial when it has a thick hair coat. Areas generally considered include the last half of the ribs, edge of the loin, spinous processes, and the hooks and pins, as well as tail-head, brisket, and shoulder area.

It is generally accepted that a change of one body condition score on this system equates to 75 to 80 lb. change in body weight on a 1050 to 1100 lb. cow.

**Body Condition Scoring System (BCS) for Beef Cattle**
(Richards et al., 1986. J. Anim. Sci. 62:300.)

| Condition | BCS | Description |
|---|---|---|
| **Thin** | | |
| | 1 | **Emaciated** – Cow is extremely emaciated with no palpable fat detectable over spinous processes, transverse processes, hip bones, or ribs. Tail-head and ribs project quite prominently. |
| | *2* | **Poor** – Cow still appears somewhat emaciated but tail-head and ribs are less prominent. Individual spinous processes are still rather sharp to the touch, but some tissue cover over dorsal portion of ribs. |
| | *3* | **Thin** – Ribs are still individually identifiable but not quite as sharp to the touch. There is obvious palpable fat along spine and over tail-head with some tissue cover over dorsal portion of ribs. |
| **Borderline** | | |
| | 4 | **Borderline** – Individual ribs are no longer visually obvious. The spinous processes can be identified individually on palpation but feel rounded rather than sharp. Some fat cover over ribs, transverse processes, and hip bones. |
| **Optimum/moderate** | | |
| | 5 | **Moderate** – Cow has generally good overall appearance. On palpation, fat cover over ribs feels spongy and areas on either side of tail-head now have palpable fat cover. |
| | *6* | **High moderate** – Firm pressure now needs to be applied to feel spinous processes. A high degree of fat is palpable over ribs and around tail-head. |

**Fat**

| | |
|---|---|
| *7* | **Good** – Cow appears fleshy and obviously carries considerable fat. Very spongy fat cover over ribs and around tail-head. In fact, "rounds" or "pones" beginning to be obvious. Some fat around vulva and in crotch. |
| *8* | **Fat** – Cow very fleshy and over-conditioned. Spinous processes almost impossible to palpate. Cow has large fat deposits over ribs and around tail-head, and below vulva. "Rounds" or "pones" are obvious. |
| *9* | **Extremely fat** – Cow obviously extremely wasty and patchy and looks blocky. Tail-head and hips buried in fatty tissue and "rounds" or "pones" of fat are protruding. Bone structure no longer visible and barely palpable. Animal's mobility might even be impaired by large fatty deposits. |

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## Measures of Sire or Herd Reproductive Efficiency

Several measures can be computed to describe reproductive efficiency (or inefficiency) of herds or bull mating groups. Identification of bull or overall herd problems will allow breeders to determine where action should be taken to improve reproduction in their herds. Measures to calculate are as follows:

Number of cows exposed. This is the number of cows exposed for either A.I. or natural service breeding, either in the present year's breeding season or in the past year's breeding season. This figure should be calculated on a bull-mating-group basis.

Percent diagnosed pregnant. This is a measure of the success of the breeding season. It is calculated as follows:

$$\text{Percent Diagnosed Pregnant} = \frac{\text{No. of cows diagnosed pregnant}}{\text{No. of cows exposed}} \times 100$$

Live calving percent. This is a measure of success of the breeding and calving seasons. It is calculated as follows:

$$\text{Live Calving Percent} = \frac{\text{No. of live calves}}{\text{(No. of cows exposed} - \text{No. of cows sold or died} + \text{No. of pregnant cows purchased)}} \times 100$$

Weaning percent. Also called “percent calf crop weaned”, this is a measure of overall reproductive efficiency. It is calculated as follows:

$$\text{Weaning Percent} = \frac{\text{No. of calves weaned} + \text{No. calves sold preweaning}}{(\text{No. cows exposed} - \text{No. cows sold or died} + \text{No. of pregnant cows purchased})} \times 100$$

**Genetic Predictions of Cow Reproductive Efficiency**

Traditional prediction methods to estimate breeding values for reproductive traits have not been widely employed. Many such traits are lowly heritable. Also, records necessary to compute the estimates have not been available from non-inventory based breed association improvement programs. New statistical estimation procedures (using threshold models to analyze calving success vs failure, for example) and inventory-based performance recording make it likely that EPDs for reproductive traits will become more readily available. As of this writing, several breed associations are publishing expected progeny differences for three fertility-related traits.

Heifer pregnancy. Heifer pregnancy EPDs estimate differences among individuals in the proportion of their daughters that will successfully conceive to calve at two years of age. Computation of these EPDs requires exposure data gathered by the previously described heifer exposure inventory and pregnancy diagnosis results.

Stayability. Stayability EPDs quantify expected differences among individuals in the probability of their daughters staying in the herd to at least six years of age. The primary reason for culling a cow before six years of age is her failure to become pregnant. Consequently, the stayability EPD is primarily a prediction of sustained female fertility. The unbiased prediction of this trait requires inventory data for females of each breeding age best gathered from WHR systems.

Calving ease. Calving ease EPDs are expressed as differences among individuals in the expected proportion of unassisted calvings. Calving ease direct EPDs estimate differences among individuals in the calving ease of their progeny. Alternatively, calving ease maternal EPDs reflect differences among individuals in the ease with which their daughters bear calves (i.e., calving ease as a trait of the dam). Estimates for both traits require collection of calving ease scores, as described earlier, and may utilize calf birth weight data as well.

# CHAPTER 3- ANIMAL EVALUATION

## Contemporary Grouping for Beef Cattle Genetic Evaluation

Every weight or measurement of an animal is an observation of its phenotype. However, not all of an animal's phenotypic superiority or inferiority for a trait is caused by genetics; part is due to environmental circumstances. A calf's superiority or inferiority for weaning weight, for example, is dependent not only upon its genetic potential for growth but also upon the environment that it experienced, including the herd, year, and season in which it was born, its weaning age, its access to nutrition, and the milk yield of its dam.

Proper genetic evaluation of beef cattle is complex. However, the basic initial premise is simple. Individual animals are evaluated based upon how well they performed in comparison to herd mates raised under comparable environmental conditions. In other words, how well did each animal perform within its contemporary group? Contemporary grouping in beef cattle genetic evaluations is an attempt to account for environmental effects so that remaining differences among animals more closely reflect heritable differences among them. A contemporary group is defined as a group of cattle that are of the same breed composition and sex, are similar in age, and have been raised under the same management conditions. More simply put, a contemporary group is a group of animals that have had an equal opportunity to perform.

Breed registries generally define rules for effective contemporary grouping according to breed composition, herd, sex, season, and the age range between the oldest and youngest calf within the group. After proper consideration of these factors, producers must still account for other management and environmental effects. For example, parts of the herd exposed to different levels of nutrition should be assigned to distinct contemporary groups, as should calves whose performance has been compromised by ill health or injury.

In theory, contemporary grouping is easy, but the application of contemporary grouping in real life can present many challenging decisions. A common error in building contemporary groups is breeders not assigning enough groupings to accommodate calves that have received unequal treatment. Just as damaging, some breeders create too many contemporary groups. Assignments should be as simple as possible while still accounting for major differences in management. A useful method to aid in contemporary grouping is to assign distinct contemporary group codes to animals that are exceptions to regular management practices. For example, calves that received preferential treatment (cattle being fitted for show, for example) should be placed within their own contemporary group.

It is important to note that contemporary groups never increase in size after the calving season is over. A contemporary group may, however, decrease in size. As calves get older, contemporary groups often will decrease in size due to culling, injury, sickness, death, or assignment of calves to different sub-groups that reflect different management

treatments. Contemporary groups cannot be recombined once animals have been defined to be members of separate groups.

Reporting data from all eligible animals is an important aspect of contemporary grouping that deserves special attention. Breeders may be tempted to economize by recording and registering only the better performing calves within their herd. They might also worry that recording data on poorer performing calves will reflect unfavorably on their herd. Both of these conclusions are incorrect. Unless inventory and performance data are submitted on every calf born in a herd, subsequent genetic evaluations will be based on less information and consequently will be less accurate than would otherwise have been possible.

Even worse, genetic evaluations may be biased. If only calves with good performance are reported, they may not get the credit they truly deserve. Suppose, for example, that a contemporary group of 10 bull calves had adjusted weaning weights as shown in the following table. Average weaning weight is 625 pounds. The lightest calf is 101 lb. below the group average (ratio of 84), while the heaviest calf is 117 lb. above the average (ratio of 119). Calf number 6 is 14 pounds above group average (ratio of 102). It is important to remember that National Cattle Evaluation programs focus on the deviation (or difference) of calf weights from the contemporary group average rather than each calf's adjusted weight.

Suppose now that the producer had reported only highest ranking 50% of calves for weaning weight. That group average would have been 675 lb. Within this new, highly selected contemporary group, the heaviest calf would have a deviation of only +67 lb and a ratio of only 110. Calf 6, close to average performance in the original contemporary group, would have a deviation of -36 pounds and a ratio of 84. When data are submitted only on selected calves, subsequent selection, culling, and merchandizing decisions will be flawed.

**Weaning Weight Contemporary Example**

| | | All Calves Reported | | Top Half Reported | |
|---|---|---|---|---|---|
| **Calf ID** | **Adj. 205d. Weight** | **Deviation** | **Ratio** | **Deviation** | **Ratio** |
| 1 | 524 | -101 | 84 | | |
| 2 | 562 | -63 | 90 | | |
| 3 | 578 | -47 | 93 | | |
| 4 | 605 | -20 | 97 | | |
| 5 | 606 | -19 | 97 | | |
| 6 | 639 | 14 | 102 | -36 | 95 |
| 7 | 643 | 18 | 103 | -32 | 95 |
| 8 | 655 | 30 | 105 | -20 | 97 |
| 9 | 694 | 69 | 111 | 19 | 103 |
| 10 | 742 | 117 | 119 | 67 | 110 |
| **Average Deviation and Ratio** | | **0** | **100** | **0** | **100** |
| **Average Weight** | | **625** | | **675** | |

Many national cattle evaluations now include the option to include performance data from Embryo Transfer (ET) calves, and special contemporary grouping criteria apply to them. Each ET calf is raised on a recipient dam rather than its own genetic dam. In this case, breed composition of the recipient dam become part of the contemporary group definition, thus separating ET calves into contemporary groups in which all recipient dams share the same breed composition. Each recipient dam should be assigned a permanent ID so that she can properly be accounted for in subsequent evaluations. Many sire evaluation programs, particularly those for carcass merit, also consider breed composition of dam as part of the contemporary group definition.

As discussed in Chapter 5, multi-breed genetic evaluations are becoming more common. It is not necessary to define contemporary groups based on breed composition in such evaluations. Rather, proportions of breed ancestry must accurately be documented for each individual and dam.

The livestock producer or herd manager is the only person that knows exactly how calves have been managed. It is their responsibility to ensure that contemporary groupings accurately reflect that knowledge. Common contemporary grouping criteria used in genetic evaluations for various traits are listed below. Helpful tips are then provided for breeders to use in creating contemporary groups.

**Contemporary grouping criteria for various traits.**

Calving Ease (Direct), Calving Ease (Maternal), and Birth Weight
1. Breeder-Herd Code
2. Year
3. Season (January-June, July-December)
4. Sex (Bull, Heifer)
5. Breed Composition
6. Birth Management Code
7. Service Type (Embryo Transfer Calves)

Weaning Weight
1. Birth Weight Contemporary Group Criteria
2. Management/Pasture Code
3. Date Weighed
4. Weaning Sex (Bull, Heifer, Steer)
5. Breed Composition
6. Service Type (Embryo Transfer Calves)

Yearling Weight and Frame Score
1. Weaning Weight Contemporary Group Criteria
2. Management/Feeding Unit Code
3. Date Weighed
4. Yearling Sex (Bull, Heifer, Steer)

Carcass Traits
1. Weaning or Yearling Weight Contemporary Group Criteria
2. Management/Pen/Feeding Unit
3. Days on Feed
4. Harvest Date
5. Grading Date
6. Carcass Sex (Bull, Heifer, Steer)
7. Date on Feed
8. Breed of Dam

Ultrasound Body Composition Traits
1. Weaning or Yearling Weight Contemporary Group Criteria
2. Management/Feeding Unit Code
3. Date Scanned
4. Sex (Bull, Heifer, Steer)

Heifer Pregnancy
1. Yearling Weight Contemporary Group Criteria
2. Heifer Pregnancy Management Code
3. Breeding Season Start and End Dates
4. Exposure
5. Breeding Pasture and/or Sire Effect

Mature Cow Weight, Height, and Body Condition Score
1. Breeder-Herd Code
2. Year
3. Date Measured
4. Age at Measurement (Years)
5. Breed Composition
6. Birth Management Code

Stayability
1. Breeder-Herd Code
2. Birth Year
3. Code of the Breeder-Herd in which the Cow Produced a Calf
4. Breed Composition

Feed Efficiency
1. Weaning or Yearling Weight Contemporary Group Criteria
2. Feed Efficiency Management/Feeding Unit Code
3. Days on Feed (or Date on Feed)
4. Date Scanned or Harvested
5. Sex (Bull, Heifer, Steer)
6. Breed Composition

**A guide to contemporary grouping.**

1. Use group codes on registration application or performance data submission forms to assign calves to contemporary groups.

2. Use the group codes to put a sick or injured calf into a single animal contemporary group if the illness or injury affected the calf's performance.

3. Take weaning weights and measurements on all calves on the same day (when a majority of the calves are between 160 and 250 days of age), including as many calves in each contemporary group as legitimately possible.

4. Weigh all animals in a group before separating them, especially before separating show calves or bulls for a test station.

5. If the age spread of calves in greater than 90 days, choose two or more weigh dates, using as few as possible.

6. Have progeny from two or more sires in each contemporary group (although not necessary when using the animal model for genetic evaluation).

7. When calves are within an appropriate age range for each trait, record yearling weight, height, scrotal circumference, pelvic area, and ultrasound measurements on the same day.

8. If carcass data are to be collected on cull bulls, heifers, or steers, report weaning weights on all animals. These data allow selection of replacement females and bulls to be accounted for in genetic evaluations and help prevent bias in the predictions.

9. Do not weigh each calf individually as it reaches 205 days of age. Rather weigh each calf individually when calves in a group average approximately 205 days of age.

10. Do not include calves receiving special treatment (show, bull test, and sale) in the same group with those that did not receive an equal opportunity to perform.

**Rate and Efficiency of Gain**

Growth rate and efficiency of gain are of major economic importance to the beef industry. Growth rate has a direct effect on net return and is positively correlated with efficiency of gain, weight, and value of retail product. Efficiency of gain has a direct effect on cost of production and net return. Selection response for preweaning and postweaning growth is influenced by how records are processed with respect to sex of animal and age of dam and upon proper assignment of each animal to a contemporary group, as discussed above. Procedures recommended in this chapter are based upon research and experience tempered by the need for cost-effectiveness and practicality. They will help to improve the rate of response to selection.

**Birth weight.** Calf birth weight in relation to dam weight is a good indicator of calving difficulty. If calving difficulty is a problem in the herd, selection of breeding animals for lighter birth weight may be an effective strategy to improve direct calving ease. However, single trait selection for lighter birth weight or shorter gestation intervals may reduce calf viability and growth rate from birth to weaning.

Both sex of calf and age-of-dam influence birth weight of the calf. The factors for adjusting birth weights for differences caused by age-of-dam are given in Appendix 3.1. BIF recommends the use of additive rather than multiplicative age-of-dam adjustment factors for weaning weight, because research indicates that they are more appropriate. Birth and weaning weight adjustments for age-of-dam can differ from one breed to another. Some breed associations have developed adjustments using their own data. These should be substituted for the BIF standard whenever possible. All breed associations are encouraged to develop their own age-of-dam adjustment factors for birth and weaning weight.

Adj. Birth Wt. = Birth Wt. + Age-of-Dam Adj.

BIF age-of-dam categories are listed below:

**Classification of Age-of-Dam**

| Age-of-Dam Range (days) | Age-of-Dam (years) |
|---|---|
| Less than 1,004 | 2 |
| 1,004 to 1,338 | 3 |
| 1,339 to 1,703 | 4 |
| 1,704 to 3,561 | 5 to 9 |
| 3,562 to 3,926 | 10 |
| 3,927 to 4,292 | 11 |
| 4,293 to 4,657 | 12 |
| More than 4,657 | 13 |

Season of birth also has an important influence on birth weight. Research indicates that summer- and fall-born calves have lighter birth weights than spring-born calves. Adjusted birth weight ratios calculated within season/sex contemporary group can be

used to compare calves from the same herd born in different seasons. It is recommended that adjusted birth weight ratio be computed as follows:

$$\text{Adj. Birth Wt. Ratio} = \frac{\text{Individual Adj. Birth Wt.}}{\text{Group Average Adj. Birth Wt.}} \times 100$$

**Weaning weight.** Weaning weights are used to evaluate differences in growth potential of calves and the milking ability of dams. In order to evaluate differences in weaning weights, individual calf records must be adjusted to a standard basis. It is recommended that weaning weights be standardized to 205 days-of-age and a mature age-of-dam basis. Weaning weights should be taken when a contemporary group of calves averages about 205 days of age. Adjusted weaning weights should be calculated for calves within an age range of 160 to 250 days of age. Records on calves weaned outside this range should be given a special management code and handled as a separate management group. They should not be adjusted for age of dam, because appropriate correction factors are not available.

Adjusted 205-day weaning weight is computed on the basis of average daily gain from birth to weaning, using the formula:

$$\text{Adj. 205-Day Wean Wt.} = \frac{\text{Wean Wt.} - \text{Birth Wt.}}{\text{Weaning Age}} \times 205 + \text{Birth Wt} + \text{Age-of-Dam Adj.}$$

If actual birth weight is not available, the appropriate standard birth weight designated by the respective breed association for the sire breed of calf may be used (see Appendix 3.1).

Individual animal records for adjusted 205-day weaning weight and adjusted 205-day weaning weight ratio should be calculated and reported separately for bulls, steers and heifers. The ratio should be calculated with the following formula.

$$\text{Adj. 205-Day Weaning Wt. Ratio} = \frac{\text{Individual Adj. 205 Weaning Wt.}}{\text{Group Average Adj. 205 Weaning Wt.}} \times 100$$

Adjusted 205-day weaning weight ratios document each animal's percentage deviation from the average of its contemporaries and are useful in ranking individuals within each sex for making selections. For weight ratios to be of value, contemporaries should be herd mates, similar in age, and raised under the same management and environmental conditions.

**Yearling weight (365, 452 or 550 days).** Yearling weight at 365 days or long yearling weight at 452 or 550 days is an important trait, because it has a high heritability and substantial genetic association with efficiency of gain and yield of trimmed, boneless retail beef.

Yearling weight should be adjusted to a standard animal age and age-of-dam. Adjusted yearling weights should be calculated and reported separately for each age/sex/management contemporary group. In on-farm tests, the postweaning period should start on the date weaning weights are obtained with actual weaning weight as the initial or on-test weight.

Adjusted 365-day yearling weights should be used for animals that received a high energy diet during the postweaning gain period. The following formula should be used to calculate adjusted 365-day yearling weight:

$$\text{Adj. 365-day Yrlg. Wt.} = \frac{\text{Final Wt} - \text{Weaning Wt}}{\text{No. of Days Between Wts.}} \times 160 + \text{205-day Adj. Weaning Wt.}$$

The period between weaning weight and final weight should be at least 160 days. The recommended age range for adjusted 365-day yearling weight is 320 to 410 days with the average age for each sex-management group at least 365 days. The number of days between weaning and final weight should be the same for all animals within the same contemporary group.

Adjusted 452-day yearling weights should be used for animals developed more slowly on diets with moderate energy levels. Animals should be at least 400 days of age when final weights are taken, and the contemporary group should average at least 452 days of age. The following formula should be used to calculate adjusted 452-day yearling weight:

$$\text{Adj. 452-day Yrlg. Wt.} = \frac{\text{Final Wt} - \text{Weaning Wt}}{\text{No. of Days Between Wts.}} \times 247 + \text{205-day Adj. Weaning Wt.}$$

Adjusted 550-day yearling weights should be used for animals developed on low energy levels of nutrition. Animals should be at least 500 days of age when final weights are taken, and the contemporary group should average at least 550 days of age. The following formula should be used to calculate adjusted 550-day yearling weight:

$$\text{Adj. 550-day Yrlg. Wt.} = \frac{\text{Final Wt} - \text{Weaning Wt}}{\text{No. of Days Between Wts.}} \times 345 + \text{205-day Adj. Weaning Wt.}$$

Regardless of level of nutrition and formula used to calculate adjusted yearling weight, yearling weight ratios should only be computed within weaning/sex/management contemporary groups.

Frequently in on farm testing, only the heavier calves in a weaning sex-management contemporary group are retained for a postweaning gain test. When this occurs, the yearling weight ratios of the calves in the postweaning contemporary group can be biased downwards, compared to what they would have been if the entire (unselected) weaning contemporary group had been tested. Research has indicated that if 25%,

50%, or 75% of the lightest calves were culled at weaning, the yearling weight ratio of the typical surviving calf would be underestimated by 3, 6, and 9 %, respectively.

The following formula is recommended for calculating the corrected adjusted yearling weight ratio of on farm tested animals to eliminate the bias due to culling of lower weight calves at weaning:

$$\text{Corrected Adj. Yearling Weight Ratio} = \frac{W + P}{W_u + P_s} \times 100$$

- W = adjusted 205-day weight of the calf
- P = the postweaning gain of the calf, calculated as 160-, 247- or 345-days x postweaning average daily gain
- $W_u$ = the average 205-day adjusted weaning weight of all calves in the calf's weaning contemporary group
- $P_s$ = the average postweaning gain of all calves in the calf's postweaning contemporary group.

**Postweaning feed efficiency.** To evaluate cattle for feed efficiency, estimates of individual feed consumption and gain must be available over the same time interval. For more information on testing procedures, see the "Central Testing" section of this chapter.

Choice of interval of evaluation or the end point for a postweaning gain test has an important influence on ranking of animals and breeding groups for feed efficiency. If the objective is to rank animals for efficiency of lean meat production, a time constant or weight constant endpoint is appropriate. If, however, the objective is to rank animals for efficiency of production of meat of a constant fat-to-lean ratio, then the endpoint for postweaning evaluation should be a constant carcass fat composition.

For either weight-constant (for example, 1,100 lb.) or time-constant (for example, 365 days) endpoints, faster-gaining cattle tend to have greater feed efficiency. These cattle are characterized by larger mature size, heavier carcasses, a higher percentage of retail yield, a lower percentage of fat trim, and lower marbling scores. Variation in feed efficiency and the correlation between feed efficiency and growth rate is maximized in weight-constant intervals (for example, 500 to 1,100 lb.). Faster growing cattle tend to require less feed per unit of gain as in weight-constant intervals, because they are on feed fewer days and thus require less feed for maintenance.

The ranking of animals for feed efficiency in a time-constant interval is positively correlated with feed efficiency ranking in a weight-constant interval. Faster gaining cattle tend to be more efficient in a time-constant interval. However, the variation in feed efficiency and its association with growth rate are reduced, because larger, faster-gaining animals are heavier throughout the time-constant test and therefore require more feed for maintenance. BIF recommends that feed consumption per unit of gain (feed/gain) evaluated in time-constant intervals be adjusted for differences in

maintenance requirement by a ratio of test group average metabolic weight ($W^{0.75}$) to individual metabolic weight ($W_i^{0.75}$) (or pen averages, if tests are on pens of animals), as follows:

Adj. Feed Efficiency = ($W^{0.75}$ / $W_i^{0.75}$) x (Feed / Gain),

where W = Mid-test Weight = (Initial Weight + Final Weight) / 2.

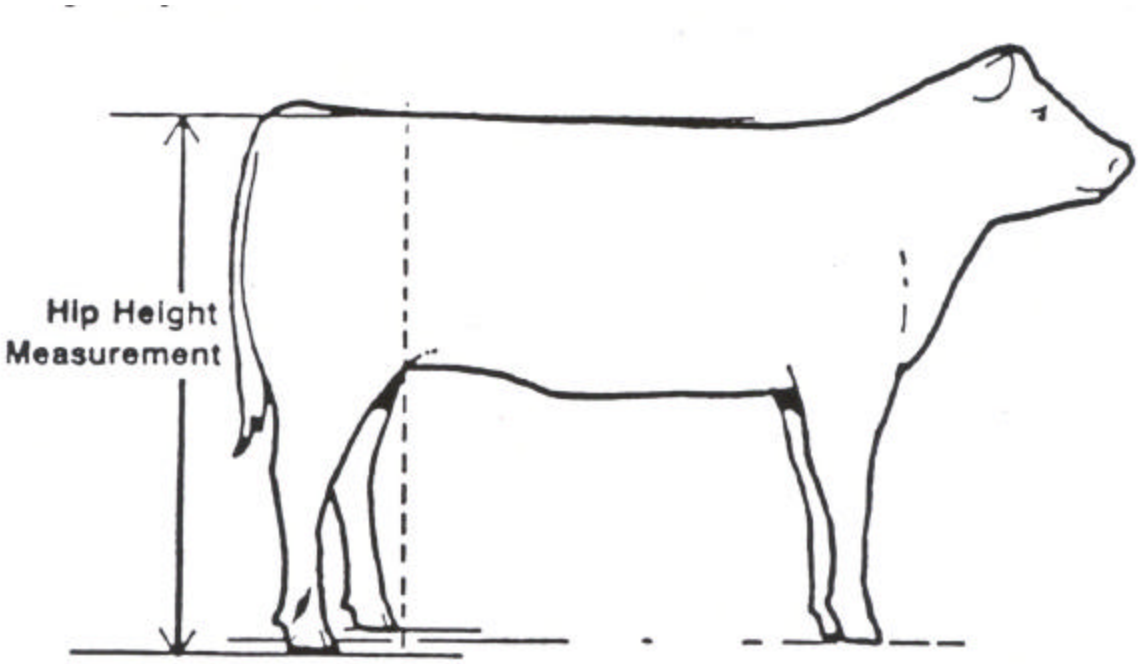
This procedure adjusts feed/gain of heavier than average groups downward and feed/gain of lighter than average groups upward. It also assumes maintenance requirements are proportional to weight raised to the 0.75 power. Results indicate that this adjusted feed efficiency closely approximates feed efficiency estimates evaluated in a weight-constant interval. Adjusted efficiency in a time-constant interval is usually easier to evaluate than feed/gain in weight-constant intervals**.**

Feed efficiency can also be evaluated to fatness endpoints such as a Small degree of marbling, which corresponds to the USDA Choice quality grade, or to a fat thickness of 0.35 inches. Animals with the greatest propensity to fatten are the most efficient when evaluated to a fatness endpoint because they require fewer days and less feed for maintenance to reach that point. It appears that feed efficiency to fatness endpoints is not strongly associated with growth rate or size.

**Frame score.** Hip height converted to frame score is a linear measurement that helps cattle producers evaluate lean-fat ratio potential of an individual animal in a performance program. No one frame size will be best for all feed resources, breeding systems, and markets. Large-framed animals tend to be heavier at all weights, leaner, and later maturing. Small framed animals tend to be lighter, fatter, and earlier maturing. Frame scores can be monitored to maintain body size, fatness level, and maturing rate within the optimum ranges dictated by the resources, breeding system, and market specifications of a herd.

Frame score is a convenient way of describing the skeletal size of cattle. With appropriate height/growth curves, most animals should maintain the same frame score throughout their life, regardless of when they are evaluated. However, frame scores may change for animals that mature earlier or later than average for their breed.

The recommended site for hip height measurement is a point directly over the hooks. This measurement should be adjusted to a weaning age-endpoint of 205 days and to yearling age endpoints of 365, 452 or 550 days. The same age range guidelines as for weaning and yearling weights should be used. It is recommended that the actual hip height and adjusted hip height be printed in national cattle evaluations rather than the height ratio.




**Height Measurement**

The following tables give current estimates of cattle height, along with adjustment equations for bulls and heifers. Values for steers are not available; however, bull height estimates may be used as approximations for steers.

## Hip Heights (inches) and Frame Scores for 5-21 Month-Old Bulls

| Age (months) | Frame Score | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 |
| 5 | 33.5 | 35.5 | 37.5 | 39.5 | 41.6 | 43.6 | 45.6 | 47.7 | 49.7 |
| 6 | 34.8 | 36.8 | 38.8 | 40.8 | 42.9 | 44.9 | 46.9 | 48.9 | 51.0 |
| 7 | 36.0 | 38.0 | 40.0 | 42.1 | 44.1 | 46.1 | 48.1 | 50.1 | 52.2 |
| 8 | 37.2 | 39.2 | 41.2 | 43.2 | 45.2 | 47.2 | 49.3 | 51.3 | 53.3 |
| 9 | 38.2 | 40.2 | 42.3 | 44.3 | 46.3 | 48.3 | 50.3 | 52.3 | 54.3 |
| 10 | 39.2 | 41.2 | 43.3 | 45.3 | 47.3 | 49.3 | 51.3 | 53.3 | 55.3 |
| 11 | 40.2 | 42.2 | 44.2 | 56.2 | 48.2 | 50.2 | 52.2 | 54.2 | 56.2 |
| 12 | 41.0 | 43.0 | 45.0 | 47.0 | 49.0 | 51.0 | 53.0 | 55.0 | 57.0 |
| 13 | 41.8 | 43.8 | 45.8 | 47.8 | 49.8 | 51.8 | 53.8 | 55.8 | 57.7 |
| 14 | 42.5 | 44.5 | 46.5 | 48.5 | 50.4 | 52.4 | 54.4 | 56.4 | 58.4 |
| 15 | 43.1 | 45.1 | 47.1 | 49.1 | 51.1 | 53.0 | 55.0 | 57.0 | 59.0 |
| 16 | 43.6 | 45.6 | 47.6 | 49.6 | 51.6 | 53.6 | 55.6 | 57.5 | 59.5 |
| 17 | 44.1 | 46.1 | 48.1 | 50.1 | 52.0 | 54.0 | 56.0 | 58.0 | 60.0 |
| 18 | 44.5 | 46.5 | 48.5 | 50.5 | 52.4 | 54.4 | 56.4 | 58.4 | 60.3 |
| 19 | 44.9 | 46.8 | 48.8 | 50.8 | 52.7 | 54.7 | 56.7 | 58.7 | 60.6 |
| 20 | 45.1 | 47.1 | 49.1 | 51.0 | 53.0 | 55.0 | 56.9 | 58.9 | 60.9 |
| 21 | 45.3 | 47.3 | 49.2 | 51.2 | 53.2 | 55.1 | 57.1 | 59.1 | 61.0 |

Frame Score = -11.548 + (0.4878 x Ht) – (0.0289 x Age) + (0.00001947 x $Age^2$) + (0.0000334 x Ht x Age), where Age = days of age.

## Hip Heights (inches) and Frame Scores for Mature Bulls

| Age (months) | Frame Score | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 |
| 24 | 46.4 | 48.3 | 50.3 | 52.3 | 53.9 | 56.0 | 58.0 | 60.0 | 52.0 | 64.0 | 66.0 |
| 30 | 47.3 | 49.3 | 51.3 | 53.2 | 54.9 | 57.0 | 59.0 | 61.0 | 63.0 | 65.0 | 67.0 |
| 36 | 48.0 | 50.0 | 51.9 | 53.8 | 55.5 | 57.5 | 59.5 | 61.5 | 63.5 | 65.5 | 67.4 |
| 48 | 48.5 | 50.4 | 52.3 | 54.1 | 55.9 | 58.0 | 60.0 | 62.0 | 63.9 | 65.8 | 67.7 |

## Hip Heights (inches) and Frame Scores for 5 - 21 Month-Old Heifers

| Age | Frame Score | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| (months) | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 |
| 5 | 33.1 | 35.1 | 37.2 | 39.3 | 41.3 | 43.4 | 45.5 | 47.5 | 49.6 |
| 6 | 34.1 | 36.2 | 38.2 | 40.3 | 42.3 | 44.4 | 46.5 | 48.5 | 50.6 |
| 7 | 35.1 | 37.1 | 39.2 | 41.2 | 43.3 | 45.3 | 47.4 | 49.4 | 51.5 |
| 8 | 36.0 | 38.0 | 40.1 | 42.1 | 44.1 | 46.2 | 48.2 | 50.2 | 52.3 |
| 9 | 36.8 | 38.9 | 40.9 | 42.9 | 44.9 | 47.0 | 49.0 | 51.0 | 53.0 |
| 10 | 37.6 | 39.6 | 41.6 | 43.7 | 45.7 | 47.7 | 49.7 | 51.7 | 53.8 |
| 11 | 38.3 | 40.3 | 42.3 | 44.3 | 46.4 | 48.4 | 50.4 | 52.4 | 54.4 |
| 12 | 39.0 | 41.0 | 43.0 | 45.0 | 47.0 | 49.0 | 51.0 | 53.0 | 55.0 |
| 13 | 39.6 | 41.6 | 43.6 | 45.5 | 47.5 | 49.5 | 51.5 | 53.5 | 55.5 |
| 14 | 40.1 | 42.1 | 44.1 | 46.1 | 48.0 | 50.0 | 52.0 | 54.0 | 56.0 |
| 15 | 40.6 | 42.6 | 44.5 | 46.5 | 48.5 | 50.5 | 52.4 | 54.4 | 56.4 |
| 16 | 41.0 | 43.0 | 44.9 | 46.9 | 48.9 | 50.8 | 52.8 | 54.8 | 56.7 |
| 17 | 41.4 | 43.3 | 45.3 | 47.2 | 49.2 | 51.1 | 53.1 | 55.1 | 57.0 |
| 18 | 41.7 | 43.6 | 45.6 | 47.5 | 49.5 | 51.4 | 53.4 | 55.3 | 57.3 |
| 19 | 41.9 | 43.9 | 45.8 | 47.7 | 49.7 | 51.6 | 53.6 | 55.5 | 57.4 |
| 20 | 42.1 | 44.1 | 46.0 | 47.9 | 49.8 | 51.8 | 53.7 | 55.6 | 57.6 |
| 21 | 42.3 | 44.2 | 56.1 | 48.0 | 50.0 | 51.9 | 53.8 | 55.7 | 57.7 |

Frame Score = -11.7086 + (0.4723 x Ht) – (0.0239 x Age) + (0.0000146 x $Age^2$) + (0.0000759 x Ht x Age), where Age = days of age.

## Hip Heights (inches) and Frame Scores for Mature Cows

| Age | Frame Score | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| (months) | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 |
| 24 | 43.1 | 45.0 | 46.9 | 48.8 | 50.7 | 52.5 | 54.5 | 56.4 | 58.2 | 60.1 | 62.0 |
| 30 | 43.8 | 45.8 | 47.5 | 49.4 | 51.3 | 53.1 | 55.1 | 57.0 | 58.9 | 60.8 | 62.5 |
| 36 | 44.2 | 46.1 | 48.0 | 49.8 | 51.8 | 53.6 | 55.5 | 57.2 | 59.2 | 61.0 | 62.8 |
| 48 | 44.6 | 46.5 | 48.2 | 50.0 | 52.0 | 53.9 | 55.8 | 57.5 | 59.4 | 61.2 | 63.0 |

**Most probable producing ability (MPPA).** In commercial herds, it is recommended that MPPA be included on produce-of-dam summaries to rank cows for productivity based on adjusted 205-day weaning weight ratios of their progeny. This allows a fair comparison among cows of different ages and with different numbers of calf records. MPPA is computed by the following formula:

$$MPPA = 100 + \frac{N \times 0.4}{1 + [(N - 1) \times 0.4]} \times (C - 100)$$

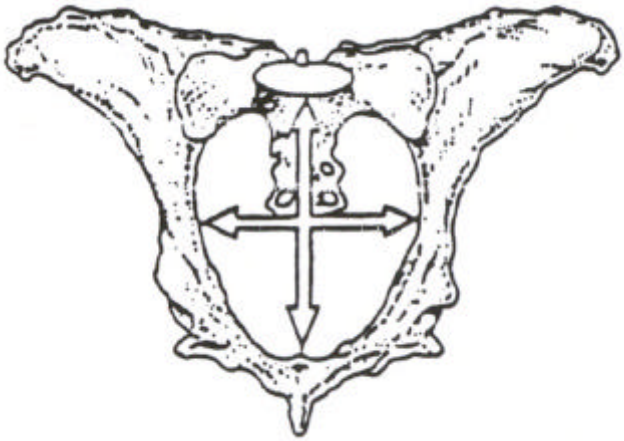
N = No. of calves included in the cow's average
C = Average weaning weight ratio for all calves the cow has produced
0.4 = Repeatability for weaning weight ratio

**Yearling pelvic area.** Most calving difficulty or dystocia occurs in two-year-old, first-calf heifers. Research indicates that disproportion between calf size (birth weight) and size of the female birth canal (pelvic area) is a major contributor to calving difficulty. As a result, producers may use yearling pelvic measurements as a culling tool to reduce the potential incidence and severity of calving difficulty among first-calf heifers in their herds.

Pelvic measurements, as shown below, should be taken between 320 and 410 days of age. Estimated pelvic area is the product of vertical and horizontal measurements. To evaluate yearling bulls and heifers, it is adjusted to 365 days of age according to the following formulas:

Bull Adj. 365-Day Pelvic Area = Actual Pelvic Area ($cm^2$) + [0.25 x (365-Age in days)]

Heifer Adj. 365-Day Pelvic Area = Actual Pelvic Area ($cm^2$) + [0.27 x (365-Age in days)]



**Pelvic Measurements**

**Yearling scrotal circumference.** A bull's yearling scrotal circumference provides an indication of his ability to produce sperm and is related to his own age at puberty and that of his daughters. The measurement should be taken at the largest diameter of the scrotum. A flexible measuring tape should be placed snugly around the scrotum after the testicles have been positioned beside each other in the scrotum. Actual scrotal circumference (YSC) in centimeters, the bull's age in days, and BIF (see following table) or other adjustment factors are used in the following formula to calculate adjusted 365-day yearling scrotal circumference:

Adj. 365-Day Yearling Scrotal Circumference = YSC + [(365 – Age) x Age Adj. Factor].

Several breed associations have developed their own age adjustment factors from the data collected through their performance records programs. Some breeds have also developed age-of-dam adjustment factors for yearling scrotal circumference. Whenever possible, the breed association adjustments should be used rather than the BIF adjustments.

## Age Adjustment Factors for Scrotal Circumference

| Breed | Adjustment |
|---|---|
| Angus | 0.0374 |
| Red Angus | 0.0324 |
| Brangus | 0.0708 |
| Charolais | 0.0505 |
| Gelbvieh | 0.0505 |
| Hereford | 0.0425 |
| Polled Hereford | 0.0305 |
| Limousin | 0.0590 |
| Salers | 0.0574 |
| Simmental | 0.0543 |

Geske, J.M., R.R. Schalles, and K.O. Zoellner. 1995. Yearling scrotal circumference prediction equation and age adjustment factors for various breeds of beef bulls. Ag. Exp. Sta., Kansas State Univ. Rep. of Progress 727:99.

**Behavioral traits**. Important behaviors to beef cattle production include reactions to processing through a squeeze chute, maternal instincts at calving, newborn calf vigor, bull serving capacity, and foraging behavior. Since these are distinctly different behaviors, different strategies are necessary to quantify differences among animals.

Among the most important of behavioral traits, temperament reflects the ease with which animals respond to handling, treatment, and routine management. Animals with disposition problems are a safety risk to handlers, themselves, and other animals in the herd. Disposition affects handling equipment requirements, operation liability exposure, beef quality assurance, and performance. The scoring system provided below is designed to subjectively evaluate differences in disposition when animals are processed

through the squeeze chute. Because an animal's behavior can be influenced by past experiences, scoring should be conducted at weaning or yearling ages. This will reduce the extent to which current behavior has been influenced by prior handling experiences.

Score 1 - Docile. Mild disposition. Gentle and easily handled. Stands and moves slowly during processing. Undisturbed, settled, somewhat dull. Does not pull on headgate when in chute. Exits chute calmly.

Score 2 - Restless. Quieter than average, but may be stubborn during processing. May try to back out of chute or pull back on headgate. Some flicking of tail. Exits chute promptly.

Score 3 - Nervous. Typical temperament is manageable, but nervous and impatient. A moderate amount of struggling, movement and tail flicking. Repeated pushing and pulling on headgate. Exits chute briskly.

Score 4 - Flighty (Wild). Jumpy and out of control, quivers and struggles violently. May bellow and froth at the mouth. Continuous tail flicking. Defecates and urinates during processing. Frantically runs fence line and may jump when penned individually. Exhibits long flight distance and exits chute wildly.

Score 5 - Aggressive. May be similar to Score 4, but with added aggressive behavior, fearfulness, extreme agitation, and continuous movement which may include jumping and bellowing while in chute. Exits chute frantically and may exhibit attack behavior when handled alone.

Score 6 - Very Aggressive. Extremely aggressive temperament. Thrashes about or attacks wildly when confined in small, tight places. Pronounced attack behavior.

**Beef Carcass Evaluation**

The ultimate goal of all beef cattle production systems is to efficiently produce a high yield of palatable beef. Meat quality and the quantity of edible portion are basic factors used to assess carcass merit. However, the relative emphasis to be placed on quality and quantity are subject to change with changing market demands.

The methods recommended for carcass evaluation were chosen because of their wide use and ease of application. For further information on carcass and meat evaluation systems, contact the nearest State Cooperative Extension Service, Animal Science Department, a breed association representative, the American Meat Science Association, or the American Society of Animal Science.

Not all beef producers need complete carcass data. Careful thought should be given to the specific information that will be useful. Increasing the amount of traits to be

recorded on large numbers of carcasses adds to the time required, costs, and likelihood of errors and may reduce a beef processor's interest in cooperating. Only trained personnel should be contracted to do this in the large processing plants.

**Product quality.** Quality refers to the overall appearance and palatability of the edible portion of the carcass. The 1997 USDA Quality Grades for young beef (A and B maturity) — Prime, Choice, Select, and Standard — are recommended as the basis for quality evaluation. The grades are determined by visual evaluation of maturity, marbling, color, firmness, and texture of lean. Generally, marbling is the main factor determining quality grade of young cattle.

**Maturity**, an estimation of the physiological age of the carcass, is determined by evaluating the size, shape, and ossification of the bones and cartilage and the color and texture of the lean. Physiological age may not be the same as the actual age of the animal in months and years; however, in most cases, they are roughly the same. There are five degrees of maturity — A, B, C, D, and E. Approximate chronological age groupings for "A" and "B" maturity carcasses and recommended numerical scores are shown in the following table:

**Numerical Scores and Maturity/Age Groupings**

| Maturity | Score | Age |
|---|---|---|
| A | 1.0 – 1.9 | 9 – 30 months |
| B | 2.0 – 2.9 | 30 – 42 months |

A numerical score of 1.5 would suggest that the carcass was in the middle of "A" maturity, while a score of 1.9 would be appropriate for a carcass at the upper end of "A" maturity but not quite into "B" maturity. Initial maturity score is determined by the skeletal characteristics with adjustments made according to characteristics of the lean tissue. However, lean characteristics cannot be used to adjust final maturity of the carcass more than one full maturity group.

**Marbling**, the flecks of fat in the lean, is the primary factor determining quality grade after maturity has been determined. Marbling is evaluated visually in the ribeye muscle, which is exposed between the $12^{th}$ and $13^{th}$ ribs. Marbling contributes to meat tenderness and is also associated with the palatability traits of juiciness and flavor. There are nine degrees of marbling, ranging from Practically Devoid to Abundant. It is recommended that marbling be given a decimalized numerical score corresponding to the relative development within that degree. For example, a Small-20 equates to a numerical score of 5.2 or 520 (5.2 × 100), as in the accompanying table.

Quality grades vary in the number of degrees of marbling within a grade. Although marbling is the primary determinant of quality grade, and numerical scores for grade can be determined from the following marbling table, final quality grade can be lowered for carcasses of B maturity, 'dark cutters', or those with soft, coarse textured lean.

Recommended descriptive and numerical marbling scores for quality grades of A maturity carcasses are given below. See Appendix 3.2 for a comparison of marbling standards for U. S. and Canadian carcass grades.

**Numerical Scores**

| Quality Grade* | Marbling | Score |
|---|---|---|
| Prime | Abundant | 10.0 – 10.9 |
| Prime | Moderately abundant | 9.0 – 9.9 |
| Prime | Slightly abundant | 8.0 – 8.9 |
| Choice | Moderate | 7.0 – 7.9 |
| Choice | Modest | 6.0 – 6.9 |
| Choice | Small | 5.0 – 5.9 |
| Select | Slight | 4.0 – 4.9 |
| Standard | Traces | 3.0 – 3.9 |
| Standard | Practically devoid | 2.0 – 2.9 |

Relationships between marbling scores and intramuscular fat percentages are shown below:

**Marbling and Intramuscular Fat**

| Marbling Score | Intramuscular Fat, % |
|---|---|
| Slightly Abundant | 10.13 |
| Moderate | 7.25 |
| Modest | 6.72 |
| Small | 5.04 |
| Slight | 3.83 |
| Traces | 2.76 |

It is recommended that a representative of the USDA Agriculture Marketing Service or a highly trained person be used to assess quality grade factors when collecting carcass data.

**Color** of the ribeye is used as an indicator of maturity or physiological age. The eye appeal of beef at the retail counter is highly dependent on desirable color. Dark cutters are carcasses that produce lean tissue that is dark red to almost black and often result from cattle that have been stressed prior to slaughter. Meat from dark cutting carcasses is safe to eat and its palatability is not seriously affected. However, the color reduces consumer acceptability and lowers carcass value dramatically.

**Firmness of lean** refers to the relative firmness or softness of the ribeye.

**Texture of lean** refers to the apparent fineness or coarseness of muscle bundles within the ribeye.

Recommended numerical scores and descriptions for color, firmness, and texture of lean are as follows:

| Scores for Lean Tissue | | | |
|---|---|---|---|
| Score | Color | Firmness | Texture |
| 7 | Light cherry red | Very firm | Very fine |
| 6 | Cherry red | Firm | Fine |
| 5 | Slightly dark red | Moderately firm | Moderately fine |
| 4 | Moderately dark red | Slightly soft | Slightly fine |
| 3 | Dark red | Soft | Slightly coarse |
| 2 | Very dark red | Very soft | Coarse |
| 1 | Black | Extremely soft | Very coarse |

More direct measures of palatability than quality grade include Warner-Bratzler shear tests for tenderness assessment, and trained sensory panel evaluation for tenderness, flavor, and juiciness. However, cost and availability will restrict usage of these methods.

**Quantity of retail product** is the amount of salable meat the carcass will yield. Two alternatives are suggested for evaluating differences in yield of salable meat:

- USDA Yield Grade (an estimate of the relative proportion of closely trimmed, boneless retail cuts from the round, loin, rib, and chuck), or
- Total percentage of retail product based on closely trimmed (no more than 0.25 in. surface fat), mostly boneless cuts, and a standardized fat content (perhaps 20 %) for ground beef.

Dikeman et al. (1996, J. Anim. Sci. 76:1604-1612) developed an equation that uses traits in the USDA Yield Grade system to predict percentage of total retail product trimmed to zero (0.0) in. of surface fat, as follows ($R^2 = 0.54$):

% Total Retail Product = 65.59 – (9.93 × Adj. fat thickness, in.)
– (1.29 × Kidney knob, %)
+ (1.23 × Ribeye area, sq. in.)
– (0.013 × Hot carcass wt., lb.)

If cattle are slaughtered at a plant that uses hot fat trimming, the following equation by Apple et al. (1991, J. Anim. Sci. 69:4845-4857) can be used ($R^2 = 0.75$):

% Total Retail Product = 78.95 – (0.005 × Hot carcass wt., lb.)
– (1.56 × Hot fat trim, %)
+ (0.516 × Ribeye area, sq. in.)
– (1.14 × Marbling score: 4.0 to 4.9 = slight, etc.)

**USDA yield grade** can be expressed in whole numbers from one to five or in tenths of a grade. Expressing yield grade in tenths of a grade is desirable in making

comparisons, although in retail marketing, decimals are dropped. Yield grades are calculated by the following formula:

Yield Grade = 2.50 + (2.5 × Adj. fat thickness, in.)
+ (0.2 × Kidney, pelvic, and heart fat, %)
+ (0.0038 × Hot carcass wt., lb.)
– (0.32 × Ribeye area, sq. in.)

**Adjusted fat thickness** is an estimate of external fat, which is the most important factor in determining retail yield. It is measured at the 12$^{th}$ rib, perpendicular to the outside fat at a point three-fourths of the length of the ribeye muscle from the backbone. This measurement often is adjusted to reflect unusual fat distribution of the carcass. As external fat increases, the percentage of retail product decreases.

**Estimated percentage of kidney, pelvic, and heart fat (KPH)** estimates fat in the kidney knob, pelvic, and heart areas as a percentage of carcass weight. As KPH fat increases, the percentage of retail product from the carcass decreases.

**Ribeye area** is an indicator of muscling. The longissimus or ribeye muscle is measured at the 12$^{th}$ rib by using a grid or a ribeye tracing that is measured with a compensating polar planimeter or image analysis system. As ribeye area increases, retail product yield increases.

**Hot carcass weight** is recorded as the carcass leaves the slaughter floor. Generally, as animals increase in weight, the percentage of retail product decreases because of increased fat deposition.

## Guidelines for Structured Sire Evaluation to Determine Carcass Merit

Both seedstock and commercial cattle breeders must be concerned about the genetic merit of cattle that they produce. Major beef processors are entering into programs of buying cattle and selling meat products based on carcass specifications, so there is little doubt that seedstock producers must be in a position to produce animals with predictable carcass merit.

Recent advances in technology have allowed national cattle evaluation for birth weight/calving ease, growth, and maternal value from field data, but it still is essential to follow structured guidelines for seedstock carcass evaluation.

### Specific testing guidelines.

1. Reference ('Tie') sires. To obtain a fair genetic evaluation of a sire for carcass merit, the testing scheme begins with the breeding season. Under ideal circumstances, enough females should be randomly mated to allow for the evaluation of at least 25 progeny to be slaughtered by a test sire and a combined

total of at least 20 progeny to be slaughtered by two reference sires. The use of reference sires is recommended and serves to tie together new information and to connect new data to existing databases in order that comparative genetic values may be calculated. A reference sire is defined as any sire that has been previously evaluated for carcass merit.

2. Contemporary grouping. A contemporary test group is a set of cattle of the same sex that have been raised together and have received equal treatment up to the point of slaughter. All progeny within a contemporary group should be born within a 90-day period, and male calves must be castrated prior to 150 days of age. A contemporary group up to the time of weaning would be subdivided if some go on feed as calves and others are started on feed as yearlings, and if the cattle are then split into two or more slaughter groups. The minimum contemporary group size is 20 steer or heifer calves in a slaughter group, to include both test- and reference-sire calves. Birth date, identification of sire and dam, breed of dam (or breed proportions in crossbred dams), and age of dam should be recorded on all progeny.

3. Sex of calf and selection. All test and reference sire progeny (male and female) may be utilized in the evaluation. Sex of calf will be used in the definition of the contemporary group, meaning that data from heifers will not be adjusted to a steer equivalent. All non-replacement individuals may enter the program, such as non-replacements heifers. However, when herd replacements are removed from contemporary groups, it is suggested that weaning and yearling weights on all progeny in the initial growth contemporary group be recorded and provided to the recording organization. This is necessary in an attempt to correct for bias in the data due to selection. Weaning weights must be taken on all cattle between 160 and 280 days, and yearling weights must be taken between 320 and 440 days, or according to established procedures.

**Finishing and slaughter guidelines.**

1. Cattle should be slaughtered when the test group averages 0.35 – 0.40 in. backfat, or prior to 18 months of age, or a maximum of 1,350 lb. live weight, whichever occurs first. This corresponds to at least 100 days on feed for yearling cattle and 180 days on feed for calves. Depending on the weight ranges of the cattle as they go on feed and the number of cattle involved, two to three slaughter dates may be required. Contemporary group identification will include slaughter date; therefore, each slaughter group must include both test- and reference-sire progeny.

2. All progeny can go on feed directly after weaning, or they may be backgrounded and placed on feed after the yearling weight is taken.

3. To facilitate record keeping, cattle should be grouped for finishing at centralized locations within a state or geographic region. The location of the feedlot should

be in close proximity to a processing plant that has agreed to participate in carcass data collection. All health and feeding practices must be consistent with normal industry standards and FDA regulations.

**Test herd alternatives.**

1. The objective of all sire evaluation programs is to arrive at unbiased predictions of genetic merit for each sire tested. However, there are economic constraints that preclude this from always being completely possible. The genetic makeup and identification of the test herd is one area where it is not always possible to have an ideal testing environment. The following test-herd alternatives are listed from the most to the least desirable:

    a. Registered cows – no selection of replacement heifers and all males castrated.
    b. Commercial cows of the same breed as that of the sires to be tested.
    c. Crossbred cows or cows of another breed.
    d. Registered cows – replacement heifers are selected and steers are the culled bulls.

    Alternative (a) is consistent with current National Cattle Evaluation procedures, whereas alternatives (b), (c), and (d) would be strictly for genetic evaluation of sires for carcass traits.

2. Regardless of the test herd alternative used, sires must be assigned mates at random, i.e., there can be no preferential matings. In each contemporary group, all test and reference sires should be evenly represented.

**Data collection.**

1. In addition to growth data, standard carcass data will include:

    a. Slaughter date
    b. Hot carcass weight
    c. Marbling score and maturity score
    d. Fat thickness
    e. Ribeye area
    f. Percent pelvic, heart and kidney fat
    g. Length of chill (24 / 48 hours).

2. Date on feed, time on feed, and feeding program must be documented for each feeding test.

**Standardized Warner-Bratzler Shear Force Procedures for Sire Evaluation**

An initiative to standardize the protocol for Warner-Bratzler shear force determinations was identified at the National Beef Tenderness Plan conference in April, 1994. The purpose of this protocol is to facilitate consistent collection of Warner-Bratzler shear force determinations across institutions for comparative evaluation. These data can be used in progeny testing and in the development of carcass EPDs to improve meat tenderness. Any institution abiding by these guidelines can be certified to collect Warner-Bratzler shear force determinations for the beef industry.

**Collection of rib or shortloin cuts.** Not all beef processing plants allow rib or shortloin sections to be collected for determination of Warner-Bratzler shear force or for trained sensory panel evaluations. When possible, a two-inch section of the rib at the 12$^{th}$ rib region of the forequarter or two-inch section of the loin at the 13$^{th}$ rib region of the hindquarter should be obtained. However, this reduces the value of the remaining rib or loin to the processor, requires skilled personnel and much planning and coordination to achieve, and may not be an option for most producers. A second option would be to retrieve the entire wholesale rib or shortloin. Although beef processors are more likely to agree to this option, it requires more personnel and time to follow carcasses through fabrication. This frequently occurs on the day after carcasses are graded. There would be a significant initial investment to purchase the rib or shortloin, and the remainder would then be fabricated and merchandized in order to recuperate most of the initial investment. This would have to be done in a state or federally inspected facility. Either option requires beef processor cooperation, extra labor, and financial investment.

**Steak preparation**. Consistent sample collection and preparation are critical to obtaining repeatable and consistent Warner-Bratzler shear force determinations. The following procedures should be utilized when preparing steaks for shear force determinations:

1. Steaks 1.0 in. thick should be removed from the longissimus lumborum between the 12$^{th}$ rib and the 5$^{th}$ lumbar vertebrae of the carcass. Only one steak per animal is needed for evaluation. Steaks should be trimmed free of fat and bone. The rib or shortloin sections or the 1.0 inch steaks should be vacuum packaged and aged 14 days at 32 to 35°F prior to shear force determinations. A cutting guide should be used to cut unfrozen muscle into steaks, and a band saw should be used for frozen product in order to obtain uniformly thick steaks.

2. Steaks can either be cooked and sheared after the 14 day aging period, or they should be frozen at day 14 postmortem to -20°F or lower until they can be evaluated at a later date. Steaks should be frozen individually without stacking to ensure uniform, rapid freezing.

3. Internal temperature of the sample at the initiation of cooking can affect tenderness; thus, this variable must be standardized. Frozen samples should be

thawed at 35 to 40°F until an internal temperature of 35 to 40°F is reached. For 1.0 in. thick steaks, this requires approximately 24 to 36 hours. During thawing, avoid steak overlap and stacking to improve the consistency of the thawing process. Steaks should not be thawed at room temperature.

4. To increase consistency among institutions, steaks must be broiled on an electric broiler or oven-broiled. Steaks should be cooked to an internal temperature of 104°F, turned and cooked to a final internal temperature of 160°F (removed from the heat at 160°F). For consistency in cooking, do not cook more than four steaks at a time on a Farberware grill. When oven broiling, it is important to minimize the number of times and length of time the door is opened.

5. Temperature will be monitored with iron- or copper-constantan thermocouple wires with diameters less than 0.02 cm., and special limits or error of less than 2°F. A metal probe, such as a 15-guage spinal needle with a stylet (plunger), should be used to insert the thermocouple into the geometric center of the steak. Push the probe (with the stylet inside) completely through the meat, remove the stylet and thread the thermocouple wire into the needle through the pointed end. Remove the needle and pull the end of the thermocouple back into the center of the meat. Temperature can be monitored using a potentiometer or hand-held temperature recorder.

**Core preparation.**

1. Cooling temperature and time after cooking until cores are taken should be standardized. Two methods of cooling are recommended. Either chill samples overnight at 35 to 40°F before coring (wrap with plastic wrap to prevent dehydration) or cool samples to room temperature prior to coring. Cooling samples to room temperature should be conducted so that a uniform temperature is obtained throughout the steak before coring. At least a 4-hour cooling time is required for 1.0 in.-thick steaks. Both procedures will remove variation in shear force caused by variation in core temperature at shearing. Steaks should not be held in foil or other types of containers prior to cooling because these processes affect cooling rates. Laboratories should intermittently check to assure that the cooling method they are using is providing an even temperature throughout the steak prior to coring. Adjusting the cooling or chilling time should be implemented if the previous time intervals are not long enough.

2. Cores should be 1.27 cm. (0.50 in.) in diameter and removed parallel to the longitudinal orientation of the muscle fibers so that the shearing action is perpendicular to the longitudinal orientation of the muscle fibers. Cores can be obtained using a hand-held coring device or an automated coring device. Coring devices must be in good condition and sharp; otherwise core diameters will vary, causing an increase in variation of shear values.

3. Six to eight cores should be obtained from each steak. Cores that are not uniform in diameter, that have obvious connective tissue defects, or that otherwise would not be representative of the sample should be discarded. All values obtained should be used for mean calculations, unless visual observation indicates that a value should be discarded (e.g., a piece of connective tissue).

4. Shear each core once in the center to avoid the hardening that occurs toward the outside of the sample during cooking.

5. Shearing must be done by using a Warner-Bratzler shear machine or an automated testing machine such as an Instron with a Warner-Bratzler shear attachment with the crosshead speed set at 20 – 25 cm./min.

**Data to record.** In addition to the Warner-Bratzler shear values, frozen weight, thawed weight, thawed temperature, time-on, time-off, final temperature, and cooked weight should be collected on each steak. Warner-Bratzler shear force typically is reported as the mean of all core values.

**Certification of Warner-Bratzler shear force.** Certification of institutions that perform Warner-Bratzler shear force measurement is important in determining that the above procedures are being adhered to and to ensure that consistent, reliable data on meat tenderness are being collected. Certification requires that individuals performing Warner-Bratzler shear force tests at each institution maintain a shear force repeatability of 0.65 or higher on duplicate steaks from the same animal.

In the absence of a standard material, cooked meat from the same animal must serve as the standard. All shear force values will be adjusted to a MARC-shear-force equivalent. Institutions interested in certification should obtain four steaks from each of 15 animals, arrange to send one pair of steaks to MARC personnel for shear force determination, and analyze the second pair of steaks themselves. The coefficient of variation of shear force for the certification steaks must range between 20% and 35%, because the amount of variation affects repeatability. MARC personnel will calculate a repeatability value and an adjustment factor, if needed, to equate each institution's mean shear force to a MARC basis.

For more information, or to make arrangements to send meat for certification, contact:

Sensory Lab Manager
USDA-ARS US Meat Animal Research Center
Spur 18 D
Clay Center, NE 68933-0166

**Ultrasound Scanning to Measure Body Composition**

Real-time ultrasound technology has advanced to the state whereby accurate measurements of several body composition traits can be made on live beef animals. These traits include 12th-13th rib fat thickness, rump fat thickness, ribeye area, and intramuscular fat percentage (marbling). Each of these traits is significant in the determination of quality and red meat yield for individual animals, and each is at least moderately heritable.

Accurate collection and interpretation of ultrasound images is critical to the successful application of ultrasound. Accuracy is highly dependent upon ultrasound technician skill. Only certified, highly skilled technicians should be retained for the collection and interpretation of images. Many breed associations publish a list of technicians that have demonstrated proficiency and have received certification status. They also have additional guidelines for ultrasound that are breed specific, especially for age of cattle to scan and adjustment factors for adjusting data to a common age endpoint.

**Ribeye area.** Accurate live animal, ultrasound estimation of ribeye area is dependent on three major items: clear and distinct medial and lateral end borders, not being over any portion of 12th or 13th rib, and good transducer-animal contact. The presence of well-defined intercostal muscles under the longissimus dorsi is an indication that the transducer is properly aligned directly between the 12th and 13th ribs for this measurement. Ribeye area is measured by placing the ultrasound transducer at position 2 in the accompanying figure.

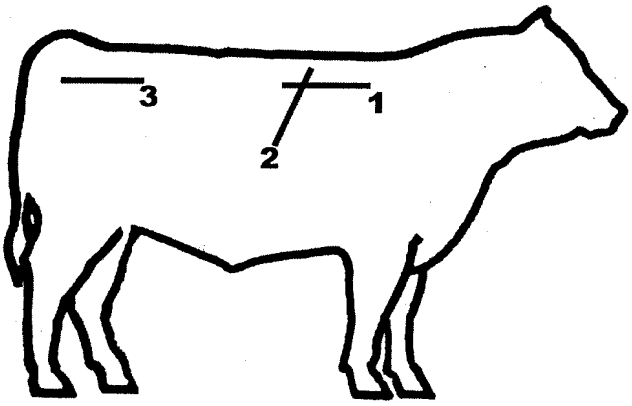



**Image Scanning Locations on the Live Animal**

**12th-13th rib fat thickness.** The ultrasound rib fat thickness measurement can be made from the same image (position 2) used to estimate ribeye area. Fat thickness at the 12th-13th rib is measured at a point three fourths of the distance from the medial end of the longissimus dorsi muscle (12-13th rib interface) and perpendicular to the surface of the hanging ribbed carcass. Ultrasound scanning protocol requires the collection of an

image made between the 12th-13th ribs using a linear-array transducer and standoff guide that conforms to the curvature of the animal's back.

**Rump fat thickness.** Rump fat thickness is a fat depot that is highly related to 12th-13th rib fat thickness (genetic correlation exceeding .70). This measurement can be beneficial when scanning very lean animals such as yearling bulls and can be used to improve the overall accuracy of external fat estimation. To collect this image, the ultrasound transducer should be placed at position 3 in the above figure, which is aligned directly between the hooks and pins without a standoff guide.

**Percent intramuscular fat.** Percent intramuscular fat (% IMF) is a trait that is highly correlated with USDA Marbling Score. It is the most difficult of all ultrasound traits to measure accurately. Equipment calibration, animal preparation, electrical power signal noise, existence of atmospheric radio waves, and transducer-animal contact are some of the factors that can influence measurement accuracy. A minimum of four independent images should be collected and the resulting % IMF predictions averaged for this trait. The % IMF measurement is made from an image that is collected across the 11th-13th ribs (or 12th-13th ribs) at a lateral position from the animal's midline at a point three fourths of the distance from the medial end of the longissimus dorsi muscle (position 1 in the accompanying figure).

**When to scan seedstock**. Body composition measures determined from individual animal ultrasound images must be adjusted to a common endpoint for accurate genetic comparisons. The endpoint must have relevance to traits of economic importance in the carcass. Research has shown that yearling bulls and developing replacement heifers can be scanned at approximately 365 days of age to provide a good indication of how sibling steer and heifer mates will perform in the carcass. Each breed association has developed an age at scanning window that must be met in order for the data to be used in national cattle evaluation.

**When to scan feedlot cattle.** The endpoint for adjusting ultrasound measures in feedlot animals will vary by breed association ultrasound program. Generally, the scanning endpoint should be consistent with the association's carcass data collection program and associated endpoint. Endpoints might include:

(a) scanning all animals within a feedlot contemporary group when the group averages 0.35 inches of external fat thickness over the 12th-13th rib,
(b) scanning all animals when a contemporary group achieves some average designated age or average weight endpoint, or
(c) scanning all animals within a contemporary group just prior to the time when the first animals within the group are to be harvested.

**Adjustment factors.** Adjusting individual animal ultrasound measures to a common endpoint allows for the fairest comparison among animals within a contemporary group. Factors such as an animal's age, age-of-dam, weight, and weight gain may affect its

ultrasound measures. Therefore, a scanning weight should be recorded within 7 days of when cattle are scanned.

Gut fill can have a significant impact on an animal's weight when compared to contemporaries, creating a biased measurement and comparison. Therefore, the scanning weight should be an empty body weight taken when the animal has been held off feed over night before scanning.

Many adjustment formulas may also use rate of gain to adjust ultrasound measurements to a common endpoint. It is recommended that an additional weight and date be recorded at weaning for seedstock animals being measured at one year of age, and for feedlot animals a weight and date should be recorded when animals go on feed.

**Contemporary groups.** The development of body composition EPDs requires that scanned animals be associated with a well-defined contemporary group. Animals of the same sex, reared and managed together up until the time of scanning form a contemporary group. Additionally, it is suggested that breeders define only calves that are within a 60-day age window as a contemporary group. Scanning contemporary group definition includes the following: herd code, weaning date or weaning lot date, weaning management group (pasture, creep, non-creep, etc.), scanning date or scanning lot date, and post-weaning management group designation. The lot date is used in lieu of actual measurement date when weaning or scanning of a contemporary group must occur over more than one consecutive day.

For animals scanned at a central test, the contemporary group definition for an animal must include its herd of origin and other birth and weaning contemporary group information.

National cattle evaluation requires that performance records be tied across contemporary groups or herds. The pedigree relationship matrix used in the prediction methodology allows for many indirect ties to be established. However, the best ties are made when sires have progeny represented across contemporary groups, herds, and years. All scanning contemporary groups must have at least two sires represented, and at least one of those sires should be used in another herd that is also participating in scanning for national cattle evaluation.

**Facilities and animal preparation**. It is the breeder's responsibility in most cases to insure that the cattle handling facilities for scanning are adequate for animal restraint and for safety of the animal handlers, ultrasound technician, and the cattle. A squeeze chute with fold-down side panels is required for scanning beef cattle. The chute should be located under a roof that can block direct sunlight and provide protection from rain or other inclement weather conditions. A clean and grounded power signal (110v) is required chute-side. It is best if the electrical circuit is a dedicated line to the chute, free from the interference of other electrical equipment such as motors.

Most ultrasound equipment does not operate efficiently and accurately when the ambient air temperature falls below 45°F. The breeder should make provisions to keep the facility heated in these situations.

Animals are to be clipped at the scanning sits to enhance contact between the transducer and wave-guide and the hide. Length of hair coat should be no more than ½ inches in the area to be scanned.

**Equipment**. Currently in the USA, most beef cattle scanning is done with an Aloka 500 V with a 17cm linear array 3.5 MHz transducer or with a Classic Scanner 200 with a 18 cm linear array 3.5 MHz transducer. The type of ultrasound equipment and software used to collect and interpret ultrasound images can have an impact on measurement accuracy.

**Image interpretation**. As in scanning, accurate interpretation of real-time ultrasound images for external fat thickness, ribeye area, and % IMF requires a high degree of skill by ultrasound technicians. Within the industry, there currently are two methods of processing images. First, technicians are solely responsible for the collection and subsequent interpretation of images. Second, a centralized processing facility may work with field technicians with the primary objective of interpreting images and reporting the data. Each method should strive to provide an accurate and timely assembly of data. There are programs currently recognized within the beef cattle industry that technicians can participate in to obtain training and certification in beef cattle scanning and interpretation.

**Technician and equipment proficiency.** The Beef Improvement Federation encourages the development and expansion of ultrasound proficiency testing programs. Strict protocol should be followed to insure fair and unbiased testing of technicians, equipment, and software used for the collection and interpretation of images. Technicians should certify with the same ultrasound equipment and interpretation software they would be using to commercially scan cattle in the field.

For certification proficiency testing, a technician should scan approximately 20 animals and then repeat scan the same animals in random order so that repeatability can be evaluated. Although additional statistics and stricter standards may be used for proficiency evaluation, the following requirements should be met.

| Trait | Standard Error of Prediction | Standard Error of Repeated Measures | Bias |
|---|---|---|---|
| Fat Thickness | $\leq$ 0.10 | $\leq$ 0.10 | $\leq$ 0.10 |
| Ribeye Area | $\leq$ 1.20 | $\leq$ 1.20 | $\leq$ 1.20 |
| % IMF | $\leq$ 1.20 | $\leq$ 1.10 | $\leq$.70 |

**Reporting of data.** It is recommended that scanning results (data) be electronically transferred, in a standard format, directly by the technician or centralized lab to the respective breed association. Data should include ranch name, membership number, address, and telephone number, technician name and telephone number, ultrasound equipment, and software used. Animal information should include the date measured, association registration number, individual herd identification number, date of birth, association number of sire and dam if registration is not available on the animal, sex, management codes, contemporary group codes, actual measurements for ribeye area, fat thickness, % IMF, rump fat, and weight.

**Archiving data and images.** Images and data should be archived in central locations at the discretion and direction of the breed association or cattle improvement association involved. This may be a valuable resource as new technology is developed.

## Central Bull Test Stations

Central bull test stations are facilities where bulls from different herds are assembled to evaluate performance under uniform conditions. Even under consistent conditions in a central test, however, not all pre-test environmental effects can be eliminated. In addition to their primary function of evaluating bulls for postweaning performance, test station programs educate purebred breeders and commercial cattlemen about the value and utilization of performance records and expected progeny differences. For purebred operations too small to support an on-farm test, they provide an opportunity to evaluate and market bulls and to advertise their programs. Test stations provide an opportunity for new breeders to introduce their breeding programs to potential customers.

**General procedures.** Although objectives and procedures may vary from station to station, the following procedures and policies are recommended for all types of central bull tests.

1. Bulls consigned to central tests should meet realistic qualifications for age, weaning performance, and soundness.
2. Calves should be 180–270 days of age at time of delivery to the test.
3. Calves within a test group should have a maximum age range of 90 days.
4. Ratios to relate individual to group performance should be calculated only within contemporary groups composed of animals of the same breed and similar age.
5. All consignors' herds should be enrolled in their respective breed association or state beef cattle improvement association performance program. Calves should complete the weaning phase of the performance recording program with their entire contemporary group.
6. Initial and final test weights to compute test average daily gain may be either full or shrunk weights. If full weights are utilized, initial and final weights should be an average of weights taken on two consecutive days to minimize fill effects. Otherwise, a single weight after a 12-hour shrink is adequate.

7. Nutritional programs should provide adequate levels of protein and energy to allow for expression of genetic differences in growth between bulls. Test station ration composition and analysis should be stated in the sale catalog.
8. Sire-group testing - a minimum five sons per sire - is more desirable than individual testing, because it provides more information to both breeders and prospective buyers.
9. All bulls sold in a central test station sale should be evaluated for structural soundness by competent personnel.
10. Yearling ultrasound and scrotal circumference measurements should be taken at the end of the test or on the first weigh day after the bulls average 365 days of age.
11. All bulls sold in a central test station sale should undergo a breeding soundness examination (Appendix 6.1) conducted by a qualified veterinarian or reproductive physiologist.
12. Expected progeny differences (EPDs) and their corresponding accuracies should be provided in test reports and sale catalogs for birth weight, weaning weight, yearling weight, maternal milk, and (if available) scrotal circumference, direct calving ease, maternal calving ease, and ultrasound carcass merit.
13. A table of breed average EPDs for non-parent bulls born in the same year as the bulls being tested should be included in the sale catalog for buyers' information.
14. Because of differences in environmental conditions and testing procedures. direct comparison of performance of animals tested at different stations, in different contemporary groups, or at different times is not valid.

**Processing of test data.** The following formulas are recommended for processing data from central bull tests. Breed association rather than BIF adjustment factors to adjust weaning weight and yearling scrotal circumference for age-of-dam should be used whenever possible.

1. ADG (average daily gain)
   ADG = (Final weight – Initial weight) / days on test
2. ADGR (average daily gain ratio)
   ADGR = (ADG / Breed-test group average ADG) x 100
3. WDA (weight per day of age)
   WDA = Final weight / Final age
4. WDAR (weight per day of age ratio)
   WDAR = (WDA / Breed-Test group average WDA) x 100
5. AYWT (adjusted 365- or 452-day yearling weight)
   AYWT = [(Final Weight – Birth Weight) / Final Age] x {365 or 452}
   + Birth Weight
   + Age-of-Dam Weaning Weight Adjustment

   An alternative equation that has the favorable effect of standardizing length of pre-test and on-test periods may be used:

   AYWT = [(Final Weight – Initial Weight) / Days on test] x {160 or 247}
   + Adj. 205-day Weaning Weight

6. AYWR (adjusted 365- or 452-day yearling weight ratio)
   AYWR = (AYWT / Breed-Test group average AYWT) x 100
7. AYSC (adjusted 365-day yearling scrotal circumference, cm)
   AYSC = YSC + [(365-Final Age) x Age Adjustment Factor]

**Full-feed central bull test programs.** The following procedures and policies are recommended for full-feed central bull tests:

1. Following delivery of the bulls to test station facilities, there should be a minimum pre-test adjustment period of 21 days.
2. The minimum length of the test should be 112 days.
3. Test rations with 60% to 70% TDN (total digestible nutrients) on an as-fed basis should be fed free-choice.
4. Because weight differences affect feed requirements for maintenance, efficiency of feed conversion should be expressed as pounds of feed (as-fed) per pound of gain adjusted to a common body weight.
5. To facilitate reproductive performance, full-fed, centrally tested bulls can benefit from a four to six week post-test period of increased exercise and reduced grain intake prior to cow herd exposure.

**Forage-based bull test programs.** Central tests can be used to evaluate the performance of bulls under grazing conditions similar to those used by commercial cow-calf producers in an area. Test gain is measured for a longer period because the bulls are on moderate rather than high levels of nutrition.

The following procedures are specifically recommended for forage bull tests:

1. A year-round grazing program on high quality forages is necessary for such tests to be feasible.
2. A backup forage supply of silage or hay is necessary, because environmental factors limit availability of continuous grazing for some portions of most years.
3. A minimum suggested test length is 168 days.
4. Because of this extended time for testing, a pre-test adjustment period of 14 or 21 days is optional. Bulls may begin the test immediately upon delivery to the station.
5. Because of their advancing age, bulls may fight and ride one another during part of forage central bull tests. Test managers and consignors should anticipate that some injuries will occur. The problem is most prevalent when the supply of grazing is inadequate and bulls are constantly hungry. These social problems may be minimized if bulls are provided a backup forage supply or limited supplemental feed.
6. If a test ration of 60-70% TDN (total digestible nutrients) on an as-fed basis is provided, it should be limit-fed.
7. BIF recommends that forage central bull test programs report and adjust yearling weight, yearling weight ratio, and yearling hip height to 452 days of age.

**Test station reports.** Test reports should be provided in a logically organized and clearly readable format. The following information should be included if available:

1. Test tag number
2. Pen number
3. Sire's name
4. Bull's tattoo/brand number
5. Horned, polled, scurred (HPS) status
6. Birth date (month-day-year)
7. Actual birth weight
8. Adjusted 205-day weaning weight
9. Adjusted 205-day weaning weight ratio
10. Number of weaning contemporaries – "ET" for embryo transplant calves
11. Birth weight EPD
12. Weaning weight EPD
13. Yearling weight EPD
14. Maternal milk EPD
15. Initial (on-test) weight
16. Final (off-test) age - days
17. Final (off-test) weight
18. ADG (average daily gain)
19. ADG Ratio
20. WDA (weight per day of age)
21. WDA Ratio
22. AYSC (adjusted 365-day yearling scrotal circumference) – cm.
23. AYWT (adjusted 365- or 452-day yearling weight)
24. AYWT Ratio
25. AYHT (adjusted 365- or 452-day yearling hip height)
26. AYFS (adjusted 365- or 452-day yearling frame score)
27. Feed conversion (lbs. feed / lb. gain) – adjusted to a common body weight
28. Adjusted 365-day yearling ultrasound ribeye area – sq. in.
29. Adjusted 365-day yearling ultrasound % intramuscular fat
30. Adjusted 365-day yearling ultrasound $12^{th}$ rib fat thickness – in.
31. Station Index

# CHAPTER 4 - BIOTECHNOLOGY

DNA technology has developed rapidly in the past decade and now has a variety of applications. For beef cattle genetic improvement, the primary areas of application are pedigree validation, parentage determination, and gene-based (genotypic) selection. Individual and parentage verification are now routine practices, while gene-based selection is in the early stages of development. This chapter describes current uses of DNA technology and provide an overview of applications currently under development.

## Types of DNA Markers

Analytical techniques to differentiate DNA of individuals or populations require genetic markers, which are defined as identifiable DNA segments that differ in nucleotide sequence from one individual to the next. Two types of markers may be used: microsatellites and single nucleotide polymorphisms (SNPs). Both create uniquely identifiable DNA patterns that may be used to follow the transmission of specific chromosomal regions from parents to progeny.

Microsatellite markers are segments of chromosomal DNA that include a variable number of repeated two to six nucleotide base sequences. Such markers are interspersed throughout the genome and are generally found in non-coding regions. These repetitive regions are subject to additions and subtractions in the number of tandem repeats of the basic two to six nucleotide segment, and this creates uniquely identifiable alleles at each site within the genome at which the particular microsatellite is found. Microsatellites routinely have been used in parentage analysis, because the multiple alleles generally found at each locus make them highly informative. They have provided the basis for individual and parentage identification in humans, dogs, cattle, and many other species. The approximately 2,100 microsatellite loci that have been identified and mapped in cattle are referenced at the following web address: (http://locus.jouy.inra.fr/cgi-bin/lgbc/mapping/bovmap/Bovmap/main.pl)

Single nucleotide polymorphisms are the other marker. As the name implies, they are a change (mutation) from the specific nucleotide originally present in a particular location in an individual to a different nucleotide at that same site and can be transmitted from parent to offspring, just like any other gene. Across evolutionary time, thousands of SNPs have been created by mutation such that they now can be found every 100 to 300 bases throughout the genome. Over 2.8 million SNPs have been placed in the human SNP database (http://www3.ncbi.nlm.nih.gov/SNP/), and a similar number are likely to exist in cattle. Because SNPs are widely distributed, it is likely that any gene of economic importance is located closely adjacent to several of them that can be used to mark its presence.

SNP markers promise to be increasingly useful in the future for developing high-resolution maps. They are becoming a popular marker because of their high throughput

capability and potentially low cost. With the availability of whole genome sequences, SNPs that are dispersed across all chromosomes have been identified, presenting important advantages as markers for genome analysis.

Some SNPs are located within the coding region of a gene and can affect the structure and function of a protein. This type of variation may be directly responsible for differences among individuals in phenotypic merit for economically important traits. Other SNPs occur either “upstream” or “downstream” of the coding region of a gene but may influence the regulation of gene expression. Others occur in locations that do not interfere with the structure or production of a protein. SNPs have the advantage that they are less likely to undergo a spontaneous mutation than microsatellites; thus they are inherited with greater stability.

**DNA Collection**

DNA is found in every nucleated cell in the body. It has been extracted from semen, muscle, fat, white blood cells found in blood and milk, skin, and epithelial cells collected from saliva. Minute amounts of tissue, such as a single drop of blood or several mucosal cells, are all that are required for routine DNA analysis. Common collection methods include a drop of blood blotted on a paper that is dried, covered, and stored at room temperature, ear tag systems that deposit a tissue sample in an enclosed container with bar code identification, and hair follicles. Techniques have been developed that allow for rapid release of DNA from cells and immediate analysis of the samples.

**Uses of DNA Technologies**

DNA-based technologies have been used for animal identification or source verification, parentage verification or identification, diagnosis of genetic diseases, genotyping for simply inherited traits, and marker-assisted selection. Animal identification and parentage verification have been used for a number of years and the techniques for analysis are well developed. Genotypes for some genetic diseases can be identified by DNA analysis, and many others are under study. Marker-assisted selection is still in the research and development phase but will likely become an important technology in the future.

Whether a particular use of DNA technology is practical, useful, and cost-effective in beef cattle improvement depends upon the individual operation and the role of the cattle producer (e.g., seedstock, multiplier, or commercial) and whether he/she will retain calf ownership or contribute to a partnership program like an alliance. Producers are encouraged to evaluate the potential benefits of the individual technologies and incorporate them when they are likely to improve profitability of an operation.

Animal identification and source verification are becoming increasingly important around the world. There are standard procedures that match specific marker genotypes from birth with those taken later in life or matching harvested product back to an original source. Either microsatellites or SNPs can be used effectively to compare DNA samples, and the probability can be calculated that the two samples are from the same source. DNA remains constant in the tissues of an animal throughout life; it cannot be altered. Thus, it is the ideal basis for animal identification.

DNA technology is commonly used for parentage verification and identification. Parentage verification provides pedigree assurance and has been used to guarantee the parentage of embryo transfer calves and of registered bulls used in AI programs. Breed associations have used this technology to guarantee the integrity of pedigree information and provide assurance to buyers. DNA samples from the sire, dam, and progeny are compared at a number of marker loci to determine the probability that the calf was in fact produced by a mating between its assumed parents

In many commercial enterprises, dams are matched to progeny at birth, but the sire is unknown. In such herds, parentage identification analysis assigns sires to calves by comparing the genotype of the progeny at a number of marker loci to genotypes of a panel of potential sires. Bulls are excluded until only one bull remains that has a genotype consistent with the genotype of the calf. To correctly match calves with sires, therefore, DNA samples must be included from all potential sires.

DNA typing can be used as a progeny testing tool by assigning calves to their individual sires based on inheritance of markers. For traits easily measured in the bull (like weaning and yearling weights and growth rate), this additional information may add little accuracy to the estimate of genetic merit of a sire. However, for those traits that cannot be measured directly on the bull (carcass or milk production traits for example), parentage verification could provide additional information for genetic evaluation. Marketing cattle through strategic alliances and retained ownership programs provide commercial cattle producers incentives for improving the genetic merit of bulls for postweaning traits. DNA parentage identification technology will allow producers to identify bulls not suited to their marketing or management program.

Blood-type markers traditionally have been used for parentage verification and are reliable for most parentage disputes. However, with only 12 blood-group systems available to determine the genetic profile of an individual animal, this method is limited in parentage disputes involving closely related individuals or in large mating groups. DNA markers provide a virtually unlimited number of genetic determinants that can be used to follow the transmission of specific chromosomal segments between parents and progeny. The International Society of Animal Genetics (ISAG) has identified a panel of markers recommended for this purpose and provides a laboratory certification program (guidelines available at http://www.wisc.edu/animalsci/isag/guidelines.html).

A parentage identification kit is available from Applied Biosystems that utilizes a panel of 11 ISAG microsatellite markers (StockMarks II), and Celera AgGen has developed a

10 microsatellite marker kit especially designed for high throughput analysis (AgGen Panel III). Using allele frequency data from 10 divergent breeds, simulation work was conducted to determine the power of these kits to correctly discriminate among potential parents of calves. When a potential and the actual parent were unrelated and the genotype of the other parent (e.g., the dam) was known, the probability always exceeded .99 that either kit would exclude the incorrect parent. When one parent (e.g., the dam) was not known and there was only one potential sire, probabilities of correct exclusion ranged from .95 to .99. These technologies thus provide a highly accurate method for identifying parentage across a wide array of breeds.

In the future, SNP markers could replace microsatellite markers for parentage identification if warranted by costs. Across existing cattle breeds, a panel of 70 to 100 SNP markers would be needed to assign parentage at the same level of discrimination as the StockMarks II or AgGen Panel III kits described above.

**Marker Assisted Selection**

Genetic markers can be used to identify transmission of specific genes from parents to progeny. In some cases, a marker will identify a change in DNA nucleotide sequence that causes a unique phenotype of interest. In such cases it can be used directly in selection decisions. Examples would be diagnostic tests for recessive, single-gene effects such as bovine leukocyte adhesion deficiency, double muscling, and the recessive allele responsible for red coat color. Many of these tests have been patented, so to use the test, a royalty must be paid to the owner of the patent. Such tests have been invaluable in identifying animals (carriers) that are heterozygous for recessive genes. When available, they are quicker and much more economical than a progeny testing program to identify carriers of the mutant gene.

In other cases, the marker will not be located physically within a gene of economic importance but will be close to it on the chromosome. Once a marker of this sort has been identified and validated, it can serve as an indicator for the presence or absence of a quantitative trait locus or QTL in an individual. (A QTL is defined as a gene having a measurable influence on the phenotype of a measured, usually economically important trait.) Marker-assisted selection may be used within a family that contains two or more alleles at such QTL, one preferred over the others. The genetic marker can be used to determine whether progeny are likely to have inherited the favorable form.

Marker-assisted selection requires a three-phase development and testing program. First, in a preliminary screening procedure locations of QTL within the genome must be identified, using widely distributed markers in a reference population of known family structure. In this initial screening, the impact of marker loci genotypes on phenotypes for the economically important trait also is estimated. (If the QTL accounts for little of the variation seen in the trait, it will not be cost effective to use the test in a selection program; traditional selection will be more cost effective.) QTL locations must then be refined by identifying flanking markers on each side of the QTL. These flanking markers

must be in close proximity to ensure high accuracy in identifying the presence of the favorable allele in candidates for selection. In the second phase, the presence and phenotypic impact of QTLs must be verified or validated in commercially relevant populations. Only after the location and effects of the QTL are validated can the third phase be undertaken, commercial application of marker assisted selection in the population at large.

SNP maps provide an opportunity to create a unique tool for identifying QTLs without relying on within family studies. Because SNPs are found in greater frequency than microsatellite markers, a map of SNP markers could be created of such a density that QTLs could be identified across a commercial population without its family structure being known. The QTLs could be identified directly in the population of interest, and all QTLs influencing a trait could be evaluated in a single analysis. These types of studies are called association studies and have been used to identify disease causing variations in humans.

SNP diagnostic markers may be used in the future to identify animals with genetic potentials appropriate to meet specific management requirements and market specifications. For example, if DNA analysis predicts that a group of animals has the genetic potential to achieve marbling standards for choice and prime beef, producers could manage them to develop high marbling and market them on a quality grid pricing program. Likewise, if a group of cattle had outstanding predicted genetic merit for lean meat production but low predicted genetic merit for propensity to marble, they could be aggressively implanted, fed fewer days, and marketed on a red-meat grid pricing system. In the past, breed or crossbred group has been the primary determinant for predicting feedlot performance, quality grade, and yield grade. Although breeds do differ for these traits, there also is substantial within breed variation. Genotyping animals as they enter the feedlot could help to sort them into the most profitable management and marketing groups.

In the future, producers are likely to have a multitude of genetic markers available to them. It remains to be seen how they will be used in genetic improvement programs. Markers may improve the accuracy of selection of individual animals when combined with classical methods of genetic evaluation, but the increase in accuracy may not be worth the cost. For easily measured and highly heritable traits, markers probably will not provide any economic advantage over traditional estimates of genetic merit. Even for traits that are not easily measured in the animal, unless there is a set of markers that accounts for a substantial portion of genetic differences, marker-assisted selection may not be predictive of overall genetic merit.

# CHAPTER 5 - NATIONAL CATTLE EVALUATION

The genetic prediction committee that produced this and contributed to other chapters of these Guidelines evolved out of the Beef Improvement Federation sire evaluation committee that was formed in 1968. The first guidelines for national sire evaluation were published in 1971. The speed of technology transfer through cooperation between the academic community and breed association leadership using the sire evaluation and genetic evaluation committees as forums to share experiences is unprecedented. Through the implementation of genetic evaluation programs, breed associations have produced Expected Progeny Differences that are economically important to the beef industry.

## Basic Considerations

The goal of the National Cattle Evaluation (NCE) program is to produce the best possible genetic predictions of breeding values on all animals available as breeding stock for traits of economic importance in commercial beef production. Breed associations are encouraged to develop these programs to provide the beef industry with information to enhance selection decisions in seedstock and commercial operations and to provide genetic information to facilitate use of crossbreeding systems in commercial beef production. A critical part of a sound national cattle evaluation program is the use of common sires, via artificial insemination, that produce progeny in many herds. The use of common or reference sires across herds to allow direct comparisons among animals provides the foundation for genetic evaluation programs.

The genetic values published from beef genetic evaluation programs and used by the industry are Expected Progeny Differences (EPDs). An EPD is a prediction, based on available data, of one-half the breeding value of an animal, which is what the animal is expected to transmit to its future offspring. EPDs are used to compare animals. For example, the difference in EPDs between two bulls is a prediction of the difference between the future performance of their progeny. The EPDs depend on heritability of the trait, correlations with other traits included in the evaluation, and on the number of records, relationships among animals with records, and distribution of the information across herds.

Each EPD has an accuracy value that can vary from 0 to 1. This value is also based on the amount and quality of the data used to predict the EPD. Since EPDs already incorporate all available information, they can be compared fairly without adjustment for accuracy. What accuracy provides the user is an indication of the likelihood of possible change in the EPD when more information becomes available. Accuracy near 1 indicates little change in EPD would be expected but accuracy near 0 would indicate that much change could be expected.

Data from breed performance programs are used to predict EPDs for all animals of the breed on traits that are routinely measured. Genetic evaluations are done for carcass

traits by some breed associations. Because EPDs for many traits can be generated from national evaluation programs, computers are needed to summarize information to make selections. Because of the importance of sire selection, sire summaries are published for proven and young bulls. Interim EPDs can be computed between routine runs of national cattle evaluation analyses to approximate predictions for young animals using their records and the EPDs of their parents.

## Performance Traits

Historically, national cattle evaluations have reported those traits recorded in traditional breed association performance programs. EPDs for birth, weaning, and yearling weights are standard, and a number of breeds produce calving ease EPDs. Many traits affect beef production efficiency, however, so these traits alone cannot sufficiently characterize the genetic merit of seedstock. Conspicuously missing from many sire summaries are important traits related to fertility, maintenance costs, and carcass value. In addition, some breeds need EPDs for traits of particular relevance to them, such as temperament and sheath/navel scores.

Some traits have both direct and maternal components. The direct component refers to the effect that an individual's own genes have on its performance. Thus the direct component for weaning weight measures genetic potential of the animal for growth to weaning. The maternal component refers to the effect that genes of the dam have on the environment influencing the offspring's performance. The maternal component for weaning weight is essentially a measure of milk production.

Carcass traits are presumed to be measured on an age-constant basis. Carcass measures could be from slaughter data, live animal data (ultrasound, etc.), or a combination of both data types.

Not all economically relevant traits can yet be evaluated because data do not exist for some of them, and not all are needed for every breed. If EPDs were reported for all traits, breeders might suffer from information overload. Some traits are alternative measures of the same underlying function, so it may be wise to select the best alternative. Reduction of the total number of EPDs reported by combining EPDs for related traits into composite indexes might be advisable.

## Data Preparation and Editing

**Data checks and edits.** National cattle evaluation programs mainly use field data collected by breeders. Therefore, data editing is an important part of data management prior to any analysis. Standard data checks and edits will be needed for all field data. Among the most important are:

1. Pedigrees must be checked and verified because correct identification of animals, and their sires and dams, is necessary for the relationship matrix to be correct. Errors such as reporting an animal as its own parent, an animal as both a sire and a dam, and the same animal with different sires or dams can occur. If an animal's data are being submitted to a breed association other than the one in which either parent is registered, the breed and registration number from the other breed association should also be recorded.

2. Birth dates should be included and checked to ensure that parents are older than their offspring and that cow ages are consistent with ages of their calves. Calving intervals must be at least 280 days unless some calves are either ET or multiple-birth calves, which must be indicated.

3. Duplicate records must be removed. Data from multiple births should be removed.

4. Records from embryo transfer (ET) calves are removed from most association's analyses. However, data from such calves could be included if maternal effects are properly accounted for. Schaeffer and Kennedy (1989; J. Anim. Sci. 67:2536) and Van Vleck (1990: J. Anim. Sci. 68:4026) presented models for incorporating records of ET calves into genetic evaluation programs. At the very least, birth date or age, breed or breed cross, and unique identification of the recipient dams need to be recorded. Performance records for ET calves contribute progeny information to the prediction of the direct breeding values of donor dams. Records from ET calves, however, do not contribute information directly to the prediction of maternal breeding values of donor dams because the dams do not provide the prenatal and postnatal maternal environment.

5. Records and calf ages should be checked. A good rule is first to eliminate weight records that are obviously out of an acceptable range of weights for the breed. Next, records of extreme magnitude within a contemporary group should be corrected if possible or eliminated. The record might be corrected by setting it to some predetermined value. Some breeds adjust records that are outside a set number of standard deviations (i.e., two standard deviations from the contemporary group mean) back to the standard deviation limit. Some breeds eliminate records within a contemporary group that are outside the ratios 60 to 140 of the record divided by the contemporary group average or outside three or four standard deviations. Such animals should remain in the pedigree file even if their records are not used. The recommended age range for weaning weight is 205 ± 45 (160 to 250) days, and for yearling weight is 365 ± 45 (320 to 410) days. These ranges allow for the use of a linear adjustment for age. Some breeds use non-linear adjustments to adjust weaning and yearling weights for calves outside of this range and then include them in the analyses.

**Contemporary group formation.** A contemporary group should consist of calves of the same sex and breed composition percentage, that were raised under the same management and environmental conditions, and that are within an acceptable age

range. The information used to determine contemporary groups should be maintained in the data bank if changes in contemporary grouping might be made in the future. Contemporary groups as small as two are useful in cattle evaluation. A single calf in a contemporary group should remain in the pedigree file, but its record would not contribute to the genetic evaluation. Some items to consider when forming contemporary groups are:

1. Contemporary groups at birth are formed using herd, year, season, sex, breed composition, and perhaps embryo transfer status and breeder-provided pasture or management group codes. The most common season grouping is January – June and July – December; although some associations use 90- or 120-day season groupings or group calves together that are born in a 90-day period. Birth and weaning contemporary groupings should be developed separately to facilitate inclusion of birth weights from calves that die before weaning. Ranges of birth weights within contemporary groups should be examined. In cases where there is no variation, the entire contemporary group should be eliminated from the analysis but not from the pedigree file. This rule should also be considered for contemporary groups for weaning and yearling weights.

2. Contemporary groups at weaning are formed using herd, year, sex, breed composition, weaning management code (usually creep vs non-creep), and date that the entire contemporary group was weighed or processed. Embryo transfer status, breeder-provided pasture or management group codes, and record processing dates are also used when available and appropriate. Large operations may not be able to weigh all calves on the same day. Calves weighed or processed within a five day period may be included in the same weaning or yearling contemporary group if management has been the same for all calves.

3. Yearling contemporary groups are formed using the weaning contemporary group with additional yearling management codes and yearling weigh or processing dates. Embryo transfer status, breeder-provided pasture or management codes, yearling sex, and record processing dates are also used when available. Data from central test stations can be used if at least two of the animals were in the same weaning contemporary group and were contemporaries in the central test.

4. For sire models, connectedness of sires across contemporary groups should be checked. When the animal model with a complete relationship matrix is used in a breed that has a substantial number of breeders that use artificial insemination, only a small percentage of the animals are likely to be disconnected.

**Analysis Considerations**

**Animal model and reduced animal model.** An animal model is a model that can predict direct genetic effects (breeding values) and for some traits, maternal genetic effects for all animals in a breed or population. A reduced animal model is sometimes used to predict breeding values. The reduced animal model uses mathematical and

genetic principles to transform the animal model so that only parent breeding values are computed directly. This substantially reduces the number of equations that must be solved simultaneously. Breeding values for non-parent animals are then computed in a second step using the predicted parent breeding values. The reduced animal model is equivalent to the animal model. Both result in the same predictions of breeding values.

**Effects in an animal model.** Effects included in an animal model can be divided into three types: fixed, random genetic, and random non-genetic effects. Whether an effect is considered to be fixed or random depends on the data and inferences to be made about the estimated effects.

1. Some important fixed effects include:

   a. Contemporary groups. Groups are defined such that records are grouped into similar management and(or) environmental units. (See Contemporary Group Formation.)

   b. Genetic groups. Genetic groups can be included to account for 1) genetic trend in unknown foundation animals (phantom parents), 2) differences among individuals in the expected expression of heterosis, 3) genetic differences among subpopulations, and 4) genetic differences in imported animals.

   c. Age of calf and age of dam. Almost all traits measured after birth of the animal are affected by ages of the animal and its dam. The usual procedure is to pre-adjust records for age of calf using some type of continuous adjustment. Traits that are affected by maternal effects are usually adjusted for age of dam. Alternatively, age of dam effects could be included directly in the animal model.

   d. Other. Sex (for traits where sex is not a part of the contemporary group definition) and sex by age of dam and management-type by age of dam interaction effects may be included as fixed effects.

2. Random genetic effects for a within-breed animal model

   a. Direct breeding value for the trait of interest. Every animal in the pedigree file will have a breeding value prediction based on all available information, such as records of the individual, progeny, parents, and other relatives.

   b. Maternal breeding value. For traits such as weaning weight that are affected by mothering ability, a maternal genetic effect should be included to obtain better predictions of direct breeding values and to provide predicted breeding values for maternal ability. Predictions of maternal breeding values for bulls and females without progeny will be based on relationships with females that are parents.

   c. The correlation between direct and maternal genetic values will mainly influence predictions of maternal breeding values for animals that are not mothers or do not have progeny that are mothers. Each breed association needs to determine the most appropriate correlation to use in evaluations for that breed.

3. Other random effects

   a. Maternal permanent environment. This effect accounts for permanent environmental factors that affect the expression of a dam's maternal ability such as losses in milk production caused by chronic mastitis or even preferential treatment.

   b. Genotype x environment interactions. Research suggests that the magnitude of sire x contemporary group, sire x herd, or sire x region effects may be large enough for some breeds to consider including them in an animal model analysis. Such effects may partially adjust for preferential treatment. Such effects have not been regularly included in within-breed NCE analyses. If across-country or across-breed analyses are conducted, these effects may need to be included.

   c. Residual error. Unknown or unaccounted for sources of variation will be partitioned into a term called residual error.

A general animal model in matrix notation is presented in the Appendix Table 5.1, and in Appendix Table 5.2, direct and maternal heritabilities, the direct x maternal genetic correlations for weaning weight, and genetic correlations between weaning weight and postweaning gain used by several breed associations are presented.

**Multiple-trait models.** Multiple-trait models provide simultaneous solutions for direct (and maternal) EPDs of two or more traits from a single analysis. Multiple-trait models are used to account for selection and reporting bias caused by selection practices and incomplete reporting of data. Multiple-trait models may also provide for increased accuracy of breeding value estimation. Since overcoming bias from incomplete reporting and selection is the principal reason for using multiple-trait models, at least one of the traits analyzed should be completely reported. Weaning weight is the trait that usually is most completely reported. It should be used in multiple-trait analyses with postweaning traits such as yearling weight, scrotal circumference, and carcass merit, to account for selection that occurs at weaning. Weaning weight also is useful in combination with birth weight to overcome incomplete and inaccurate reporting of animals that had heavy birth weights or high calving difficulty scores.

The combination of traits to include in a multiple-trait analysis depends on both computational feasibility and the combinations of traits that best overcome potential biases and lead to the greatest increases in accuracy. The amount of computing work required to solve multiple-trait models increases approximately as an $N^2$ function, where N is the number of effects in the model for one trait. Multiple-trait models also tend to require many more rounds of iteration for convergence. Depending on the computing power available, a trade-off may be necessary between improved accuracy and reduced bias from incorporating additional traits vs the increase in costs due to number of equations and number of iterations.

**Threshold model.** Traits such as calving ease and calving expressed as a success or a failure are measured using scores such as "zero or one". Analysis of such variables

using a linear model does not yield optimal solutions. A threshold model that assumes an underlying unobservable normal distribution for a categorical trait may yield more accurate predictions of genetic values. Research using simulation has indicated that for calving ease, the linear model and the threshold model tend to rank sires the same, especially if only first-calving data are used, and that both models identify the extremely bad calving-ease bulls. However, the threshold model does a better job of identifying the "easy calving" sires. Further information on threshold and survival models is given in Appendices 5.3 and 5.4, respectively.

**Solution methods.** Because of the number of equations involved in most national cattle evaluation programs, solutions are obtained by iteration. Iteration is based on the principle of successive improvement from one round of approximate solutions to the next. In practice, continuation of iteration will result in the same solutions as direct methods based on inversion or Choleski factorization of the coefficient matrix, but direct methods are not feasible with more than a few thousand equations.

## Reporting EPDs

**Base.** All EPDs are reported relative to a base population. The definition of the base is arbitrary. Most commonly used bases are obtained by forcing the EPDs of all animals born in a particular year to sum to zero. Thus, EPDs reported for animals born in a current year are relative to average genetic merit of animals born in the base year. Changing the base year for populations undergoing genetic trend will change all EPDs by a constant value (the difference in the average genetic merit of animals born in the old and new base years) but will not change the difference between the EPDs of any pair of animals. A recommendation is that the base year be changed every 5 years (base year of 1991 for evaluations done in 1996-2001 and a base year of 1996 for evaluations in 2001-2005 for example).

**Accuracy.** Information used to calculate EPDs for a particular animal can include pedigree information, own performance data, and information on descendants for the trait of interest and correlated traits. Accuracy is dependent upon the value (amount and quality) of the information used for EPD calculation.

Accuracy for an EPD is calculated as:

$$\text{Accuracy} = 1 - \sqrt{\frac{\text{Prediction error variance}}{\text{Additive genetic variance}}}$$

Theoretically, the prediction error variance is obtained from the inverse of the coefficient matrix of the mixed model equations. However, in most applications the coefficient matrix is too large to invert and approximations are generally used.

**Possible change.** A confidence range, which is a measure of the possible difference between the EPD and the true progeny difference, can be constructed for each EPD. The confidence range depends on the standard error of prediction (the square root of

prediction error variance) and a factor associated with probability of a change. The confidence range for an EPD is:

$CR = EPD \pm t(1 - \text{accuracy})\ \sigma_A/2,$

where t is a number associated with the probability desired for the confidence range and $\sigma_A$ is the standard deviation of breeding values for the trait of interest. For most applications t is 1.0 so that the confidence range is equal to the EPD plus and minus the standard error of prediction. This range provides a 68% chance of including the true progeny difference.

Using accuracy as defined by BIF, the standard error of prediction is linear with respect to the accuracy value. The term "possible change" is used in lieu of confidence range. Accuracy values range from zero to one for all traits and the meaning of a numerical value of accuracy is the same regardless of the trait. Possible change values are different for each trait, reflecting the units of measurement and amount of genetic variation associated with each trait (the $\sigma_A$).

**Interim Predictions**

Most beef cattle breed associations have genetic evaluation systems as a part of their performance recording programs. These National Cattle Evaluation (NCE) programs provide EPDs for sires, dams, and non-parents on an annual or biannual basis. Interim EPDs can be calculated for calves recorded during the time period between NCE runs, from records of calves within contemporary group adjusted for factors such as age, sex, and age of dam, from EPDs of sire and dam, and from estimates of maternal permanent environmental effects of dams. Interim EPDs provide breeders a way to make early selection decisions on calves prior to the next run of the breed NCE.

The individual's own records and current EPDs of the parents from the NCE are used to calculate interim EPDs as a routine part of an association's record processing program. The interim EPDs are the individual's current evaluation until the next NCE run.

The interim EPD is illustrated as follows:

$EPD_I = 0.5\ EPD_s + 0.5\ EPD_d + 0.5\ \phi$

where $EPD_s$ and $EPD_d$ represent sire and dam EPD, respectively, and $\phi$ is the individual's Mendelian sampling effect. The Mendelian sampling effect is a prediction of how much the individual's own genetic value deviates from the average value of its parents ($0.5*EPD_s + 0.5*EPD_d$). How the Mendelian sampling effect is estimated is shown in Appendix 5.1.

Interim EPDs can be calculated on a single-trait or multiple-trait basis. Single-trait interim EPDs ignore the genetic and environmental correlations that may exist between

traits, whereas multiple-trait interim EPDs use information from all evaluated traits. Wilson and Willham (1988; J. Anim. Sci. 66:618) developed procedures to calculate single-trait interim EPDs using results from NCE programs. The methods used to calculate multiple-trait interim EPDs are based on procedures described by R. L. Quaas.

**Accuracies for interim EPDs.** An accuracy value is provided with each EPD to assess the risk associated with making selection decisions. For non-parent EPDs and interim EPDs, the information used to compute EPDs are the animal's pedigree index (sire and dam EPD) and the animal's own record. As a routine part of NCE, accuracies are provided for non-parent EPDs. For the accuracy of interim EPDs, two methods are recommended to provide some measure of reliability: 1) use of a letter designation to distinguish between interim and non-parent EPDs or 2) use of a numerical value for accuracy which accounts for pedigree index only or pedigree index and own record.

A letter designation for interim EPD accuracy can be used to denote pedigree index only or pedigree index and own record for a particular trait. To designate that an interim EPD was based on pedigree information, a designation of P or I can be used for the interim accuracy. For animals with an individual performance record along with pedigree information, a P+ or an I+ can be used to designate the accuracy of the Interim EPD.

**Recommendations for computing interim EPDs.**

1. Methods used to calculate interim EPDs should be similar to the procedures used to calculate non-parent EPDs from the breed's NCE program. The interim EPDs should use the same genetic and environmental (co)variances that are used in the NCE.

2. For interim accuracies, a letter designation, such as P or I for pedigree only, and P+ or I+ for pedigree and own performance, should be sufficient to indicate the information used to calculate the interim EPDs. A numerical accuracy can be used if the interim accuracies are computed from the accuracies of the parent EPDs.

3. Parents with interim EPDs should not be used in the pedigree index of a calf for calculating interim EPDs. If either parent is not included in the previous NCE run, they should be assumed to be unknown in the interim system. For animals that were not evaluated as non-parents in the NCE run that do become parents at a later date (e.g., embryo-transfer calves), their evaluation from the NCE will be a pedigree index. For these cases, the EPD based on pedigree information could be used in the interim values of their progeny.

**International Cattle Evaluations**

There are several reasons for developing systems to conduct international cattle evaluations. International evaluations could provide breeders with a much larger gene pool from which to select breeding stock. Such evaluations provide a way to standardize evaluation procedures and reports. A more practical reason is to reduce the number of

country-specific EPD values that are reported for any one animal. Pooling records across countries also will increase accuracies of evaluation for some individual animals.

Reference to a country or region in the following paragraphs is in reference to a within-country (region) breed organization. That organization is assumed to be responsible for maintaining the breed pedigree file. The organization or an affiliate also is assumed to maintain pedigree and performance files in a computerized database for accessing and maintaining the data.

**Requirements to participate**. Requirements for any country or region to participate in an international genetic evaluation are basically the same as for an in-country performance recording and genetic evaluation program: (1) a viable method of collecting accurate performance measurements; (2) a computerized data storage and retrieval system; (3) appropriate fixed effect (age, sex, age-of-dam, etc.) adjustment procedures; and (4) an efficient method for disseminating and explaining the evaluations.

To conduct an across-country (region) genetic evaluation, a computerized system is required for merging the independent data sets. This must include a master file that cross-references individual animals that are identified with different country-specific registration numbers.

**Considerations and issues.** There is no reason to expect that these considerations or issues will be insurmountable or any more significant than those that exist within current national genetic evaluation programs. One of the first questions is whether genotype × environment interactions exist, and if they do exist, are they significant enough to require adjustment of the evaluation procedures. Additionally, only common traits can be adequately evaluated. Do these common traits exist? Are the endpoints the same for each common trait? Contemporary group definition differences will probably exist for some of the traits being evaluated. Such differences will need to be resolved with definitions agreed on and consistently implemented by the participating parties. Are fixed effect adjustments made on some of the performance measurements, and what is the consequence of using different adjustment procedures for the same trait? A minor consideration is provision for conversion between English and metric units for the EPD values.

The data bases for countries participating in an international genetic evaluation must be tied together, generally through common or reference sires. Sufficient direct ties must exist to adjust adequately for environmental and management differences that influence performance in different regions. With widespread use of artificial insemination, this should not be a problem with most of the major beef breeds. However, breeds with small populations may not be adequately tied across countries.

**BIF role.** It is recommended that the Genetic Prediction Committee establish a subcommittee to develop guidelines. It should include representatives from at least the following organizations: Agriculture Canada, Animal Genetics and Breeding Unit

(AGBU) and Breedplan (Australia), Cornell University, University of Georgia, Iowa State University, Colorado State University, and the U. S. Meat Animal Research Center.

**Multi-Breed Genetic Evaluation**

A multi-breed evaluation is something the industry has wanted for years, or if not a true multi-breed evaluation (MBE), then at least EPDs that are comparable across breeds. Several institutions have developed such systems of evaluation.

First, however, what are some of the factors motivating breed association interest in an MBE? The main reason is that in many databases, performance records exist for a multiplicity of breeds and especially for their crosses. For example, in the American Simmental Association database there are nearly 70 breed codes. Why is this?

1. Many associations have open herd books and have recorded various percentage animals created during grading up. An MBE can do a better job of evaluating percentage animals by accounting for breed differences and heterosis.

2. There are increasing numbers of composites. In addition to the traditional Brahman-influenced breeds – Brangus, Braford, etc. – there are also growing numbers of individual breeders who are creating their own composites. Many of these would like EPDs on their cattle but have no place to have them computed. Processing records of composite breeders along with their own could be beneficial for a breed association by expanding their database and by providing a source of income, contacts, and goodwill.

3. Another increasingly common phenomenon is the $F_1$ bull. To evaluate such individuals, an MBE is necessary to account for breed composition.

4. Many data sets now have common sires. Angus sires, especially, tie together different record sets.

5. Finally, from the perspective of the group doing evaluations, an MBE has a logistical advantage (and some disadvantages) in that EPDs for multiple breeds can be computed simultaneously.

What additional fixed effects need to be included in a model for MBE? For direct effects, these include breeds of founders and heterosis for both direct and maternal effects plus an age of crossbred dam effect.

**Age of dam effect.** Based on work done at the University of Georgia, a 4$^{th}$ order polynomial curve for the impact of age of dam on growth traits can be adapted to account for crossbred dams. Because there are typically too many kinds of crosses to fit a separate curve for each cross, a crossbred curve is assumed to be the weighted average of straight-bred curves. The weighting comes from the breed composition of the dam. For birth weight and post-weaning gain: $z = \bar{b}_0 + \bar{b}_1 x^1 + \bar{b}_2 x^2 + \bar{b}_3 x^3 + \bar{b}_4 x^4$ where $\bar{b}_0$ = average breed maternal effect and x is age of dam. Because there is a random maternal component for weaning weight with a mean (i.e., a group effect), the

weaning weight polynomial needs no intercept: $z = \bar{b}_1 x^1 + \bar{b}_2 x^2 + \bar{b}_3 x^3 + \bar{b}_4 x^4$. For example, the quadratic term for a ¾ Simmental, ¼ Angus dam is $\bar{b}_2 x^2 = \left(\frac{3}{4} x^2\right) b_2^S + \left(\frac{1}{4} x^2\right) b_2^A$. Coefficients for all the commonly represented breeds can be estimated; less common breeds may need to be grouped.

**Heterosis effects.** The assumption for heterosis follows results from the U. S. Meat Animal Research Center in attributing heterosis primarily to dominance effects so that the fraction of maximal heterosis is proportional to the probability that an individual has genes from different breeds at a random locus. This fraction (H) can be computed as $H = \sum_{i \neq j} f_i^{sire} \times f_j^{dam}$ where the f's are the fractions that different breeds contribute to the sire and dam. Because it is not feasible to estimate $F_1$ heterosis for every possible breed combination, grouping of 'similar' breeds is necessary, e.g., four breed types: Continental, British, Zebu, and Other. With four breed types, there would be ten distinct heterosis effects:

| | |
|---|---|
| Continental x | Continental, British, Zebu, and Other |
| British x | British, Zebu, and Other |
| Zebu x | Zebu and Other |
| Other x | Other |

The following hypothetical example illustrates an animal whose composition includes six of the above ten categories and shows the fraction (coefficient) of each combination in the regression model that describes expected heterosis expression in the calf's record.

| Dam breed composition | Sire breed composition | |
|---|---|---|
| | 1/2 Charolais | 1/2 Shorthorn |
| 3/4 Brahman | 3/8 (Continental ×Zebu) | 3/8 (British × Zebu) |
| 1/8 Texas Longhorn | 1/16 (Continental × Other) | 1/16 (British ×Other) |
| 1/8 Hereford | 1/16 (Continental × British) | 1/16 (British ×British) |

Coefficients for the four combinations not represented would be zero.

To fit this model and compute heterosis fractions for direct effects requires knowledge of the breed composition of each sire and dam; to compute heterosis fractions for maternal effects, the breed composition of each maternal grandsire and maternal granddam must be known.

There are at least three options for dealing with heterosis effects. Option 1 is to pre-adjust the data with values from the literature. Option 2 is to include heterosis effects in the model and estimate them simultaneously with breeding values and other effects. However, breed association data with many different kinds of crossbreds but a preponderance of animals from purebred sires are not ideal for estimating heterosis. (Not to mention that many of the combinations of breeds are infrequent.). Good estimates of heterotic effects require both straightbreds and reciprocal crosses. The NCE data are primarily from purebred (predominately of one breed) and backcross animals.

The third option is a Bayesian approach to combine prior (published) information with information in the data. Published priors have means and variances. The variances reflect 'belief' or certainty about the prior mean. A large variance suggests uncertainty.

Fitting normal priors with non-zero expectations for mean effects requires a simple modification to the mixed model equations (MME). Priors for mean heterotic effects (in actual units of measurement for the trait) can be obtained from published studies. Specifying the priors for the variances is harder. One option is to specify variance $= \sigma^2_{e_i} / N_i$ for the $i^{th}$ trait. This lets the $\sigma^2$ do the scaling among traits and the $N_i$ can be thought of, perhaps crudely, as how many independent observations were available to provide the prior mean. In reality, however, the $N_i$ are arbitrary. Larger values indicate greater belief in the prior means: as $N_i \rightarrow \infty$, the data are completely ignored; as $N_i \rightarrow 0$, the prior means are completely ignored. The whole problem is that $N_i$ is a somewhat nebulous arbitrary constant that Baysians gloss over.

**Breed of founder effects.** Account must be taken of breed differences. Because NCE data do not contain a representative sample of most breeds, it is perhaps better to call the differences "founder effects." For example, breed differences cannot be estimated as could be done with U. S. Meat Animal Research Center data. However, the estimate of the difference between an average Simmental and the average Angus used by Simmental breeders can be estimated. Angus founders in early years were mostly commercial females while recently they are mostly registered A.I. sires. In neither case were they a random sample of the registered Angus population; hence they represent founder effects and not breed effects. The 1970 Angus founders were not likely to have had the same genetic merit as those in 2000. To allow for a trend in founder effects, founder effects can be defined by breed $\times$ year subclasses. (Again uncommon breeds would need to be grouped.)

Again a Bayesian approach can be used. The priors among breeds are assumed independent, e.g., no correlation between prior guesses (beliefs) of the genetic merit of, for example, Charolais and Gelbvieh. In contrast, year differences within-breed are less

likely to be unrelated. For a given breed of founder, a constant mean year effect (which implies no trend) can be obtained from published studies. An autoregressive covariance structure can be specified for the year within breed effects with a 'large' variance and a high correlation among adjacent years (0.95). This procedure is equivalent to the heuristic conclusion that the size of the effects is uncertain but that their magnitude doesn't change dramatically from one year to the next. The operational effect is that the year $\times$ breed effects are smoothed when plotted as a curve unless there is sufficient information from the data to dictate otherwise. As with the heterosis effects, the variance is taken as $\acute{o}^2_{e_i} / N_i$ although the N's are not the same as for heterosis effects. The NCE data are structurely more amenable to estimating 'breed' effects than heterosis effects, but separating direct and maternal effects can be a problem.

A question arising with an Multi-Breed Genetic Evaluation: "*Is an EPD an EPD?"* In the computations, heterosis is adjusted out of phenotypes to make fair comparisons in prediction of additive breeding values, but it is not added back to an "Expected Progeny Difference" to account for heterosis expected in the progeny. Therefore, depending on breed of cow and of sire, EPD-based comparisons among sires may not be reliable. This omission should be easy to fix but needs to be done electronically and interactively so that a user can specify the breed composition of the dam and sire when comparing EPDs of potential sires. Obviously, a unique sire summary cannot be produced that is specific for every type of cow.

Finally, although there is a savings in doing only one computational run in MBE, the logistics of getting all data and pedigrees ready at the same time and in the appropriate format is challenging. The process could be made somewhat easier by storing data and pedigrees in a relational database.

**Across-Breed EPDs**

Across-breed EPDs can be used by commercial producers as a tool to optimize performance levels in commercial herds, especially in herds using crossbreeding systems to exploit heterosis and match genetic potential to climate, environment, feed resources, and market targets. Across-breed EPDs are used to compare EPDs of animals of different breeds on the same scale. In time, with experience and use, commercial breeders will be able to decide on optimal ranges in across-breed EPDs for birth weight, direct and maternal weaning weights, and yearling weights for their specific requirements. Across-breed EPDs are most useful to commercial producers purchasing bulls of two or more breeds for use in systematic crossbreeding programs. Uniformity of across-breed EPDs should be emphasized in selection of bulls for use in rotational crossbreeding systems to improve uniformity of calves produced in successive generations of the rotation. Relative to EPDs of maternal breed bulls to produce replacements, selection of bulls for terminal crossing should emphasize across-breed EPDs for greater weaning and yearling weights and greater retail product yield.

**Adjustment of breed EPDs to compare animals of different breeds**. National cattle evaluations produce EPDs to compare bulls (and cows) within each breed. To compare bulls across-breeds, adjustment factors are needed for the within-breed EPDs. Computation of the adjustment factors requires direct comparison of progeny of sires of those breeds when all sires are mated to dams with the same breed composition. Currently those comparisons are available only from the Germplasm Evaluation Program at the U.S. Meat Animal Research Center (USMARC). Those breed solutions then are updated to what they would have been if a current group of those bulls had been used in the project. The updating requires the average EPD of the bulls used at USMARC and the average EPD of all animals born in a current year (which is the same for all breeds). The USMARC breed solutions and the difference in average EPDs (current bulls and bulls actually used earlier) are then used to calculate adjustment factors for each breed which, when added to the within-breed EPD, result in across-breed EPDs for comparison of bulls of all breeds. For example, the 2001 adjustment table that follows is based on the average EPDs of Angus calves born in 1999 forced to equal zero.

| **2001 Additive Adjustment Factors to Compute Across-Breed EPDs** | | | | |
|---|---|---|---|---|
| Breed | Birth wt. | Weaning wt. | Yearling wt. | Milk |
| Angus | 0.0 | 0.0 | 0.0 | 0.0 |
| Hereford | 3.6 | 0.4 | -8.8 | -14.4 |
| Shorthorn | 7.4 | 28.0 | 39.1 | 13.1 |
| South Devon | 6.8 | 20.1 | 36.0 | 2.2 |
| Brahman | 13.1 | 34.1 | -9.1 | 24.6 |
| Simmental | 6.8 | 20.7 | 18.1 | 13.2 |
| Limousin | 5.9 | 22.1 | 16.2 | -1.0 |
| Charolais | 10.5 | 37.7 | 50.8 | 6.0 |
| Maine Anjou | 6.5 | 16.0 | 0.7 | 10.8 |
| Gelbvieh | 5.8 | 8.1 | -19.9 | 13.1 |
| Pinzgauer | 7.6 | 26.1 | 21.3 | 7.2 |
| Tarentaise | 3.7 | 28.5 | 10.5 | 17.2 |
| Salers | 5.1 | 26.9 | 35.1 | 12.4 |
| Red Angus | 3.3 | -4.0 | -5.7 | --- |

Application of the adjustments would not change differences in EPDs among bulls of the same breed. It would, however, change differences among bulls of different breeds.

As an example of the application of this table, consider the following three bulls:

| Bull/Breed | Within-breed EPD | Adjustment | Across-breed EPD |
|---|---|---|---|
| Angus | 2.6 | 0 | 2.6 |
| Hereford | 3.9 | 3.6 | 7.5 |
| Simmental | 3.2 | 6.8 | 10.0 |

Although the bulls in the example had similar within-breed EPDs, their across-breed EPDs are quite different.

The accuracies of across-breed EPDs depend on within-breed accuracies and the accuracy of the estimate of the breed differences. The last part is not usually very important. Thus, if accuracies of across-breed EPDs are considered, a guideline would be to use the accuracy of the bull with the lowest within-breed accuracy in computing ranges of possible changes.

**Data needed for across-breed EPDs.**

1. Within-breed EPDs estimated from field data from breed associations.

    a. EPDs from the most recent NCE for sires used in experimental herds.
    b. Mean EPDs of non-parents for each breed from the most recent NCE for animals born in the birth year providing most recent 365-day weights (e.g., if 365-day weights taken in 2001 are the most recent data available for analysis, the mean non-parent EPD for all calves born in 2000 should be used).

2. Data used for estimation of across-breed EPDs should be obtained on topcross progeny produced by mating two or preferably many sires with current EPDs of two, or preferably more, sire breeds to dams of a different breed or specific cross and managed in a contemporary environment in experimental or industry herds. All progeny should be topcrosses out of dams of a breed composition different from the sire breeds (e.g., two-way $F_1$ crosses or three-way crosses) to avoid confounding of additive breed effects with general effects of heterosis and breed maternal effects. Straightbred and backcross matings must be avoided. If not, records must be corrected for differences in direct and maternal heterosis. If contemporary groups of dams are all comprised of the same breed (e.g., Angus or Hereford) or the same specific cross (e.g., Hereford × Angus), no adjustment of data is required for general heterosis effects or for breed maternal effects. These records must not be used in calculation of within-breed EPDs (see, 1 above).

The following data should be recorded:

a. Registration number of sire of calf (only records of calves of sires with most recent EPDs can be included)
b. Unique calf identification
c. Location
d. Birth date of calf (year and date within year are required to account for year of birth, season of birth, and age of calf)
e. Sex of calf
f. Age of dam
g. Breed composition of dam
h. Contemporary group codes (e.g., creep vs no creep, pasture environments, etc.)
i. Dam of calf

3. With the analytical procedures used presently, across-breed EPDs can be computed only for traits for which within-breed EPDs are available. These include:

   a. Birth weight
   b. 205-day weaning weight
   c. 365-day yearling weight
   d. Total maternal weaning weight
   e. Net maternal weaning weight ("Milk")

**Other important traits.** To date, across-breed EPDs generally have not been estimated for reproductive traits, calving ease, or carcass and meat characteristics. EPDs have been available only for a limited number of sires of a few breeds for carcass and meat traits such as marbling, estimated cutability, and yield grade and for reproductive traits such as scrotal circumference and calving ease. Until sufficient data are available, experimental results such as those from direct comparison of breeds in the MARC Germplasm Evaluation Program for reproduction and maternal performance, growth and feed efficiency, and carcass and meat traits should be summarized by BIF for use by commercial cattlemen.

# CHAPTER 6 - UTILIZATION

## Selection Practices

**Sire selection.** In order to make sustained contributions to the breeding program, bulls should be structurally and reproductively sound. Approximately 20% of all beef bulls have some degree of infertility. A thorough breeding soundness examination, performed by an experienced veterinarian or other competent personnel, can detect the majority of bulls having obvious fertility problems and should be performed annually on all bulls two to four weeks before the start of mating. As described in Appendix 6.1, components of the breeding soundness examination include a physical examination, measurement of scrotal circumference, rectal palpation of internal organs, and examination of semen for progressive linear motility and normal morphology.

Sound feet and legs are essential in order for a bull to cover many acres of pasture, both for obtaining adequate nutrition and mating cows. Structural soundness is not an all-or-none phenomenon; rather it is expressed in various degrees. Bad feet, pigeon toes, excessively straight or sickle hocks, and loose or pendulous sheaths are examples of some of the more common structural problems of bulls. Because many structural problems become worse as bulls grow older and heavier, it is particularly important to critically evaluate young bulls.

Structural soundness of bulls that are candidates for selection should be evaluated in a systematic manner. Inspect each bull's feet, toes, heels, pasterns, knees, hocks, and sheath. When viewed from the front, the feet should point straight ahead, both when the bull is standing and walking. The feet should be large and round with a deep heel and with toes that are similarly sized. When viewed from the rear, the legs should be equally far apart at the hocks and pasterns and then toe out slightly from the pasterns to the ground. The bull should move freely with each hoof striking the ground evenly.

Many structural problems are partially heritable and should be particularly discriminated against when daughters will be kept for replacements. However, structural problems that do not compromise longevity or ability to service cows are of little consequence in the selection of terminal sires.

Evaluating bulls for structural soundness also provides an opportunity to gauge a bull's temperament or disposition, a moderately heritable trait. A bull with poor disposition may be dangerous or difficult to work, and his daughters may be difficult to manage as well.

For traits for which they are available, EPDs most efficiently combine phenotypic performance data, records from all related animals, and information from genetically correlated traits to predict the relative performance of future progeny of candidates for selection. Information from these sources is optimally combined into a single predictor of genetic merit. Therefore, there is no advantage in using information from sources that contribute to the EPD when the EPD itself is available. For example, if the EPDs for

birth weight are available on two candidates for selection, then these statistics provide a more accurate indication of the difference in birth weights of future progeny than the actual or adjusted birth weight records of the candidates themselves. Likewise, if the selection criterion is calving ease and calving ease EPDs are available, then consideration of birth weight EPDs is unwarranted.

Ratios of animal records to their contemporary group average describe the magnitude of an individual's phenotype relative to other animals managed in a similar fashion. In calculating contemporary group ratios, no information is used from related animals in other contemporary groups or from genetically correlated traits. Contemporary group ratios are most useful when EPDs are not available for an economically important trait.

Appropriate use of performance records and EPDs allows producers to increase genetic potential for profit. Profit is determined both from income (a function of reproductive rate, growth rate, and product quality) and expense ( a function of feed requirements and managerial interventions). Thus, in order to improve genetic potential for profit, selection decisions must consider several traits simultaneously. Because genetic antagonisms exist among some of the traits influencing profit, selection for extreme phenotypes or genotypes frequently is not warranted. It is far more likely that the greatest profit will be realized from cattle with an optimal balance among traits.

Many traits have intermediate optima. Examples include:

1. Birth weight. Calves that are too heavy at birth experience increased dystocia, require higher management input, and suffer higher mortality. Conversely, calves that are too light at birth are more prone to starvation and thermal stress, with similar consequences.

2. Leanness. Concerns about the relationship between diet and health have led consumers to favor leaner beef. However, cows that lack the ability to conserve energy as fat are at risk of impaired fertility during lactation and may require increased supplemental feeding in harsh environments. When fed cattle are marketed, premiums are paid for increasing levels of intramuscular fat or marbling, but increasing levels of intermuscular fat are discounted.

3. Age at puberty. Heifer calves that reach puberty at extremely young ages may become pregnant before being weaned and require increased managerial intervention to assure the survival of the heifer and her calf. However, heifers reaching puberty at too advanced an age are at increased risk of not becoming pregnant as a yearling to calve first at two years of age, thereby reducing lifetime productivity.

4. Mature size. Increasing growth rate and mature size result in greater throughput in a beef production system and allow producers and processors to capture economies of scale. However, faster growing and larger cattle have greater feed requirements and thus cost more to maintain than smaller cattle.

Beef producers are constantly challenged by the question of how much relative emphasis to put on each trait in a selection program. Selection for several traits at a time will slow progress for each individual trait but is the most efficient way to improve a complex breeding objective. To make the problem more difficult, some traits are genetically antagonistic to one another. If one trait is improved, then another may deteriorate. Notable genetic antagonisms include:

1. Milk production and body weight vs maintenance requirements. Selection for increased productivity through increased milk production or growth rate results in increased proportions of metabolically active tissues that must be maintained. This requires additional feed energy. Thus, gains from selection for additional productivity must be more than sufficient to offset the correlated increases in feed cost.

2. Growth rate vs calving ease. Selection for increased growth rate generally results in increased size at all ages, including birth. Particularly in temperate regions, birth weight is a major determinant of calving ease. Thus, selection for increased growth rate may also result in deterioration of calving ease.

3. Lean yield vs carcass quality. Improvement in lean yield, as indicated by USDA Yield Grade, results from reducing waste fat in the carcass. However, USDA Quality Grade is improved through increasing intramuscular fat deposition. Selection for reduced fat deposition will improve carcass value by increasing lean yield but may simultaneously reduce marbling.

4. Leanness vs fertility. Increased carcass leanness is desired in many situations. However, daughters of sires selected for reduced fat trim of steer progeny may reach puberty later, require more services per conception, and have a longer first gestation, resulting in a heavier calf at birth being born with greater difficulty.

It is important to note that these genetic antagonisms are not absolute. It is possible, for example, to identify sires with desirable genetic merit for both carcass quality and lean yield. However, identifying sires with favorable EPDs for genetically antagonistic traits will be challenging to the breeder.

Selection for more than one trait at a time is optimally implemented using selection index methods. When EPDs are available for all economically relevant traits, calculating the sum of the products of EPDs weighted by their relative economic values provides a single straightforward criterion for evaluating candidates for selection. If the EPDs result from a multiple trait genetic evaluation system in which all economically relevant traits have been considered, then this criterion is the best linear unbiased prediction (BLUP) for economic merit.

**Replacement female selection.** Many of the concepts involved in the selection of sires are equally appropriate to selection of replacement females. In general, female selection is less intense than selection of males. Therefore, most genetic progress

results from sire selection. From an economic perspective, it is important that the selected replacement females calve first at two years of age, reproduce annually thereafter, and remain in the herd for an extended period of time.

Because the postpartum interval for first calf heifers is longer than for mature cows, it is important that heifers calve early in their first calving season. Thus, virgin heifers must have reached puberty and be exhibiting regular estrous cycles before the start of their first breeding season. Age at puberty is primarily a function of age and weight. It is generally recommended that replacements be selected from among the older available heifers and developed to reach 55 to 60% of their anticipated mature body weight by the start of their first breeding season. Pelvic area measurements may be warranted in herds with a history of dystocia problems or when high birth weight/low calving ease sires are used.

Failure to become pregnant is the leading cause for females to leave the breeding herd. Sustained reproduction is compromised when genetic potential for production of the female is mismatched with the nutritional environment in which she is expected to function. Thus, the desirable EPD profile for a replacement female is dependent upon the resource base of the farm or ranch. Optimum EPDs for growth and milk production under harsh conditions are lower than in better environments. Also, the ability to deposit fat under good nutritive conditions may be valuable for females that must endure seasonal periods of energy deficit.

Beyond the ability to reproduce annually, replacement females should remain functionally sound to advanced ages. Proper foot, leg, and udder structure is important. A cow's udder should be well attached, level across the bottom, and have small to moderate sized teats that are not excessively long. In general, soundness of the udder deteriorates with age. At present, there is no EPD for udder quality. In selection of sires producing replacement daughters, perhaps some emphasis should be given to sons of cows that remained sound to advanced ages.

**Cow culling decisions.** Removal of cows from the herd is largely an economic decision, because it has limited influence on genetic improvement. In most cases, it has been recommended that nonpregnant cows routinely should be culled. However, systems analysis studies have not always shown this to be a profit maximizing decision, particularly for young cows and when the difference in value between cull cows and replacement heifers is large.

Functionally unsound cows should almost always be culled. Cows with impaired mobility or unsound mouths are unlikely to harvest sufficient nutrients to maintain body condition and be productive. Newborn calves may have difficulty nursing from large teats or pendulous udders. In either case, economic consequences of the unsoundness are profound. However, few commercial cows should be culled for low productivity. Only in extreme cases will the income lost due to low future production be greater than the cost of developing a replacement heifer to replace that cow. Record keeping that includes

production information could be valuable, however, to aid decisions during years when extra culling is necessary.

Calf weaning weight typically begins to decrease when cows reach about eight years of age. Several studies indicate that in commercial production, the optimal economic culling age is between eight and 11 years. When calf prices are low, the optimum culling age decreases. When calf prices are high, there is some advantage to keeping slightly older cows.

## Guidelines for Seedstock Performance Programs

The primary responsibility for maintaining or improving traits associated with efficient beef production lies in the hands of seedstock producers. Only 3% of the U.S. national cow herd is owned by registered cattle breeders. Genetic change in the commercial beef cattle population is controlled by the genetic merit of bulls produced by these breeders. It is their responsibility to know the specific needs of their customers and to produce registered cattle that can help to fulfill those needs.

There are two aspects of performance programs for seedstock producers: (1) programs for individual herds, which are planned and controlled by individual breeders, and (2) the programs of seedstock organizations, which are planned and controlled by groups of breeders. These two aspects will be treated separately.

## Guidelines for Individual Herds

**Herd sires**. Sire selection is a sequential process. New herd sire candidates should initially be selected on the basis of EPDs for economically important traits, as provided by the appropriate breed association. These herd sire candidates may include both young sires produced in the herd as well as proven sires evaluated in other herds and available through A. I. Use of EPDs will facilitate comparison of such bulls from different sources. Other factors that should influence the selection of herd bulls include economically important, objectively measured traits for which EPDs are not available and subjective traits that affect the breeding program. Also, it is recommended that herd sires be structurally correct and undergo a breeding soundness evaluation prior to the start of the breeding season.

Accuracy of selection should be considered when choosing herd sires. Because EPDs are not exact predictors of true breeding values, they are subject to change after each evaluation, depending upon newly accumulated data. High accuracy sires are likely to produce progeny whose average merit closely corresponds to their EPDs. By comparison, young and low accuracy sires may produce progeny whose average merit either falls short of or exceeds prediction. Consequently, they should be used with some caution. The risk from using young sires can be decreased by selecting several whose average EPDs are equivalent to the desired standard. Progeny produced by this group should be quite similar to expectation.

**Heifer selection**. Seedstock breeders typically select replacement heifers from within their own herds as opposed to purchasing heifers from other breeders. This has the advantage of utilizing the same genetic resources that produce their marketable bulls. Selection of replacements is a multi-stage process and is similar to any other selection scheme for females. However, it is important to note that the quality of sires used to produce the heifers will greatly impact the genetic potential of future calf crops.

Heifers should be culled for structural problems that may interfere with their ability to raise a calf, breed back, and have a long productive life. They should also be selected for superior genetic merit as predicted by their EPDs. Because yearling heifers have low EPD accuracies, the accuracy of selection for an individual heifer is low. However, selection of a substantial group of heifers has a high accuracy of selection for the average of that group's EPDs.

**Merchandising for seedstock producers**. Effective merchandising depends on the integrity of the breed and breeder, coupled with a clear description of the products that are to be sold. Seedstock producers with comprehensive and accurate production records that are presented in a concise and informative manner have a valuable resource for use in the sale of animals. Credibility of the records is enhanced if the herd has a sound, progressive management program. It is becoming increasingly important to provide EPDs on several traits for effective merchandising. Seedstock customers rely on this information to assist them in making appropriate decisions.

Because the seedstock producer is selling a genetic "package," he/she must provide estimates of genetic merit for traits of interest to the customer. Whenever available, EPDs and their respective accuracies should be provided on each bull offered for sale. If EPDs are not available, ratios of adjusted performance measures may suffice. Promoting bulls with actual and/or adjusted individual performance information can be misleading, especially if contemporary group information is withheld or unknown. Performance pedigrees from breed associations can be helpful tools in promoting specific animals. They allow for the complete disclosure of information, including ancestry, as sanctioned by an official organization. Seedstock breeders should provide, at a minimum:

1. Adjusted birth weight, ratio, and EPD/ACC
2. Adjusted 205-day weight, ratio, and EPD/ACC
3. Adjusted yearling weight (365, 452, or 550 day weight), ratio, and EPD/ACC
4. Number of contemporaries at weaning and yearling
5. Sire
6. Maternal grandsire
7. Breed (or percentages of ancestral breeds)

If EPDs are available for other economically relevant traits, they should be provided as well.

Seedstock breeders should assist their customers with purchasing decisions. Some customers may need only the information on each animal before they are ready to make

a purchase. However, some customers may appreciate a more service-oriented seedstock supplier. As the number of available EPDs increases, buying decisions become more complex. In order to assist the buyer with complex decisions, the seedstock provider should:

1. Consider the production goals of the customer.
2. Match seedstock to the buyer's current cow herd.
3. Recommend specific animals for purchase.
4. Justify the recommendations in terms of genetic improvement.

This type of service requires good communication between buyer and seller. The buyer may not be able to clearly describe his/her environment or cow herd. Therefore, the seller must ask specific questions and, if possible, visit the potential customer. This type of relationship may increase the number of repeat customers for the seller.

## Guidelines for Breed Association Performance Programs

Breed associations serve several functions for the profit seeking seedstock producer. The most important function for herd/breed improvement is to provide genetic predictions to members and their customers. Data are collected from member breeders, analyzed, and returned in a summarized fashion. The ultimate goal is that all breeders and their customers are clearly informed of selection decision options. Most associations publish sire summaries that list EPDs of progeny tested sires. Technology has advanced to such a level that many breeders and bull buyers expect lists of potential seedstock sorted according to their individual specifications. The internet provides an ideal medium to service such requests. Although paper forms are adequate for some exchanges, most breeders and bull buyers will benefit from the speed and customization of browser-based internet technologies.

**Input records**. Most discussion regarding data for submission to breed associations is covered in the chapter on Animal Evaluation. Methods used to submit data should be simple. Paper forms are common but can be subject to postal delays, illegible handwriting, labor of data entry, and misinterpretation of data fields. Associations should provide internet access for data submission. There are two ways that this can be accomplished:

1. Breeders can submit data exported from a third-party herd management software package. The key to this is a standardized file format. The format should be made available to any member who wishes to create his/her own files for input, as well as files from third-party vendors.

2. Breeders can enter the data directly into a browser-based internet web site. This option has the advantage of sending data directly to the association. Also, it allows validation of selected data fields, which will allow the member to make corrections before the data are submitted to the association.

Regardless of how data are submitted (paper or electronic media), data fields should be clearly defined. Fields that require specific codes (e.g. calving ease or body condition scores, etc) need to be accompanied by definitions and examples to prevent incorrect codes from being entered.

**Output records**. Summarized data must be returned to members and sent to customers in a timely, organized fashion. Associations should offer a standard set of reports that satisfy the majority of questions regarding breeding decisions. Such a set of reports could include:

1. Progeny of Dam Summary. A listing of all progeny of a given dam with EPDs, ratios, adjusted weights, birth dates, tattoos, sex, etc. Progeny data should be averaged for each dam. Typically, associations only release this type of report to owners of the cattle listed.

2. Progeny of Sire Summary. Same as a dam summary, but for sires.

3. Whole Herd EPDs. All cattle registered to a specific owner. Fields should include tattoos, birth date, sex, name, EPDs, and accuracies. Averages of all EPDs may be helpful to the breeder/customer.

4. Registration/Performance Certificates. This report would display a three or four generation pedigree, adjusted performance data, ratios, EPDs, accuracies, name, sex, breeder, owner, and any other information the association considers important. Typically, these reports contain one animal per page.

5. Performance/Selection Worksheets. These are current documents that report the information available at the time of their compilation. Thus, when new worksheets are obtained, old ones with less information can be discarded. Typically, this is the report that would be returned to the breeder as soon as their most recent data had been incorporated into the association database. It is valuable to the breeder for validating data entry.

6. Custom Performance List. Members may request custom lists of registered animals. These reports may contain any number of fields including those found in the Progeny of Dam/Sire reports.

As required, lists of individual calves should be summarized by sire, contemporary group, breeder, or any other classification that is important to association members and their customers.

Standard reports should be offered on the internet as well as on paper. Because paper reports are static, the information they contain is not easily manipulated. Only those breeders who do not have computer or internet access should rely on paper forms. Associations that make all common reports available through the internet will benefit from reduced labor costs through automation of routine jobs. Technology and e-

commerce have matured to the point that breeders and customers can pay for reports, if necessary, via the internet.

The most general format for data is in the style of a spreadsheet. Each row contains a unique animal record, and each column represents a unique field or characteristic of an animal. This format can easily be sorted and manipulated by breeders/customers with spreadsheet applications for personalized analyses. Although spreadsheets are very flexible and powerful, not all breeders have the training to manipulate data in such a format. For those breeders, formatted reports are best. Formatted reports contain the necessary data in an eye-appealing presentation. Individual animals are easily identified and the data are labeled with column headers. Different sections of formatted reports (header, detail, and summary) are accented with lines and boxes. Formatted reports can be presented via internet browsers and printed. For large numbers of animals, however, it may still be best to request printouts from association headquarters or to request data in a spreadsheet format.

Regardless of how information is sent to members/customers, timing and ease of interpretation are critical. The beef industry runs on a timetable. A delicate balance exists between making early decisions and making accurate decisions. Associations that provide accurate, timely data will enable their members and customers to make timely and informed marketing and management decisions.

## Commercial Programs

The beef industry is becoming more consumer driven with a focus towards targeted products that are wholesome and safe. The commercial cow/calf industry plays a major role in this movement and will likely play an even larger role in the future. Commercial cow/calf production is extremely diverse, encompassing producers that sell calves directly at weaning through producers that retain ownership all the way to the retail case. Those involved in retained ownership may be involved in some form of alliance or have their own customized system. Regardless of the complexity or simplicity of their system, each producer should develop production and financial goals that are realistic, sustainable, and economically driven. In the final analysis, the goal in commercial herd improvement is to create a greater profit by increasing herd output with minimal additional cost.

## Selecting and Implementing a Performance Program

For a commercial herd, an appropriate performance testing program can take several forms depending upon herd size, management capability, and the goals set for herd improvement. Thus, performance programs are not the same for all commercial herds. Fundamental ingredients for any herd improvement program would include:

1. A controlled breeding and calving season or seasons.
2. Adoption of a mating system that utilizes heterosis.

3. Selection and use of superior sires for traits important to the system.
4. Selection of replacement females.
5. Culling of the cow herd based upon economically relevant criteria.

The commercial herd manager may elect to use one or more proven performance procedures or may use a complete performance testing program including single sire breeding pastures and individual animal weights. The manager who wishes to use a complete performance program may choose a program operated by a performance organization, such as a state beef cattle improvement association, or may use a personal computer with an appropriate software package.

Many tools are available to assist producers in achieving desired results. Already discussed in these Guidelines are selection using EPDs. This section will focus on strategies to meet specific production goals utilizing all genetic and management tools that are available. Each operation is unique in terms of the existing cow herd, environmental conditions, and available resources. It is therefore difficult to develop generic guidelines for commercial producers. The following examples illustrate methods for developing individual courses of action. They define several potential goals and present procedures that might be used to attain those goals.

| Goal: Increase Net Return from Calf Production | |
|---|---|
| Item | Procedure |
| Select bulls | Select herd sires that are reproductively and structurally sound; for use as terminal sires, select bulls with EPDs for calving ease direct, birth weight, growth, and carcass merit that are appropriate for the breed and age of their mates, prevailing environmental challenges, and market requirements; for sires that will produce replacement daughters and progeny for sale, add maternal traits to the selection criteria listed above; in either case, choose bulls with appropriate frame size, muscling, and body capacity. |
| Select replacement females | Select heifers from sires with optimum growth and milk production potential; select heifers with desirable within herd performance; select older, relatively larger heifers that are more likely to reach target weights for breeding; consider the physical structure, udder characteristics, and calf production of dams when making replacement heifer decisions. |
| Collect and utilize performance data | Permanently identify cows and calves; record calf weights at birth, weaning and yearling; record frame and muscle scores at weaning or yearling; utilize contemporary grouping and appropriate adjustments to evaluate animal production; utilize records to cull inferior bulls and cows and in replacement female selection. |
| Control the calving season | Reduce calving season to the shortest effective length; synchronize estrus to produce more calves early in the calving season. |

| Goal: Increase Reproductive Efficiency | |
|---|---|
| Item | Procedure |
| Measure reproductive performance | Permanently identify cows and calves; record breeding inventories, bull exposure dates, and A.I. breeding dates; record calving dates, calving difficulty, mothering ability, and calf survival; determine average calving date, calving interval, pregnancy rate, and weaning rate. |
| Provide adequate nutrition | Match breeding/calving seasons to nutritional resources; monitor body condition scores for rebreeding; determine nutritive value of stored feeds; sort cows by condition scores and provide better nutrition to under-conditioned cattle; maintain adequate pre- and postpartum nutrition; monitor pasture quantity and quality. |
| Select bulls and predict their fertility | Use healthy bulls with acceptable breeding soundness; match bull/cow ratio to environmental conditions; observe herd for mating activity; match bull birth weight and calving ease EPDs to intended mates; cull bulls causing increased dystocia; screen bulls for testicle morphology and scrotal circumference; if heifers are not cycling at the start of breeding, select for decreased age at puberty EPDs, increased scrotal circumference EPDs, or larger yearling scrotal circumference. |
| Pregnancy test and examine cows | Cull open females; cull cows with significant structural, eye, tooth, or udder problems. |
| Control breeding seasons | Synchronize estrus to concentrate breeding and calving; cull cows with late calves or extended postpartum interval; fit calving season to labor, feed, and environment. |
| Use crossbred cows | Use heterosis to increase reproduction and cow longevity; use breeds and crosses whose genetic potential for reproduction, milk, and growth matches feed resources. |
| Select and manage first calf heifers | Calve heifers at two years of age; select early-born replacement heifers; select daughters of sires that fit the management situation for frame size, growth, and milk yield; manage heifers to reach critical breeding weight; mate heifers two weeks before mature cows; maintain adequate nutrition for pregnancy and growth; use bulls with appropriate calving ease or birth weight EPDs; cull heifers with small pelvic areas; monitor heifers carefully at calving; manage first calf heifers separately; maintain adequate postpartum body condition. |
| Implement an effective health management program | Develop an effective vaccination program; purchase animals from herds with good health programs; maintain internal and external parasite control; obtain postmortem examination of aborted fetuses or abnormal births. |

| Goal: Maximize Net Returns and Profits | |
|---|---|
| Item | Procedure |
| Collect and utilize production and financial records | Record production records for reproductive rate, market weight, and other economically important traits; use financial accounting and records program to determine overhead, labor, health, feed, and other variable costs; monitor asset : debt ratio; determine breakeven values of production, returns to investment in land and capital, beef production per acre, and profit; identify profit centers and monitor profitability of each; monitor debt service; use information to achieve cost reductions for breeding, feeding, and management; compare costs and returns across years; adjust management to maintain profitability. |
| Reduce costs | Use financial records to determine costs of production and to identify areas for cost reduction; analyze nutritive value of stored feeds; develop a feeding program that efficiently meets feed requirements; match cow size and production potential to environmental, management, and financial limitations; use non-traditional feeds when cost effective; buy in bulk if reduction in cost is greater than increased labor cost and potential wastage; comparison shop for health, feed, equipment, supplies, and services; participate in group purchasing programs where available; compare the cost of producing versus purchasing feeds; compare the cost of raising versus purchasing replacement females; soil test and fertilize based on pasture needs; evaluate labor needs and fully utilize available labor; critically evaluate needs for buildings and equipment. |
| Increase returns | Use records to relate returns to costs; maintain reproductive efficiency; control calving season for optimal utilization of feed, labor, and management; synchronize breeding to produce a high proportion of older, heavier calves; select sires that will improve economically important traits; monitor other traits for undesirable correlated responses to selection; consider electronic, futures, and options markets and retained ownership to increase returns and/or manage risk; develop markets and marketing options; obtain information from customers to plan and adjust the breeding and management program. |

| Goal: Increase Profit through Retained Ownership - Marketing on the Rail | |
|---|---|
| Item | Procedure |
| Select bulls | Identify economically important live animal and carcass traits: choose breeds that will complement the cow herd in meeting endpoint targets; determine target percentages of British, Continental and Zebu breeding based upon cow/calf, backgrounding, and feedlot environments, genetic merit for growth, efficiency, yield, and carcass merit; select bulls with acceptable breeding soundness examinations; select bulls with EPDs (or within contemporary group performance) that will maintain acceptable growth, lean yield, and quality grade; select bulls with acceptable calving ease or birth weight EPDs, based on the females to be bred, and with optimal milk EPDs to fit the physical environment; select bulls based on visual appraisal for structural soundness, muscling, and body capacity. |
| Collect and utilize performance records | Permanently identify cows and calves; record birth, weaning, and yearling weights and reproductive performance; utilize a feedlot that will provide performance information, preferably on an individual animal basis; arrange with the feedlot and packer to obtain carcass information, particularly hot carcass weight, yield grade, and quality grade; utilize this information in conjunction with financial information to determine traits to emphasize. Necessary changes may be in pre- and/or post-harvest genetics (e.g., breeds and EPDs), preweaning management (e.g., health programs), feedlot management (e.g., change of feedlot), or pricing (e.g., change of processor and/or grid). |
| Select a feedlot | Assess costs of gain and morbidity rates of in potential feedlots over similar time periods; request references from producers in your area; determine all charges and when payment is due; determine if the feedlot will finance costs and at what rate; determine which processor will likely be used and proximity of feedlot to processor; determine whether the feedlot and the processor will share information to improve your profitability. |

## Integrated Production Systems for Cattle Improvement and Production

The systems approach to cattle production recognizes that interactions among numerous factors influence profitability of beef cattle enterprises. Genetics, management, and environment all affect input, output, and profit. The systems concept incorporates an awareness that there is more to consider in a beef cattle enterprise than simply the level of production. What is most important is the overall efficiency of the enterprise – in other words, net return. While the level of production is an important factor affecting profitability, costs of production are equally important.

The "systems" part of the concept implies that a beef operation is influenced by many components, all of which play a part in determining net return. These elements might be categorized in the following way: the physical environment; cattle biological type; mating systems; management practices; input costs; product prices; and market requirements. Typically, a beef production system is highly complex, both because of the large numbers of factors affecting the system and because of the high degree of interaction among them. For example, the management practice of creep feeding might be profitable for one type of cattle in one environment, given current feed costs and feeder cattle prices. Change the cattle, the environment, or the economics, however, and creep feeding may no longer pay.

The systems concept of beef production presents challenges to both the commercial cattleman and seedstock producer. For the commercial cattleman, the challenge is to combine cattle and management alternatives in a way which maximizes net return. For the seedstock producer, the challenge is to breed the kind of cattle which best fit the commercial cattleman's production and marketing system. This implies breeding cattle for specific environments or purposes. One breeder may be producing cattle for the Corn Belt, another for the Arizona desert. One may specialize in bulls for first-calf heifers, another in terminal sires, and another in general-purpose cattle. All, however, can be breeders of "systems cattle."

Because the seedstock breeder should be producing breeding animals with the commercial user in mind, the challenge for the seedstock producer is to determine what type of cattle fit the commercial customer's production system and still produce a product that is acceptable and marketable to the consumer. The challenge for commercial producers is to find the seedstock whose offspring will fit their production and marketing system.

The first step towards integrating the systems concept into a seedstock or commercial beef production system is to understand how components of the system might interact.

## Interactions Related to Beef Improvement

Interactions exist within any biological system. Noteworthy for beef cattle production systems are the interactions between animals' genotypes and the production

environment in which they are raised. Even more important are interactions in the production system that affect investment return and profit.

The following table attempts to characterize production environments and list likely ranges for optimum levels for several important traits within each of the environments. Production environments are characterized by feed availability and the degree of environmental stress. Feed availability refers to the quantity, quality, and regular availability of grazed and harvested forage and supplemental feed. Sources of environmental stress include heat, humidity, cold, parasites, and diseases.

**Matching Genetic Potential for Different Traits to Production Environments[1]**

| Production Environment | | Traits | | | | | |
|---|---|---|---|---|---|---|---|
| Feed Availability | Stress[2] | Milk Production | Mature Size | Ability to Store Energy[3] | Resistance to Stress[4] | Calving Ease | Lean Yield |
| High | Low | **M to H** | M to H | L to M | M | M to H | H |
| | High | M | L to H | L to H | H | H | M to H |
| Medium | Low | M to H | M | M to H | M | M to H | M to H |
| | High | L to M | M | M | H | H | H |
| Low | Low | L to M | L to M | H | M | M to H | M |
| | High | L | L | H | H | H | L to M |
| Breed role in terminal crossbreeding systems | | | | | | | |
| Maternal | | M to H | L to H | M to H | M to H | H | L to M |
| Paternal | | L to M | H | L | M to H | M | H |

[1]L = Low; M = Medium; H = High.
[2]Heat, cold, parasites, disease, mud, altitude, etc.
[3]Ability to store fat and regulate energy requirements with changing (seasonal) availability of feed.
[4]Physiological tolerance to heat, cold, internal and external parasites, disease, mud, and other factors.

Six traits are listed in the table: milk production, mature size, ability to store energy, adaptability to stress, calving ease, and lean yield. Typical ranges for low, medium and high levels of mature cow size are 800 to 1,000 lb., 1000 to 1,200 lb., and 1,200 to 1,400 lb., respectively. Ability to store energy might also be termed “do-ability” – the ability of a cow to store fat when feed is abundant for use during periods when feed resources are limited. Adaptability to stress refers to an animal’s capacity to withstand the types of stresses mentioned above.

Clearly, there are more than six traits of importance to beef production. For the purpose of this table, however, the assumption has been made that animals are sound, fertile, and marketable (range of final weights for slaughter animals: 900 to 1,400 lb.; range of carcass weights: 550 to 850 lb.).

The recommended ranges shown in the table for traits in varying production environments are appropriate for general-purpose cattle – cattle typically utilized in rotational crossbreeding systems. The lower portion of the table lists ranges for the types of cattle used in terminal crossbreeding schemes. "Maternal" refers to the mother cows in such a crossbreeding system, and "paternal" denotes the sires that are used to produce strictly market calves. The recommendations shown for these special-purpose cattle are not broken down by production environment, but it should be recognized that production environment has a bearing on optimum trait levels for these cattle, just as it does for general-purpose cattle.

Relationships between production environments and optimum levels for traits are depicted in the table. To cite a few examples, it makes little sense to run large dairy crosses under low nutrition, high heat stress conditions of the desert or small cattle with low milk yield potential in areas of plentiful, year-round feed. The better the environment, both in terms of feed availability and freedom from stress, the wider the optimum range in milk production. Optimum range in mature size changes with feed availability. Environmental stress probably limits mature size only when feed availability is low.

Ability to store energy is critical when feed availability is low. Animals without this ability often do not carry enough condition to rebreed readily. Cows that are "easy keepers" in low feed environments, however, may become overly fat in a high-feed, low-stress environment. High lean yield and propensity to store energy as fat are genetically incompatible. The optimum level for lean yield will vary with market objectives when feed availability is high. However, when feed is limited cows still need to be able to fatten easily, even if this not beneficial in their progeny at slaughter.

Ability to withstand stress is always important, particularly in high-stress environments. Heat tolerance, for example, becomes critical in hot, humid regions. Also in some instances, calving ease is increasingly important at greater stress levels. When calves sired by terminal bulls are large, or when labor at calving time is limited, calving ease becomes more critical.

Recommendations for the sires and dams in terminal sire crossbreeding programs vary somewhat from the recommendations for general-purpose cattle. "Maternal" cattle are characterized by a generally higher level of adaptability to natural environments, i. e., more ability to store fat and lower lean yield. Milk production in these cows should probably not differ appreciably from that of general-purpose cows in similar environments, but maternal cattle may be smaller in order to take advantage of the increased efficiency of producing fast-gaining terminal calves from smaller, low-maintenance cows. Calving ease is, of course, very important in these cattle, because they will be bred to large sires.

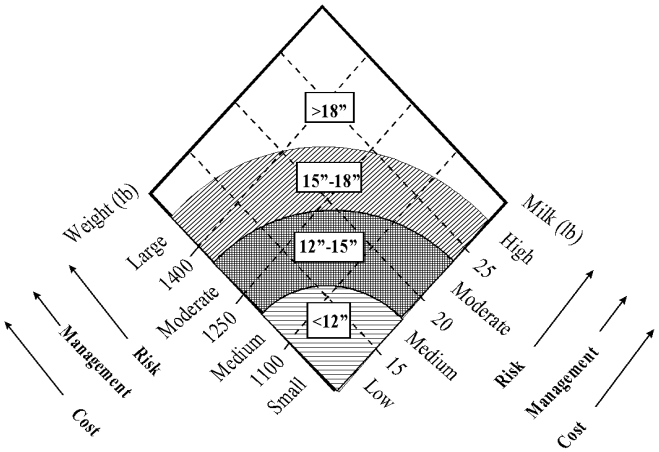
The traits to be emphasized in the terminal sires themselves ("paternal" cattle) are growth rate and lean yield (as shown in the table). Milk production and ability to store energy are relatively unimportant. Calving ease and adaptability to stress are not to be

forgotten, however. High calf crop percentage is as important in a terminal-sire system as in any other crossbreeding program.

The table on matching genetic potential for different traits is not complete and is meant only as a general guideline for making decisions in this area. There are additional aspects of the production environment beyond feed availability and environmental stress. Examples include the period of ownership (selling weanling calves vs retaining ownership to slaughter), basis for profit determination (return on investment vs return above production costs), relative costs of feeds and relative prices paid/received for different classes of cattle, and aversion to economic risk.

These factors add considerable complexity to the problem of matching cattle to the production environment. Using only cow weight, milk production, and feed availability from the above table and superimposing risk, management, and cost levels in a range environment, the following figure shows that as genetic potential surpasses resource availability, risk and cost of production can increase.

Figure 1. Matching cow biological type (weight and milk) to range environment, with associated risk, management, and cost. Ranges in inches (12"-15") are annual precipitation and/or represent availability of winter feed resource.




Thanks to Don Kress, Mike MacNeil, and the Western Coordinating Committee for Beef Cattle Breeding (WCC-1) for the graph.

For any given precipitation level (an indicator of feed availability), there exist optimal combinations of mature cow size and milk production level. For example, in areas of less than 12 inches of rainfall (smallest band—horizontal lines) the optimum cow is small to medium in size and has low to medium milk production potential. If either cow size or milk production increases beyond these levels, risk, degree of management (labor), and costs increase. In comparison, for areas with 15-18" of rainfall, a large

animal with low levels of milk production or a small animal with high levels of milk production might be appropriate, as indicated by the 15-18" band (bold striations). Because of the increased feed availability, there is more flexibility in defining an appropriate biological type. For areas with 15-18" of rainfall, if both mature size and milk production are decreased, risk and costs of production will decrease correspondingly.

Again, this figure is meant only as a rough guideline for matching cow biological type, as characterized by mature weight and milk production, to the production environment while simultaneously considering risk, level of management, and costs of production. As in the above table, this does not consider period of ownership and other factors that might modify identification of an appropriate cow type. It becomes rapidly apparent that beef production is a complex enterprise, that a multitude of factors affect profitability, and that a systems perspective of production is required.

**Conclusions from Systems Research**

1. Increasing or decreasing the genetic potential for any of the primary production characteristics (e. g. size, maturing rate, and milk production) causes changes in production that tend to have counterbalancing effects on biological or economic net herd productivity.

2. There is a level of production for each primary trait that best matches a particular set of environmental / management / economic conditions.

3. For many primary characteristics, intermediate levels of phenotypic merit tend to be optimal, but optima vary for different sets of production / economic conditions.

4. As nutritional quality, availability, and stability (across seasons and years) increase, the optimal values for primary characteristics tend to increase.

5. Production efficiency is enhanced by increasing herd production (gross revenue), decreasing herd costs, or both. Selection to attain optimum levels for primary production tends to increase herd off-take, while selection to improve secondary characteristics (disease resistance or soundness for example) tends to decrease costs.

6. Greater attention should be focused on defining the breeding objectives and selection criteria to achieve a clearly defined goal (e.g., herd profits vs individual animal performance).

7. Genotypes should be ranked based upon economic return, which may differ from breed rankings based on biological productivity. Rankings also may differ according to the economic objective (e.g., returns to land and livestock vs returns to land, livestock, labor, and management).

**The Calving Distribution Report: a Tool for Systems Analysis**

True systems compatibility is measured by net return to the beef operation. Unfortunately, an easily calculated report is not available that evaluates the contribution of different genotypes to net return, taking into consideration all of the components of the beef production system (e.g., period of ownership, resource availability, risk aversion). However, tools of varying complexity are available that begin to characterize the relationships between genetics, production environment (both natural and labor resources), and profitability.

The calving distribution report relies on reproductive performance as an indicator of compatibility of cattle with the production environment. Provided the required data have been recorded, it can be completed using a calculator or a spreadsheet program. Deviations from acceptable values can alert producers to variation in fertility caused by differences in genetic potential in other traits, or to ineffective reproductive management.

Data in the following table serve as a simple example.

**Calving Distribution Report**

| | Spring Calving Period | | | | | Fall Calving Period | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| Cow Age | No. of Cows | 1 | 2 | 3+ | Avg. Day of Calving | No. of Cows | 1 | 2 | 3+ | Avg. Day of Calving |
| 2 | 79 | 55 | 27 | 16 | 24 | 33 | 45 | 39 | 15 | 26 |
| 3 | 62 | 29 | 43 | 27 | 33 | 34 | 47 | 23 | 29 | 31 |
| 4 | 44 | 43 | 36 | 20 | 26 | 22 | 27 | 50 | 22 | 31 |
| 5+ | 70 | 60 | 21 | 19 | 23 | 52 | 29 | 40 | 31 | 33 |
| Total | 225 | 48 | 31 | 20 | 26 | 141 | 36 | 37 | 25 | 30 |

| Trait | Avg. Performance by Calving Period | | | Herd Average | Avg. Performance by Calving Period | | | Herd Avg. |
|---|---|---|---|---|---|---|---|---|
| Milk EPD | +5.0 | +3.9 | +4.1 | +4.4 | +4.0 | +4.8 | +6.6 | +4.9 |
| Weight (lb.) | 1243 | 1234 | 1233 | 1240 | 1281 | 1304 | 1247 | 1280 |
| Height (in.) | 51.9 | 52.2 | 51.9 | 52.0 | 52.3 | 52.4 | 52.4 | 52.4 |
| W/H | 23.9 | 23.6 | 23.9 | 23.8 | 24.5 | 24.9 | 23.8 | 24.4 |

The top portion of the report is used to monitor reproductive management. Cows are grouped by age in this report, although breed-of-sire and other groupings may be useful as well. The numbers in the table represent the percentage of cows calving in the 1st, 2nd, and 3rd 21-day increment of the calving season, and the average calving date. In this example, a higher percentage of cows calved early in the season during the spring compared to the fall calving season. However, there was greater difficulty rebreeding two-year-old cows in the spring than in the fall (as illustrated by the timing of calving at three years of age).

Results from the bottom part of the table can be used to alert producers to a level of genetic potential in the herd that is outside the optimum range for total production efficiency. The herd's genetic potential for a trait is within the range for optimal performance if cows calving early, late, or not at all have similar average performance or EPDs for that trait. On the other hand, herd genetic potential for a trait may surpass the range for optimal performance if there is a significant trend in performance or EPDs for cows calving early, late, or not at all. If the trend affects net profit, the producer then must determine whether it is cost effective to modify the environment to meet the needs of the cattle or to change the cattle to match their genetic potential to what the environment can support.

In this example, average hip height was very similar for cows calving in each period, indicating that herd genetic potential was not too high for prevailing conditions. However, for cows calving in the fall there was a trend of increasing milk EPDs as the calving season progressed. This does not establish cause and effect, but it suggests that higher-milking, fall-calving cows had difficulty consuming enough feed to simultaneously meet lactation and reproduction requirements.

The only true systems indicator of compatibility is the bottom line – net return to the beef operation. Therefore cattle producers that are serious about using the systems concept of beef production must keep the records necessary to analyze profitability from different types of cattle and management alternatives. And they must go one step further; they must be willing to act on the information that their analyses reveal.

**Integrated Resource Management (IRM) Tools**

Based upon the concept “if you don’t measure it, you can’t manage it", an additional set of tools has been developed by the National Integrated Resource Management Coordinating Committee (NIRMCC). These tools are designed to aid producers in gathering data necessary to develop an informed management plan that considers all farm / ranch resources and their interactions in the production model. The NIRMCC is composed of members from the National Cattlemen’s Beef Association; Cooperative Extension; veterinary, agricultural finance, and allied industries; the Beef Improvement Federation; the Society for Range Management; and the American Forages and Grasslands Council.

One of the first tools developed in the IRM program was the cow-calf Redbook. This book is designed to be carried by producers to record calving and cow herd information, as well as other daily events. The Redbook can be ordered for a small fee by calling 800-368-3138 following November 1 of each year.

Next, producers identified a need to determine cow-calf production costs. The Standardized Performance Analysis (SPA) program was developed to address this need. SPA is designed to incorporate production, feed, and financial data into a model that will calculate the unit cost of production in a commercial or seedstock cow-calf

enterprise. Calculations are based on number of cows exposed to mating and a fiscal-year cow inventory. The measure of productivity is the number and pounds of calf weaned per cow exposed to mating. The first SPA program was the Cow-Calf SPA. Subsequently the Cow-Calf Desk Record was developed and is the stay-at-home big brother to the Redbook. It contains ten sections to record information necessary to complete the SPA. SPA programs for the stocker, feeder, and seedstock enterprises are also currently available.

SPA measures provide a manager with comprehensive information that can be used to make informed decisions. Simply to eliminate expenses or cut costs without determining the impact on production is not making an informed decision. A decision to change an input based on the best information available will prevent a drop in production. Sometimes added inputs will increase costs beyond the yield of the inputs. SPA will help to identify such instances. It allows for consistent comparisons from year to year about the cattle enterprise. The year-to-year comparisons, or trend lines for a production trait, provide a reliable indication of change in the measured variable.

As goals are established for the cow-calf enterprise, SPA measures progress toward them. Seedstock producers, similar to cow-calf producers, should make changes based on economically important goals. Reducing the unit cost-of-production, or developing more efficient cattle, will enhance the profitability of the enterprise and survival of the industry. Many producers have identified low-cost, high-production cows in the herd. What is now needed are entire herds of such cows. Managing a cow herd, whether it be seedstock or commercial, without SPA is analogous to purchasing bulls without EPDs.

After the development of SPA methodology and calculation of a unit cost-of-production for commercial cattle operations, seedstock producers recognized the management value of SPA information. Consequently, the National Cattlemen's Beef Association initiated development of the IRM SPA Seedstock program. It was determined that the seedstock methodology should parallel the cow-calf program until the calves are weaned. A value is then placed on all calves, regardless of whether they are sold at weaning, retained as herd replacements, or retained for later sale. All unique costs associated with seedstock production (e.g., registration, association fees, breeding certificates, advertising, and additional feed) are accounted for in a separate module of the program. Revenue from the sale of surplus replacement heifers and herd bulls is processed in the same module.

The foregoing discussion provides a brief overview of the National IRM program, the National IRM Coordinating Committee, and some of the projects they have undertaken. As new issues are identified, the Committee will develop teams to work toward a solution. The section that follows provides a general overview of the data required to implement the seedstock SPA. As stated earlier, the Commercial Cow-Calf SPA and Seedstock SPA are identical in methodology until the calves are weaned.

**Seedstock Standardized Performance Analysis**

Implementation of Beef Cattle Seedstock Standardized Performance Analysis (SPA) requires collection of specific data to provide an accurate calculation of the chosen performance measures. In general, the seedstock production system is divided into three enterprises: breeding cows, replacement heifers, and sale bulls. To fully implement the Seedstock SPA, production data must be collected on these three enterprises and on financial measures. Seedstock SPA describes herd or production-group performance rather than individual animal performance. Individual animal data can, however, be combined to provide herd or production-group performance data.

During the annual production cycle, data for the production analysis needs to be collected during four key periods. These are during the breeding season, at pregnancy diagnosis, during calving, and at weaning. Data required include but are not limited to such items as number of females exposed, number of females diagnosed pregnant, number calving, and number weaning a calf. Based on this and other information, the seedstock cow-calf SPA produces summaries such as pregnancy percentage, percentage loss between pregnancy diagnosis and calving, calf death loss percentage, calf crop weaned percentage, cumulative calving distribution (number and percentage of calves born during the 1$^{st}$, 2$^{nd}$, and 3$^{rd}$ 21 days and after the 63$^{rd}$ day of the calving season), and a weaning production summary.

The replacement heifer enterprise also has specific data requirements which begin when the heifer is weaned and end when she enters the breeding herd (is first exposed to mating). Replacement heifer data must be kept separate from data for the breeding cows and generally require performance information on growth rate, feed use, and breeding season length in addition to records on culling/sale events. These data provide information on why and when heifers are removed from the replacement category.

The final enterprise, sale bulls, begins when a calf is selected at weaning to be raised as a bull. Data collection continues until bulls are culled, sold for breeding, or transferred to the breeding herd. Production data are recorded separately for each calving season or other production group and include records on culled bulls as well as bulls sold or transferred out of the enterprise for breeding. Similar to the replacement heifer enterprise, data must be collected on postweaning growth rates, feed use, and culling/sale events.

For financial analysis, the complete cattle herd must be inventoried. These data are required for preparation of the balance sheet, as well as for reconciliation of data in the depreciation schedule. Also, the fiscal beginning-year inventory of breeding cows serves as the divisor in determining cost and return per breeding cow. When inventorying breeding females, it is useful to identify cows as being purchased or raised, because this is how they are carried on the balance sheet.

To complete the SPA analysis, financial statements (balance sheets and income statement) must be completed. Allocations are then made to specific cow-calf, replacement heifer, and sale bull enterprises. Sources of data to prepare financial statements include the depreciation schedule and current IRS tax schedules, especially Schedule F.

The accrual adjusted-income statements can be generated from the cash accounting data with adjustments for inventory change, accounts payable, and accounts receivable. Most producers already have data necessary for the SPA financial analysis; the supporting SPA software and worksheets facilitate data processing for the managerial analysis.

Whereas requirements for the seedstock SPA may seem overwhelming at first, software is available to facilitate collection and management of the data. A list of approved software is available through the National Cattlemen's Beef Association. Also, an abbreviated SPA, SPA-EZ, is available in MS Excel 5.0 format from http://www.beef.org/business/production/irm/spa_ez/index.htm.

For more information on these and associated IRM tools, see
http://www.beef.org/library/publications/irm_news/index.htm

**Other Decision Support Systems**

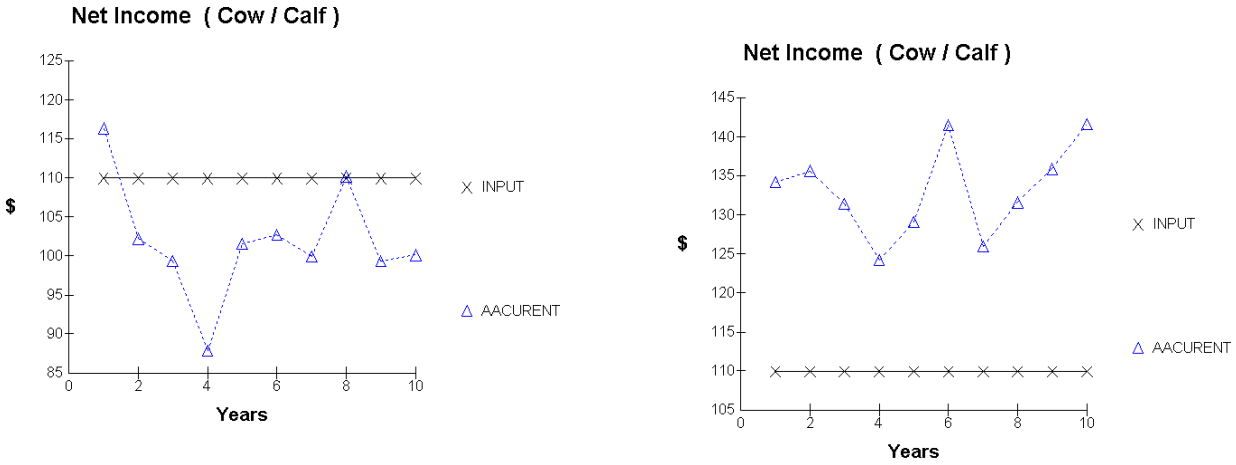
In the broad sense, a Decision Support System (DSS) can be defined as any tool (e.g., EPDs, the Calving Distribution Report, SPA analysis) that helps a producer make a strategic decision. As used here, a DSS is a computer program that assists the user in complex problem solving or decision-making. Simply put, they help producers make better decisions.

In any beef cattle production system, the physical environment, animal biological type (genotype), management, costs, prices, and market requirements all interact to determine profitability. Given this extreme complexity, the development of computer systems for decision making seems natural. With the support of the NIRMCC and the National Cattlemen's Beef Association, the Decision Evaluator for the Cattle Industry (DECI) was developed by scientists at the Meat Animal Research Center, Clay Center, Nebraska. Its goal is to evaluate the effect of management decisions (both genetic and otherwise) on production and profitability of a beef cattle enterprise.

Based upon user-supplied information, DECI is able to describe a production system over time based on genetic resources, feed availability and quality, and management practices. Once parameterized for a specific production system, individual components of the system can be modified; and the effects of those modifications on production and profitability can be predicted. This allows the producer to evaluate breeding and management decisions via simulation before they are ever undertaken "on-the-ground". Production and financial outputs are currently in line with SPA guidelines, facilitating

producer evaluation of the simulation results.

A simple example below shows one form of output that traces net income per cow for ten years of a DECI simulation. The left graph is the result of simulation of a 150 head, straightbred cow herd with moderate genetic potential for milk and growth. The line of Xs represents the average net income based on producer records, and the line of Δs represents simulation results. The right graph is the result of simulation of the same 150-cow herd, nutritional resources, and management protocol as in the first graph with the exception that in the second graph, the oldest 35% of the cow herd is mated to a terminal sire. These results indicate that implementation of a terminal crossbreeding program for a portion of the herd would increase overall profitability of the operation.




Information on DECI, with case study illustrations and procedures to obtain the software are available at http://www.marc.usda.gov .

Producers may obtain a variety of other decision support systems from university and cooperative extension personnel. The complexity and application of various programs range from addressing single problems (e.g., inbreeding management) to calculating feedlot breakeven prices to simulating an entire beef production system from birth to slaughter.

**Recommendations for Genetic Improvement with a Systems Perspective**

Based on the topics and tools discussed above and assuming the application of genetic prediction technologies discussed elsewhere in these guidelines, here are a few basic recommendations for making “Genetic Improvement with a Systems Perspective”:

1. Using production system analysis, determine customer’s needs and focus genetic improvement on those needs. In characterizing customers’ production systems, identify their economically relevant traits (traits that directly influence profitability due to their association with cost of production or an income stream) and focus on improving them.

2. If EPDs are available for the economically relevant traits, use these for selection purposes. If EPDs are not available for those traits, use EPDs for traits that are predictive of the economically relevant traits until direct EPDs become available.

3. Record cost and income data through use of SPA compatible software.

4. In so far as possible, integrate genetic and management information to make strategic breeding, management, and marketing decisions. This may be through use of DSS such as DECI or through development of profit-motivated breeding objectives.

5. Set genetic improvement objectives but be flexible enough to take advantage of opportunities for profit as they arise.

# BEEF PERFORMANCE GLOSSARY

**Accuracy (of selection)** - Correlation between an animal's unknown actual breeding value and a calculated estimated breeding value for a trait.

**Across-breed EPDs** - Procedures and adjustment factors that allow direct comparison of EPDs from animals of different breeds. They are based upon across-breed EPD adjustment factors which are added to EPDs provided by the separate genetic evaluation of each breed. The adjustment factors, which are updated each year, are based upon estimates of current performance differences among breeds and differences among breeds in genetic base for their evaluations.

**Additive adjustment factors** - A numerical quantity added to an animal's record to reflect expected performance if the animal had belonged to some baseline group. For example, 60 pounds could be added to weaning weight records of steer calves out of two-year-old dams to represent expected weaning weight if their mother had been five to nine years of age. The use of additive adjustment factors does not affect variability in the trait after adjustment.

**Adjusted weaning weight (WW)** - An unshrunk, off-the-cow calf weight adjusted to 205 days of age and to a mature dam age equivalence.

**Adjusted yearling weight (YW)** - An unshrunk weight adjusted to either 365, 452, or 550 days of age.

**Alleles** - Alternate forms of genes. Because genes occur in pairs in body cells, one gene of a pair may have one effect and another gene of that same pair (allele) may have a different effect on the same trait.

**Alliance** - A cooperative business arrangement in which a cattle producer, sometimes in cooperation with other producers, arranges for the retained ownership and/or contract sale of his/her animals before they actually are produced. The agreement typically defines the breeding system, selection methods, management conditions, and product specifications for the cattle.

**Animal model** - A genetic prediction procedure in which EPDs are directly computed for all animals in the population. See reduced animal model and sire model.

**Artificial insemination (AI)** - The technique of placing semen from the male into the reproductive tract of the female by means other than natural service.

**Average daily gain (ADG)** - Measurement of the average daily body weight change over a specified period of time of an animal on a feed test.

**Backcross** - The mating of a two-breed crossbred individual back to one of its parental breeds. Example: A Hereford-Angus crossbred cow bred back to an Angus bull.

**Base pair** – The complementary bases found within a DNA molecule. There are four different bases: adenine (A), thymine (T), cytosine (C), and guanine (G). A always pairs with T, and C always pairs with G. The base sequence ultimately determines the effect of the gene.

**Beef carcass data service** - A program whereby producers, for a fee, can receive carcass evaluation data on their cattle by using a special carcass data ear tag for their slaughter animals. See county extension director, breed representative, Beef Cattle Improvement Association representative, or area office of USDA meat grading service for information.

**Beef Improvement Federation (BIF)** - A federation of organizations, businesses, and individuals interested or involved in performance evaluation of beef cattle. It seeks to build confidence of the beef industry in the principles and potentials of performance testing. The purposes of BIF are to achieve utilization of the most efficient and effective performance evaluation methods, uniformity of procedures, development of programs, cooperation among interested entities, and education of its members.

**Best linear unbiased prediction (BLUP)** - A genetic prediction methodology providing the most accurate and precise genetic evaluations possible, given the information and family structure that are available.

**Biological type** - A group of cattle breeds having similar geographic origin and past selection history and with similar genetic potential for traits of economic importance. British general purpose beef cattle breeds, for example, have genetic potential for moderate growth, muscling, and milk yield; whereas continental European dual-purpose breeds have genetic potential for high milk yield and rapid growth.

**Birth weight (BW)** - The weight of a calf taken within 24 hours after birth. Heavy birth weights tend to be correlated with calving problems, along with other factors.

**Body capacity** - A subjective assessment of the feed intake capacity of an individual or breed, typically assessed by visually evaluating body length, body depth, and spring of ribs.

**Body condition score** - A score on a scale of 1 to 9, reflecting the amount of fat reserves in a cow's body, where 1 = very thin and 9 = extremely fat.

***Bos indicus*** - A subspecies of cattle of south Asian origin. Often known as Zebu, they have prominent humps forward of the shoulder. The Brahman breed is one example in the United States.

***Bos taurus*** - A subspecies of cattle of western Asian origin but often referred to as "European". Most breeds commonly found in the United States and Canada, and their

European ancestors, belong to this group. *Bos indicus* x *Bos taurus* crosses are viable and fully fertile and exhibit large amounts of heterosis.

**Breed** - Animals with a common origin and selection history. Animals within a breed have physical characteristics that distinguish them from other breeds or groups of animals within that same species.

**Breed association** - An organization that maintains pedigree and performance information and arranges for timely genetic evaluation of animals within that breed. Breed associations also establish regulations for registration of animals, promote the breed, and advance the interests of the breeder members.

**Breeding objective** - The goal of a breeder's selection program, for example to produce high quality, lean meat at lowest cost. It may also include a listing of the traits to be used as selection criteria to achieve the overall goal. Objectives may vary among breeders due to their genetic and physical resources and their markets.

**Breeding soundness examination** - Inspection of a bull, including evaluation of physical conformation and soundness through genital palpation, scrotal circumference assessment, and testing of semen for motility and morphological abnormalities.

**Breeding value** - Transmissible genetic merit of an individual, or the value of that individual as a parent. In the United States and Canada, genetic predictions are expressed as progeny differences rather than as breeding values. Because any parent contributes only half the genes in any one offspring, the progeny difference of an individual is half its breeding value.

**British breeds** - Breeds of cattle such as Angus, Hereford, and Shorthorn originating in Great Britain.

**Caesarean section** - A process in which the calf is surgically removed from the cow during parturition by making a large incision in the right side of the cow just above the flank.

**Calving difficulty (Dystocia)** - Abnormal or difficult labor, causing difficulty in delivering the fetus and/or placenta. Difficult births lead to increased calf and cow mortality and to more difficult rebreeding of the cow.

**Calving ease** - The opposite of calving difficulty. An easy calving is one that does not require assistance and does not impose undue strain on the calf or dam.

**Calving ease score** - A numerical score quantifying calving ease, ranging from 1 for an easy, unassisted calving through 5 for an abnormal presentation.

**Calving season** - The season(s) of the year when the calves are born. Limiting calving seasons is the first step to performance testing the whole herd, accurate records, and consolidated management practices.

**Carcass evaluation** - Techniques for measuring components of quality and quantity in carcasses and using the information for genetic prediction of carcass merit.

**Carcass merit** - Desirability of a carcass relative to quantity of components (muscle, fat, and bone), USDA quality grade, and potential eating quality.

**Carcass quality grade** - An estimate of palatability based primarily on marbling and maturity and generally to a lesser extent on color, texture, and firmness of lean.

**Carrier** - An individual that is heterozygous, having one dominant and one recessive allele at a given locus. For example, an animal with one gene for polledness and one gene for horns will be polled but can produce horned offspring when mated to another animal carrying the gene for horns.

**Central test** - A comparison conducted at a single location where animals are assembled from several herds to evaluate differences in performance traits under uniform management conditions.

**Chromosome** - Chromosomes are paired strands of DNA, with accompanying structural proteins, on which genes are located. Domestic cattle have 30 pairs of chromosomes, one chromosome of each pair having been inherited form each parent. One random chromosome of each pair is transmitted to each egg or sperm cell produced by a parent.

**Closed herd** - A herd in which no outside breeding stock (cattle) are introduced.

**cM (centiMorgan)** - The unit of length used to express locations of genes on chromosomes. One cM is approximately one million nucleotides long. The entire length of the DNA within a cattle cell is approximately 3000 cM. A gene ranges from .001 - .005 cM in length. A cM corresponds to 1% recombination between loci.

**Codon** – A specific three-base sequence in DNA that ultimately codes for a specific amino acid used in the building of a protein.

**Collateral relatives** - Relatives of an individual that are not its ancestors or its descendants. Brothers and sisters are an example of collateral relatives.

**Commercial producers** - Producers whose primary goal is to produce animals for herd replacement, feeding, and slaughter rather than breeding stock for sale to other producers. Progressive commercial producers seek bulls or semen from seedstock breeders that have comprehensive programs designed to produce animals with

optimum genetic merit for the combination of traits that increase efficiency and profit of their production system.

**Compensatory gain** - Rapid, subsequent gain of cattle that have been nutritionally deprived for some portion of their life.

**Composite breed** – A breed made up of combinations of other breeds.

**Complementarity** – The combining of breeds or individual animals that have characteristics that complement each other, thereby obtaining optimum progeny.

**Complementary DNA (cDNA)** – A DNA copy made from RNA through reverse transcription.

**Conformation** - A description of the shape of body parts of an animal.

**Congenital** - A condition that was acquired during prenatal life and therefore exists at or dates from birth. The term is often used in the context of defects present at birth.

**Contemporary group** - A group of cattle that are of the same breed and sex, are similar in age, and have been raised in the same management group (same location on the same feed and pasture). Contemporary groups should include as many cattle as can be accurately compared.

**Continental (European) breed** – Breeds originally developed on the continent of Europe. Examples include Simmental, Limousin and Charolais.

**Correlation** - A numerical measure, ranging between -1.00 and +1.00, describing how two traits are related. A high positive correlation means that as one trait increases, the other one usually does as well. For example, cattle with higher than average yearling weight generally will have larger mature size as well. When traits are negatively correlated, if one is above average, the other is likely to be below average. For example, as birth weight of a calf increases, calving ease is likely to decrease. A near zero correlation between traits means there is no particular relationship between them.

**Crossbreeding** - The mating of animals of different breeds or subspecies, frequently resulting in heterosis (hybrid vigor) for many economically important traits.

**Culling** - The process of eliminating less productive or less desirable individuals from a herd.

**Cutability** - An estimate of the percentage of salable meat (muscle) from a carcass versus percentage of waste fat. Percentage retail yield of carcass weight can be estimated by a USDA prediction equation that includes measured or estimated values for hot carcass weight, rib eye area, fat thickness, and estimated percent of kidney, pelvic, and heart fat.

**Decision Evaluator for the Cattle Industry (DECI)** - A decision support system available through the U. S. Meat Animal Research Center that simulates the impact of alternative breeding or management strategies on production and profit within a producer's herd.

**Decision Support System (DSS)** - A set of rules, usually coded into a computer program, that helps a producer evaluate the impact of alternative breeding or management strategies on one or more aspects of a beef production enterprise.

**Deviation** - The difference between an individual record and the average for that trait in the individual's contemporary group. For all animals within a contemporary group, these differences sum to zero when the correct average is used. A ratio deviation is an individual's ratio minus the group average ratio or 100.

**Direct effect** – For weaning weight that portion of preweaning growth that is due to the calf's genetics (see Maternal Effect).

**Direct EPD** - An EPD representing the effect of the individual's own genes on the trait of interest. A calving ease direct EPD, for example, represents calving ease of an individual's progeny. See also Maternal EPD.

**Disposition (temperament)** - A measure of an animal's docility, wildness, or aggression toward unfamiliar situations, human handlers, or management interventions.

**DNA (Deoxyribonucleic acid)** - The chemical compound that stores within each cell genetic information unique to an individual. A DNA molecule is composed of two strands of nucleotides bound to one another by chemical bonds between each complementary (A-T and G-C) base pair. The molecule has the appearance of a twisted ladder. The sequence of bases within DNA molecules determine amino acid sequences of proteins, control development, and establish the genetic potential for production of the individual.

**Dominant** – An allele is dominant when its presence prevents a recessive allele from affecting the phenotype of an individual heterozygous at the locus in question. For example, the allele for polledness (P) is dominant to the allele allowing growth of horns (p), so an animal with the genotype Pp shows the polled form of the trait.

**Double muscling** - A simply inherited trait evidenced by an enlargement of the muscles with large grooves between the muscle systems especially noticeable in the hind leg.

**Dressing percentage** - (Chilled carcass weight/live weight) x 100.

**Dystocia (calving difficulty)** - Abnormal or difficult labor causing difficulty in delivering the fetus and/or placenta. Difficult births lead to increased calf and cow mortality and to more difficult rebreeding of the cow.

**Economic value** - The net return within a herd for making a one unit change (pound or percentage, for example) for an economically important trait under selection.

**Economically relevant trait (ERT)** – Traits that are of direct economic importance to cattle producers.

**Effective progeny number (EPN)** - An indication of the amount of information available for estimation of expected progeny differences (EPDs) in cattle evaluation. It is a function of number of progeny of a parent but is adjusted for their distribution among herds and contemporary groups and for the number of contemporaries by other sires. EPN is less than the actual number of progeny because the distribution of progeny is never ideal.

**Electrophoresis** – A process used to separate DNA fragments by length. DNA fragments are placed at the top of a gel matrix that is then exposed to an electrical current. This causes fragments to migrate through the pores in the gel at rates proportional to fragment size. Resulting fragment location on the gel can be visualized by appropriate labeling techniques.

**Embryo transfer** - Removing fertilized ova (embryos) from one cow (the donor), generally in response to hormone-induced superovulation, and placing these embryos into other cows ( the recipients). More calves can be obtained from cows of superior breeding value by this technique

**Environment** - All external (nongenetic) conditions that influence the reproduction, production, and carcass merit of cattle. When environmental influences on phenotypic merit are not properly be accounted for in genetic evaluations, they reduce the accuracy of breeding value estimation and of subsequent selection.

**Estimated breeding value (EBV)** - An estimate of an individual's true breeding value for a trait based on the performance of the individual and close relatives for the trait itself and sometimes performance of genetically correlated traits. EBV is a systematic way of combining available performance information on the individual and sibs and the progeny of the individual. Expected progeny differences have replaced EBV's in most breed association programs.

**Exon** – Those regions of a gene in which the nucleotide sequence actually codes for a biologically relevant product.

**Expected Progeny Difference (EPD)** - The difference in expected performance of future progeny of an individual, compared with expected performance of future progeny of an individual of average genetic merit in the base time frame for the genetic evaluation. EPDs are estimated from phenotypic merit of an individual and all of its relatives and are estimates of one-half the breeding values. EPDs are generally reported in units of measurement for the trait (e.g., lb., cm., etc.).

**$F_1$** - Offspring resulting from the mating of a purebred (straight-bred) bull to purebred (straight-bred) females of another breed.

**Fat thickness** - Depth of fat in tenths of inches over the rib eye muscle at the 12th rib. It consists of a single measurement at a point three-fourths of the lateral length of the rib eye muscle from the split chine bone.

**Feed conversion (feed efficiency)** - Units of feed consumed per unit of weight gained or (less commonly in the United States) production of meat or milk per unit of feed consumed.

**Fertilization** - The union of the male and female gametes to form a new, genetically unique individual. In cattle, sperm and egg cells with 30 chromosomes each combine to form a zygote with the 60 chromosomes normal to the species.

**Fingerprint (DNA)** – Pattern of DNA fragments unique to an individual. Often produced by using restriction enzymes to cut the DNA into fragments at specific sequences of nucleotides. Using electrophoresis, these fragments can be sorted and then visualized, forming a unique “fingerprint" for each different animal.

**Frame score** - A score based on subjective evaluation or actual measurement of hip height. This score is related to slaughter weights at which cattle should grade choice or at which different groups of cattle should have comparable amounts of fat.

**Freemartin** - Female born twin to a bull calf (approximately 9 out of10 will be infertile).

**Gel (gel matrix)** – A porous substance that allows DNA fragments to migrate through it at a rate inversely proportional to fragment size, this allowing separation of DNA fragments.

**Generation interval** - Average age of parents when the offspring destined to replace them are born. It should be computed separately for male and female parents and then represents the average turnover rate of bulls and cows in the herd. When other factors are held constant, generation interval is inversely related to the rate of response to selection. That is, rapid generation turnover enhances rate of selection response.

**Gene** - A gene is a discrete segment of the DNA molecule, located at a specific site (its locus) on a specific chromosome pair. Two copies of each gene exist in each nucleated diploid cell in an animal. Only one gene of each pair is randomly transmitted to the offspring through the gamete. The unique nucleotide sequence of each gene determines its specific biological role. Many genes specify the amino acid sequence of a protein product. Others produce gene products that are involved in controlling metabolic and developmental events.

**Gene marker** – A specific sequence of nucleotides that is easily detectable and can be used to differentiate among alleles at a locus.

**General purpose breed** - A breed with acceptable genetic merit in reproductive, maternal, growth, and carcass traits, but not specialized in either terminal or maternal characteristics. Such breeds frequently are used in rotational crossbreeding programs.

**Genetic antagonism** - A genetic correlation in which desirable genetic change in one of the traits is accompanied by an undesirable change in the other. For example, because of the positive genetic correlation between milk yield potential and cow maintenance requirement, selection for increased milk would lead also to increased feed cost for maintenance.

**Genetic correlations** - Correlations between breeding values for two traits that arise because some of the same genes affect both of them. When two traits (weaning and yearling weight for example) are positively genetically correlated, successful selection for one trait will result in an increase in the other trait as well. When two traits are negatively genetically correlated (birth weight and calving ease, for example), successful selection for one trait will result in a decrease in the other. This is sometimes referred to an a genetic antagonism between traits.

**Genetic linkage map** – A diagram showing where genes and markers are located on a chromosome and their relationship to one another.

**Genetic trend** - An estimate of the annual change in genetic merit of individuals within a breed for a trait. It is computed from the average difference in estimated breeding values of animals born in a series of adjacent years.

**Genome** – The entire complement of DNA characteristic to individuals of a species.

**Genotype** - The two alleles present at a locus in an individual. For a locus with only two alleles, three genotypes are possible. For example, at the polled/horned locus in cattle, two common alleles are P ( the dominant allele preventing growth of horns) and p (the recessive allele allowing horn growth). The three possible genotypes are PP (homozygous dominant), Pp (heterozygous or carrier), and pp (homozygous recessive).

**Genotype x environment interaction** - When the difference in performance among genetic groups depends upon the environment in which they are compared. For example, the most profitable breed in the Great Plains is probably not the same as the most profitable breed on the Gulf Coast. Also, different breeds and crosses will be optimum for producing beef for different market specifications and requirements.

**Gestation** - The period of pregnancy or the period of time from conception until young are born, averaging about 285 days in cattle.

**Half-sibs** - Individuals having the same sire but different dams (or less commonly the same dam but different sires). Half-brothers, half-sisters, or half brother/sister.

**Harvest** - To slaughter an animal.

**Heat (estrous) synchronization** - Through hormonal manipulation, causing a group of cows or heifers to initiate estrous cycles at approximately the same time.

**Heifer pregnancy EPD** - Heifer pregnancy EPDs, expressed as probabilities of successful conception, predict differences among individuals in the ability of their daughters to conceive and calve at two years of age.

**Heritability** - The proportion of the differences among cattle, measured or observed, that is transmitted, on average, to their offspring. Heritability of different traits may vary from zero to one. The higher the heritability of a trait, the more accurately individual performance predicts breeding value and the more rapid should be the response to selection for that trait.

**Heritability estimate** - An estimate of the proportion of the total phenotypic variation between individuals for a certain trait that is due to transmissible genetic merit. It is the proportion of total variation for a trait caused by differences among individuals in breeding value.

**Heterosis (hybrid vigor)** - Amount by which the average performance for a trait in crossbred calves exceeds the average performance of the two or more purebreds that were mated in that particular cross.

**Heterozygote** – A genotype in which the two alleles at a locus are different, e.g. Pp.

**Homozygote** – A genotype in which the two alleles at a locus are the same, e.g. PP or pp.

**Hot carcass weight** - Weight of a carcass just prior to chilling.

**Inbreeding** - The mating together of parents more closely related than average in the population. Inbreeding decreases the proportion of heterozygous gene pairs in the offspring and increases the proportion of homozygous gene pairs. It increases the frequency of expression of genetic defects caused by recessive genes. Inbreeding may increase prepotency for simply inherited and highly heritable traits.

**Inbreeding coefficient** - A numerical measure, ranging from zero to 1.0, of the intensity of inbreeding of an individual. It represents the proportion of gene loci in the individual at which both genes are identical copies of the same ancestral gene.

**Inbreeding depression** - The reduction in performance level for many economically important traits that accompanies, on average, the increase in inbreeding coefficient.

**Incomplete dominance** - A situation in which neither of two alleles at a locus is fully dominant to the other. As a result, both are expressed. Typically the phenotype of the heterozygote is intermediate between that of the two homozygous genotypes.

**Indicator traits** – Traits that do not have direct economic importance, but aid in the prediction of economically important traits.

**Independent culling levels** - Selection based on cattle meeting specific levels of performance for every trait included in a selection program. Equivalently, culling based on the failure of cattle to meet the required standard for any trait in the program. For example, a breeder could cull all heifers with weaning weights below 400 pounds (or those in the bottom 20% on weaning weight) and yearling weights below 650 pounds (or those in the bottom 40%).

**Integrated resource management (IRM)** - Producing beef cattle in a manner that efficiently, profitably, and sustainably uses available human and physical resources.

**Interim EPD** - An expected progeny difference computed from an individual's own performance information and(or) the EPDs of its parents. Interim EPDs may be used to support selection and merchandizing decisions before EPDs from regularly scheduled national cattle evaluation runs become available.

**International cattle evaluation** - An evaluation utilizing data from more than one country, allowing comparisons of estimated genetic merit of cattle across countries.

**Intron** – DNA whose nucleotide sequence does not code for a product. An intron is transcribed but is excised and not translated. Therefore, it does not affect the sequence of sub-units in the gene product.

**Kidney, pelvic and heart fat (KPH)** - The internal carcass fat associated with the kidney, pelvic cavity, and heart. It is expressed as a percentage of chilled carcass weight. The weight of the kidneys is included in the estimate of kidney fat.

**Lactation** - The period of calf nursing between birth and weaning

**Lethal gene** - A gene or genes that cause the death of any individual in which they are expressed.

**Libido** - Sex drive. In bulls, the propensity to detect and mate estrous females.

**Linebreeding** - A form of inbreeding in which an attempt is made to concentrate the inheritance of some favored ancestor in descendants within a herd. The average relationship of the individuals in the herd to this ancestor is increased by linebreeding, but at the cost of an increased level of inbreeding.

**Linecross** - Offspring produced by crossing two or more inbred lines.

**Linkage** – The occurrence of two or more loci of interest on the same chromosome within 50 cM linkage distance of one another.

**Locus** – The specific location of a gene on a chromosome.

**Maintenance energy requirement** - The amount of feed energy required per day by an animal to maintain its body weight and support necessary metabolic functions.

**Marbling** - The specks of fat (intramuscular fat) distributed in muscular tissue. Marbling is usually evaluated in the rib eye between the 12th and 13th rib. It is a major factor in assigning USDA quality grade of a beef carcass.

**Marker Assisted Selection (MAS)** – The use of genetic markers to select for specific alleles at linked QTLs and therefore specific traits.

**Maternal effect** – For weaning weight, the dam's maternal ability which influences preweaning growth.

**Maternal EPD** - An EPD representing the effect of the genes of an individual's daughters on the trait of interest. A calving ease maternal EPD, for example, represents the ease with which an individual's daughters calves are born. See also Direct EPD.

**Maternal heterosis** - Amount by which the average performance for a trait in the progeny of crossbred cows exceeds the average performance of progeny of purebred cows of the two or more breed ancestors of the crossbred cows.

**Maternal sires** - Sires whose major function is to sire daughters (often crossbreds) with outstanding genetic merit for reproductive and maternal traits, adaptability to prevailing environmental conditions, and longevity. Such females would ideally be crossed to sires of a terminal breed with all offspring marketed.

**Maturity** - An estimation of the physiological age of the animal or carcass. It is assigned by assessing muscle characteristics and the stage of bone maturity.

**Metabolic body size** - The weight of the animal raised to the 3/4 power ($W^{0.75}$); a value indicative of the feed required to meet metabolic needs and maintain current body weight.

**Microsatellite** – A type of genetic marker. It is composed of repeating nucleotide sequences within DNA that are locus specific and variable in the number of times the sequence is repeated.

**Minisatellite** – A type of genetic marker widely used in DNA fingerprinting that consists of repeating subsets of nucleotides that are highly polymorphic and widely distributed throughout the genome.

**Morphology** - A parameter recorded during microscopic examination of semen in the standardized breeding soundness evaluation quantifying the visual characteristics of spermatozoa, expressed as the percentage that appear normal.

**Most Probable Producing Ability (MPPA)** - An estimate of a cow's future superiority or inferiority for a repeatable trait (such as progeny weaning weight) based upon the cow's past production in comparison to her contemporaries, her number of past records, and the repeatability of the trait in question.

**Motility** - A parameter recorded during microscopic examination of semen in the standardized breeding soundness evaluation quantifying spermatozoa movement, expressed as the percentage demonstrating forward progressive motility.

**Multiple breed evaluation** - A genetic prediction simultaneously utilizing data from more than one breed or crossbred group. It accounts not only for differences among animals in transmissible genetic value (EPDs) but also in breed differences and heterosis effects.

**Multiple trait evaluation** - A genetic prediction in which phenotypic merit for two or more genetically correlated traits (birth weight, weaning weight, and post-weaning gain, for example) is used simultaneously to estimate breeding values for each of the traits. Compared to single trait evaluations, multiple trait evaluations produce EPDs with higher accuracy and less bias from selection.

**Multiplicative adjustment factors** - A numerical quantity by which an animal's record is multiplied to reflect expected performance if the animal had belonged to some baseline group. For example, if calves from mature dams weighed, on average, 8% more than calves from two-year-old dams, the multiplicative factor to adjust calves from two-year-old dams to a mature age-of-dam equivalent would be 1.08. The use of multiplicative adjustment factors does affect variability in the trait after adjustment, inflating it if the multiplicative factor is greater than 1.0 and deflating it if it is less than 1.0.

**National Cattle Evaluation (NCE)** - Programs of cattle evaluation conducted by breed associations to compute estimated genetic merit of a population of animals. Carefully conducted national cattle evaluation programs give unbiased estimates of expected progeny differences (EPD's). Cattle evaluations are based on field data and rely on information from the individual animal, relatives, and progeny to calculate EPD's.

**Nonadditive gene effects** - Effects of specific gene pairs or combinations. Nonadditive gene effects occur when the heterozygous genotype is not intermediate in phenotypic value to the two homozygous genotypes. Undesirable homozygous gene combinations

lead to inbreeding depression in inbred populations; whereas favorable heterozygous gene combinations lead to heterosis in outbred herds.

**Nucleotide** – The subunit of DNA composed of a five carbon sugar, one of four nitrogenous bases (adenine, thymine, cytosine, or guanine), and a phosphate group.

**Number of contemporaries** - The number of animals of similar breed, sex, and age against which an animal was compared in performance tests. The greater the number of contemporaries, the greater the accuracy of comparisons.

**Optimum level of performance** - The most profitable or favorable ranges in levels of performance for the economically important traits in a given management system and environment. For example, although many cows produce too little milk, in every management system there is a point beyond which higher levels of milk production will reduce fertility and decrease profit.

**Outbreeding (outcrossing)** - Mating together of animals that are not closely related. Mild outbreeding is illustrated by mating cows to a sire of their own breed but who is not closely related to them. Such outcrossing may widen the genetic base in a herd and reduce inbreeding accumulation. A higher level of outcrossing is illustrated by crossing two *Bos taurus* breeds. This generally would result in beneficial heterosis for economically important traits. Crossing of a *Bos taurus* to a *Bos indicus* breed is outcrossing of an even greater extreme. These two subspecies have been genetically isolated from one another for a very long time, so heterosis is expected to be greater than from a within subspecies cross. The widest possible outcross is between genetically distinct species, cattle and bison for example. Progeny from such crosses, even when viable, frequently are sub-fertile or infertile.

**Ovulation** - Release of the female germ cell (egg or ovum) by the ovary. Cows usually ovulate several hours (up to 15 hours) after the end of estrus or standing heat.

**Palatability** - Acceptable to the taste or sufficiently agreeable in flavor to be eaten.

**Parturition** - The act of giving birth; calving.

**Pedigree** - A tabulation of names of an individual's ancestors, usually only those of the three to five closest generations. Pedigree information is used to establish genetic relationships among individuals to use in genetic evaluations.

**Percent calf crop** - The percentage cows and heifers exposed to breeding within a herd and year that produce calves.

**Performance data** - The record of the individual animal for reproduction, production, or carcass merit. The most useful performance records for management, selection, and promotion decisions will vary among purebred breeders and for purebred breeders compared with commercial cattle producers.

**Performance pedigree** - A pedigree that includes performance records of the individual, ancestors, relatives, and progeny in addition to the usual pedigree information. Expected progeny differences may also be included.

**Performance testing** - The systematic collection of comparative production information for use in genetic evaluation, selection decisions, and merchandizing.

**Phenotype** - The visible or measurable expression of a character; weaning weight, postweaning gain, or reproduction for example. For most traits, phenotype is influenced by both genotype and environment. The relative degree to which phenotypic variation among individuals is caused by transmissible genetic effects is the heritability of a trait.

**Phenotypic correlation** - The net correlation between two traits caused both by genetic factors and environmental factors simultaneously influencing both traits.

**Plasmid** – A circular piece of bacterial DNA often used as a cloning vector to produce recombinant DNA in large quantities.

**Polled** - Naturally hornless cattle. Having no horns or scurs.

**Polymerase Chain Reaction (PCR)** – A process used to rapidly amplify DNA. The original DNA is heated, causing the strands to separate. Specific primers are then added and bond to the single strands. DNA polymerase adds nucleotides to the primer, extending the new DNA strand. The PCR process can be repeated to produce many copies.

**Polymerase** – The enzyme system that facilitates the replication of DNA or RNA.

**Polymorphism** – The existence of two or more alleles at a gene locus in a population.

**Possible change** - The amount by which an individual's current EPD might reasonably be expected to change (either upwards or downwards) as more information becomes available in subsequent national cattle evaluations. This measurement of error in prediction decreases as the number of offspring per sire increases.

**Postpartum** - After the birth of an individual.

**Postpartum interval** - The number of days between parturition and the first post-partum estrus.

**Prepotency** - The ability of a parent to transmit its characteristics to its offspring so that they resemble that parent, and one another, more than usual. An individual that is homozygous for a dominant allele will show prepotency for the trait controlled by that gene, but not necessarily for any other trait. Inbred cattle, having a higher than average

degree of homozygosity, may be more prepotent than outbred cattle but only for simply inherited or highly heritable traits.

**Preweaning gain** - Weight gained between birth and weaning.

**Progeny** - The young, or offspring, of the parents.

**Progeny testing** - Evaluating the genotype or estimating the breeding value of an individual by evaluating the comparative phenotypic merit of its progeny.

**Puberty** - The age at which the reproductive organs become functionally operative and secondary sex characteristics begin to develop.

**Purebred** - An animal of known ancestry within a recognized breed that is eligible for registry in the official herd book of that breed.

**Qualitative (categorical) traits** - Those traits in which there is a sharp distinction between phenotypes, such as black vs. red or polled vs. horned. Only one or a few pairs of genes are involved in the expression of many qualitative traits.

**Quantitative traits** - Those traits, such as weaning weight, in which there is no sharp distinction in the range of phenotypes, with a gradual variation from one extreme to the other. Usually, many gene pairs are involved as well as environmental influences affect variation for such traits.

**Quantitative Trait Loci (QTL)** – A gene locus that has an effect on a quantitative trait. Often the actual nucleotide sequence is unknown, so selection is based upon genotype at a linked gene marker.

**RAPDs** – Randomly Amplified Polymorphic DNAs. Genetic markers that are randomly amplified using PCR with random primers to find polymorphic regions.

**Random mating** - A system of mating in which every female (cow and/or heifer) has an equal or random chance of being assigned to any bull used for breeding in a particular breeding season.

**Rate of genetic improvement** - The amount of improvement per unit of time (year). The rate of improvement is dependent on: (1) heritability of traits considered, (2) selection differentials, (3) genetic correlations among traits considered, (4) generation interval in the herd, and (5) the number of traits for which selections are made.

**Ratio** - An expression of an animal's performance for a particular trait relative to the herd or contemporary group average. It is calculated for most traits as:

$$\frac{\text{Individual Record}}{\text{Group Average}} \times 100.$$

**Recessive** - Recessive alleles are expressed only when homozygous. They must have been inherited from both parents before the phenotype with which they are associated can be expressed. At the locus affected the growth or absence of horns, for example, homozygous recessive pp individuals are horned whereas PP and Pp individuals are polled.

**Reduced animal model** - A genetic prediction procedure in which EPDs are computed directly for all parents in the population, while EPDs for non-parents and progeny are computed from the parent solutions. Predictions are equal and equivalent to those from the animal model. See animal model and sire model.

**Reference sire** - A bull that has previously been progeny tested and subjected to national cattle evaluation that is used concurrently with a test sire or sires in a new progeny test program. Reference sires provide genetic linkages among herds and/or existing databases, allowing indirect comparison of the test sire with bulls evaluated at other places and times.

**Regression** - A measure of the relationship between two variables expressing the expected change in one of them per unit change in the other. Using regression methods, the value of one trait can be predicted by knowing the value of others. For example, easily obtained carcass traits (hot carcass weight, fat thickness, rib eye area, and percentage of internal fat) are used to predict percent cutability.

**Relationship matrix** - A table that stores numerical values for the genetic relationships among all pairs of animals in a population. It is used in genetic prediction technology to properly predict the genetic merit of each animal from its own phenotypic merit and that of all of its relatives.

**Relative economic value** - The amount by which net income to the cattle enterprise will change, per unit change in genetic merit for a trait.

**Restriction enzyme (Endonuclease)** – One of over 150 enzymes derived from bacteria that recognizes specific DNA sequences and cuts the DNA at those sites.

**Restriction site** – The specific recognition site in DNA at which a specific restriction enzyme cuts the DNA.

**RFLP (Restriction Fragment Length Polymorphism)** – Polymorphism identified by digesting DNA with a restriction enzyme. Individuals differ in their resulting fragment patterns, which are visualized radioactively after separation through gel electrophoresis.

**Ribonucleic acid (RNA)** – A single-stranded molecule composed of ribonucleotides. RNA differs from DNA in that it contains the base uracil (U) instead of thymine (T). RNA is formed from DNA through transcription. It is involved in transferring and translating

the genetic message from a gene into a protein product with a specific physiological function.

**Rib eye area** - Area in square inches of the longissimus muscle measured at the 12th rib interface on the beef forequarter.

**Rotational crossbreeding** - Systems of crossing two or more breeds where the crossbred females are bred to bulls of the breed contributing the lowest proportion of genes to those females. Rotational crossbreeding systems maintain relatively high levels of heterosis and allow for replacement heifers to be produced from within the system.

**Scrotal circumference** - A measure of testes size obtained by measuring the distance around the testicles in the scrotum with a circular tape. Related to semen producing capacity and age at puberty of female sibs and progeny.

**Scurs** - Horny tissue or rudimentary horns that are attached to the skin rather than the bony parts of the head.

**Seedstock breeders** - Producers whose primary goal is to produce breeding stock rather than animals for feeding and slaughter. Progressive seedstock breeders have comprehensive programs designed to produce animals with optimum genetic merit for the combination of traits that will increase downstream profit of commercial beef production.

**Selection** - Choosing some individuals and rejecting others as parents of the next generation of offspring. Choosing as parents those individuals of superior estimated genetic merit for traits of interest

**Selection differential (reach)** - The difference between the average for a trait in selected cattle and the average for that same trait of the group from which they came. The expected response to selection for a trait is equal to selection differential times the heritability of the trait.

**Selection index** - A formula that combines performance records from several traits or different measurements of the same trait into a single value for each animal. Selection indexes assign relative emphasis to different traits according to their relative net economic importance, their heritabilities, and the genetic associations among them.

**Selection intensity** - The selection differential measured in phenotypic standard deviation units of the selected trait. It is inversely proportional to the proportion of available replacements actually selected to be parents of the next generation. For example, with A. I. compared to natural service, only a small proportion of bulls needs to be selected, and the selection intensity, selection differential, and selection response will be high.

**Serving capacity** - A measure of the motivation, willingness, and ability of a bull to detect and service females in estrus.

**Sibs** - Brothers and sisters of an individual.

**Sire x environment interaction** - When the difference in progeny performance among sires is dependent upon some factor of the environment under which the progeny were compared. For example, sires might rank differently for progeny performance in different contemporary groups, herds, or regions.

**Sire model** - A genetic prediction procedure in which EPDs are directly computed for all sires with progeny in the population.

**Sire summary** - Published genetic predictions (EPDs) of sires for economically important traits from national cattle evaluation programs.

**Sperm** - A mature male germ cell.

**Standardized performance analysis (SPA)** - A set of programs that allow producers to collect, process, and interpret information on biological efficiency and economic returns to a seedstock or commercial beef production enterprise.

**Stayability EPD** - The expected difference among individuals in the probability that a daughter will stay in the herd to at least six years of age. Because the majority of cows culled before the age of six are open, the EPD is primarily a prediction of sustained fertility in female offspring.

**Super ovulation** - Process by which a cow is treated with reproductive hormones to induce her to produce more eggs than normal.

**Systems approach** - An approach to evaluating alternative individuals, breeding programs, and selection schemes that involves assessment of alternatives in terms of their net impact on all inputs and output in the production system. This approach specifically recognizes that intermediate levels of performance in several traits may be more profitable than maximum performance for any single trait.

**Tandem selection** - Selection for one trait at a time. When the desired level is reached in one trait, then selection is practiced for a second trait.

**Temperament (disposition)** - A measure of the relative docility, wildness, or aggression of an animal toward unfamiliar situations, human handlers, or management interventions.

**Terminal sires** - Sires used in a crossbreeding system in which all of the progeny, both male and female, are marketed. For example F, crossbred dams could be bred to terminal sires of a third breed and all calves marketed. Although this system allows

maximum heterosis and complementary of breeds, replacement females must come from other herds.

**Threshold model** - Statistical procedures for analyzing traits that are expressed in an all-or-none fashion (alive vs dead or pregnant vs open, for example) but that probably are affected by environmental factors and by genes at many loci. When genetic predictions are conducted for such traits using the threshold model, resultant EPDs reflect the expected proportion of an individual's progeny that will vs will not express the trait.

**Transcription** – The process by which an RNA copy is made from a gene.

**Translation** – The process by which ribosomes use the nucleotide sequence in RNA to synthesize proteins.

**Ultrasonic measurements** - A non-invasive method used to estimate carcass characteristics and reproductive events. It operates off the principle that sound waves echo differently with different densities of tissue.

**USDA yield grade** - Measurements of carcass cutability categorized into numerical categories with 1 being the leanest and 5 being the fattest. Yield grade and cutability are predicted from the same four carcass traits.

**Variance** - Variance is a statistic that numerically describes the differences among individuals for a trait in a population. Without variation, no genetic progress would be possible, since genetically superior animals would not be distinguishable from genetically inferior ones.

**VNTR (Variable Number of Tandem Repeats)** – A type of minisatellite that is locus specific but cannot be generated by PCR.

**Weight per day of age (WDA)** - Weight of an individual divided by its age in days.

**Whole Herd Reporting (WHR)** – An inventory based performance recording system in which the production of all animals in a breeding herd and the performance of all progeny are accounted for annually. In calf-based systems, by contrast, progeny performance data may be recorded selectively and production information is not gathered on females who do not produce live calves. An inventory based Whole Herd Reporting system is necessary to acquire the data for genetic evaluation of some reproductive traits.

**Yield grade (see cutability)**- A numerical score ranging from 1 (high yield) to 5 (low yield) reflecting the expected proportion of boneless, closely-trimmed cuts from the beef carcass. It is estimated from a USDA prediction equation that includes measured or estimated values for hot carcass weight, rib eye area, fat thickness, and estimated percentage of kidney, pelvic, and heart fat.

## APPENDIX 1.1, BIF MEMBER BREED ASSOCIATIONS

American Angus Association
3201 Frederick Blvd.
St. Joseph, MO 64501

American Blonde d'Aquitaine Association
P.O. Box 12341
Kansas City, MO 64116

American Brahman Breeders Int.
3003 South Loop West, Suite 140
Houston, TX 77054

American Chianina Association
P.O. Box 890
Platte City, MO 64079

American Gelbvieh Association
10900 Dover Street
Westminister, CO 80021

American Hereford Association
P.O. Box 014059
Kansas City, MO 64101

American-International Charolais Association
P.O. Box 20247
Kansas City, MO 64195

American Murray Grey Association
P.O. Box 224
New Bethlehem, PA 16242

American Maine-Anjou Association
P.O. Box 1100
Platte City, MO 64079-1100

American Red Brangus Association
3995 E Hwy 290
Dripping Springs, TX 78620

American Red Poll Association
P.O. Box 147
Bethany, MO 64424

American Salers Association
19590 E Main Street #202
Parker, CO 80112

American Shorthorn Association
8288 Hascall St.
Omaha, NE 68124

American Simmental Association
1 Simmental Way
Bozeman, MT 59715

American Tarentaise Association
P. O. Box 34705
Kansas City, MO 64116-1105

Barzona Breeders Association of America
P. O. Box 631
Prescott, AZ 86302

Beefbooster Cattle, LTD
#226 1935 32nd Ave., NE
Calgary, AB T2E 7C8 Canada

Beefmaster Breeders United
6800 Park Ten Blvd. 290 W
San Antonio, TX 78123

Braunvieh Association of America
P.O. Box 6396
Lincoln, NE 68506

Canadian Angus Association
142, 6715 – 8th Street NE
Calgary, AB T2E 7H7 Canada

Canadian Charolais Association
2320 - 41st Ave., NE
Calgary, AB T2E 6W8 Canada

Canadian Gelbvieh Association
110, 2116 27 AV NE
Calgary, AB T2E 7A6 Canada

Canadian Hays Converter
650, 1207-11 AV SW
Calgary, AB T3C 0M5 Canada

Canadian Hereford Association
5160 Skyline Way, NE
Calgary, Alberta T2E 6V1 Canada

Canadian Limousin Association
2320 – 41 AV NE
Calgary, AB T2E 6W8

Canadian Simmental Association
13 - 401 19th St., NE
Calgary, Alberta T2E 7C4 Canada

Composite Cattle Breeders Alliance
2657 Village Drive
Cottonwood, AZ 86326

International Brangus Breeders Association
5750 Epsilon
San Antonio, TX 78249

North American Limousin Foundation
7383 S. Alton Way
Englewood, CO 80112

North American South Devon
2514 AV South
Santa Fe, TX 77510

Red Angus Association of America
4201 35 North
Denton, TX 76201

Salers Association of Canada
228, 2116 - 27th Ave., NE
Calgary, Alberta T2E 7A6 Canada

Santa Gertrudis Breeders Int.
P.O. Box 1257
Kingsville, TX 78364

Senepol Cattle Breeders
P.O. Box 808
Statam, GA 30666

United Braford Breeders
422 E. Main, Suite 218
Nacogdoches, TX 75961

# APPENDIX 2.1, NAAB UNIFORM CODING SYSTEM FOR IDENTIFYING SEMEN

## National Association of Animal Breeders
## Columbia, Missouri

The purpose of the NAAB Uniform Coding System for Identifying Semen is to provide a unique code number for each bull that includes: 1) identification of the source of the semen (the organization that processed the semen), 2) identification of the breed of the bull, and 3) a code number identifying each respective bull within breed within each A.I. organization.

It is recognized that the registration number for each bull is a unique number. However, it does not identify the source of the semen and in some cases is not readily recognizable by the breed. Experience has proven that individual herd owners, managers, and technicians prefer to use a more familiar code number instead of the registration number when identifying a sire used. The NAAB uniform code number will in many cases be seven or eight characters, which is equally as long as a registration number. However, since different segments of the code number have specific meanings, the entire code is much easier to remember and more acceptable by people in the field than is the registration number. In addition, by eliminating all blanks and leading zeros, the code number when written will often be shorter than most registration numbers.

The NAAB uniform code number was originally developed for use by commercial A. I. Organizations for identification of semen as it is exchanged and sold throughout the industry. In addition, the A. I. Requirements of the Purebred Dairy Cattle Association require a code identifying the source of dairy semen on each individual unit. Certified Semen Services (CSS) also requires all participating A. I. Businesses to label each breeding unit of semen produced by them with the elements of the NAAB Uniform Code. Logically, there are other needs for a code number identifying the source of semen. It would not be feasible to print a different code number for each of these and other purposes on each unit of semen in view of space availability and unnecessary duplication.

Incomplete sire identification by registration number in Dairy Herd Improvement (DHI) records has for years been a concern because of the significant loss of records that otherwise would be available for sire evaluation. Many herd owners and managers use bull code numbers instead of registration numbers when completing production record forms. Thus, it is logical that the code number be a unique number that can be uniformly converted to the correct registration number by use of a cross reference listing of each bull (i.e., the bull's code number cross referenced to his registration number). For this purpose the entire code number, including stud and breed identification and individual bull number, is necessary for the number to be unique for each bull. This system is being employed by the Dairy Record Processing Centers and there is little doubt that such a system will be useful in beef performance record programs.

The NAAB Uniform Code for Identifying Semen consists of a maximum of ten characters according to the following combination scheme:

**A.I. Center (Stud) Code**

Indicates the semen producing organization (stud) that collected and processed the semen. Stud code numbers are assigned by the NAAB to its member organizations and other semen producing organizations where warranted. It is comprised of one or more numeric characters. (Maximum of three characters).

**Breed Code**

Indicates the breed of bull. Dairy breed codes are two alpha characters and consistent with codes designed by USDA for the DHI program. Changes in dairy breed codes should be made only upon mutual agreement of the NAAB, USDA and DHI computing centers. Beef breed codes are two alpha characters and are assigned by NAAB in conjunction with Agriculture Canada and the Canadian A. I. Industry. (Maximum of two characters).

**Bull Code**

Indicates the respective bull's number assigned by the A. I. Organization collecting and processing the semen. Bull codes should be numeric codes with a maximum of five characters from 1 to 99999. All leading zeros and blanks should be omitted. If a bull is transferred to a second A.I. Organization for collection a different number should be assigned to the same bull. Since the stud code is different for each organization, it is not necessary to retain the same individual bull code when a bull is moved to a different stud. (Maximum of five characters).

**Examples**

<u>1HO777</u>

1 = Stud code for Cooperative Resources International
HO = Breed code for Holstein
777 = Bull code for Coastal Cleitus Andrew, Registration No. USA2110495

<u>109SM284</u>
109 = Stud code for Reproduction Enterprises, Inc.
SM = Breed code for Simmental
284 = Bull code for Black Knight U2, Registration No. 1138189

# NAAB UNIFORM BREED CODES

## Dairy Breeds

| Breed | Code | Breed | Code |
|---|---|---|---|
| AMERICAN LINEBACK | LD | HOLSTEIN | HO |
| AYRSHIRE | AY | JERSEY | JE |
| BROWN SWISS | BS | RED & WHITE | WW |
| GUERNSEY | GU | SHORTHORN (Milking) | MS |

## Beef, Dual Purpose, Lesser Dairy, Other Breeds

| | | | |
|---|---|---|---|
| AFRICANDER | AF | LIMOUSIN | LM |
| ANGUS | AN | LINCOLN RED | LR |
| ANKINA | AK | LOWLINE (LOALA) | LO |
| ANKOLE-WATUSI | AW | LUING | LU |
| AMERICAN BREED | AE | MAINE - ANJOU | MA |
| AMERIFAX | AM | MASHONA | MH |
| BARZONA | BA | MANDALONG SPECIAL | ML |
| BEEFALO | BE | MARCHIGIANA | MR |
| BEEF FRIESIAN | BF | MAREMMANA | ME |
| BEEFMASTER | BM | MEXICAN CORRIENTE | MC |
| BELGIAN BLUE | BB | MUESE-RHINE-ISSEL | MI |
| BELTED GALLOWAY | BG | MURRAH | MU |
| BLONDE D'AQUITAINE | BD | MURRAY GREY | MG |
| BONSMARA | NS | NELLORE | NE |
| BRAFORD | BO | NORMANDE | NM |
| BRAHMAN | BR | NORWEGIAN RED | NR |
| BRAHMOUSIN | BI | PARTHENAISE | PA |
| BRALER | BL | PIEDMONTESE | PI |
| BRANGUS | BN | PINZGAUER | PZ |
| BRAUNVIEH | BU | RANGER | RA |
| BRITISH WHITE | BW | RED ANGUS | AR |
| BROWN SWISS (BEEF) | SB | RED BRAHMAN | RR |
| BUELINGO | BQ | RED BRANGUS | RB |
| CANADIENNE | CN | RED DANE | RD |
| CHARBRAY | CB | RED POLL | RP |
| CHAROLAIS | CH | ROMAGNOLA | RN |
| CHI-ANGUS | CG | ROMOSINUANO | RS |
| CHIANINA | CA | ROTBUNTE | RO |
| CHI-MAINE | CM | SAHIWAL | SW |
| DANISH RED & WHITE | RW | SALERS | SA |
| DEVON | DE | SANTA GERTRUDIS | SG |
| DEXTER | DR | SENEPOL | SE |

| | |
|---|---|
| DUTCH BELTED | DL |
| ERINGER | ER |
| FLAMAND | FA |
| FLORIDA CRACKER | FC |
| FRIBOURG | FR |
| GALLOWAY | GA |
| GELBRAY | GE |
| GELBVIEH | GV |
| GRQUVIEH | GI |
| GRONNINGEN | GR |
| GUZERA | GZ |
| GYR (GIR) | GY |
| HAYS CONVERTER | HC |
| HEREFORD (horned) | HH |
| HEREFORD (polled) | HP |
| HIGHLAND (Scotch) | SH |
| HYBRID (Alberta) | HY |
| INDU BRAZIL | IB |
| KOBE (WAGYU) | KB |
| SHORTHORN (Beef Scotch) | SS |
| SHORTHORN (Polled) | SP |
| SHORTHORN (Illwara) | IS |
| SIMBRAH | SI |
| SIMMENTAL | SM |
| SOUTH DEVON | DS |
| SUSSEX | SX |
| TABAPUA | TB |
| TARENTAISE | TA |
| TAURINDICUS | TN |
| TEXAS LONGHORN | TL |
| TULI | TI |
| WELSH BLACK | WB |
| WEST FLEMISH RED | WF |
| WHITE PARK | WP |
| CROSSBREEDS (Twinner) | XT |
| CROSSBREEDS | XX |

## APPENDIX 2.2, INTERNATIONAL YEAR/LETTER DESIGNATIONS FOR ANIMAL IDENTIFICATION

International letters are designated for each year of birth. This option is easy to use in conjunction with numbers. For example, M001 and M002 might be used to indicate the first and second calf born in the year 2002.

| | | | | | |
|---|---|---|---|---|---|
| A | 1969 | U | 1986 | N | 2003 |
| B | 1970 | W | 1987 | P | 2004 |
| C | 1971 | X | 1988 | R | 2005 |
| D | 1972 | Y | 1989 | S | 2006 |
| E | 1973 | Z | 1990 | T | 2007 |
| F | 1974 | A | 1991 | U | 2008 |
| G | 1975 | B | 1992 | W | 2009 |
| H | 1976 | C | 1993 | X | 2010 |
| J | 1977 | D | 1994 | Y | 2011 |
| K | 1978 | E | 1995 | Z | 2012 |
| L | 1979 | F | 1996 | A | 2013 |
| M | 1980 | G | 1997 | B | 2014 |
| N | 1981 | H | 1998 | C | 2015 |
| P | 1982 | J | 1999 | D | 2016 |
| R | 1983 | K | 2000 | E | 2017 |
| S | 1984 | L | 2001 | F | 2018 |
| T | 1985 | M | 2002 | G | 2019 |

The letters I, O, Q, and V are not used.

## APPENDIX 3.1, BIF STANDARD ADJUSTMENT FACTORS FOR BIRTH AND WEANING WEIGHT

| Age of Dam at Birth of the Calf | Birth Weight | Weaning Weight | |
|---|---|---|---|
| | | Male | Female |
| 2 | +8 | +60 | +54 |
| 3 | +5 | +40 | +36 |
| 4 | +2 | +20 | +18 |
| 5 - 10 | 0 | 0 | 0 |
| 11 and older | +3 | +20 | +18 |

Note: 1) Standard birth weights are 75 lb. for males and 70 lb. for females.

2) Breed specific adjustment factors have been developed by individual breed associations from breed data. Factors used by individual breed associations are subject to change. Contact the respective breed association for more information about their birth and weaning weight adjustment factors.

3) See Chapter 3 of these guidelines for information on using adjustment factors in adjustment formulas.

# APPENDIX 3.2, MARBLING SCORES AND QUALITY GRADES IN THE UNITED STATES AND CANADA

## Canadian Marbling Standards

Canadian marbling standards were changed in 1996 and now use the copyrighted standards of the United States. The minimum marbling standards used for USDA Prime (slightly abundant), Choice (small) and Select (slight) are the same standards used in Canada to segregate youthful beef carcasses into Canada Prime, AAA, and AA quality grades, respectively. Canada A has no comparable USDA grade. Canada A is restricted to youthful carcasses that have at least trace amounts of marbling.

A 1994 comparative study of 4,600 carcasses revealed a correlation of approximately 0.85 between final United States and Canadian quality grades. It is important to note that Canada has now adopted the copyrighted USDA standards for slight, small, and slightly abundant marbling scores. Canadian standards have muscling, color, and fat thickness minimum requirements for the four quality grades of youthful beef carcasses (A, AA, AAA, Canada Prime). Whereas the USDA system are weighted and one factor may compensate for a deficiency in another factor, the Canadian system allows no "quality attribute offsets."

In the USDA system, carcasses up to 42 months of age (B maturity) can qualify for the Prime, Choice, Select, and Standard grades. In the Canadian system, however, animals showing more than 30 months of physiological age are removed from the four youthful quality grades (A, AA, AAA, Canada Prime) to either the "D" or "E" grades. The USDA quality grading system penalizes dark cutting beef by no more than one full grade. However, dark cutters in Canada are removed to the B4 grade. Further, the Canadian system recognizes yellow fat color as a quality discount and removes all carcasses with yellow fat to the B2 grade. Finally, the Canadian system removes all carcasses with deficient muscling to the B3 grade. Beef carcasses with less than firm texture are removed to the B grades in the Canadian system.

## Correspondence Between USDA and Canadian Quality Grades

The level of marbling in Canada Prime corresponds to the levels associated with USDA Prime. Similarly, marbling requirements for Canada AAA and AA correspond to requirements for USDA Choice and Select, respectively. The level of marbling required for Canada A corresponds to the upper levels required for USDA Standard. However, these grades (A, Standard) do not correspond exactly due to allowable quality defects in USDA Standard.

**Table 1. Canadian Quality Grades**

| | Youthful (≤ 30 mo) | | Mature (> 30 mo) | |
|---|---|---|---|---|
| **Characteristic** | **Level** | **Grade** | **Level** | **Grade** |
| Muscling | Good | -- [a] | Excellent | D1 |
| | Poor | B3 | | |
| Lean color | Bright red | -- | Poor | D3 |
| | Dark | B4 | | |
| Fat color | White | -- | Yellow | D2 |
| | Yellow | B2 | | |
| Fat thickness | > 4 mm | -- | ≥ 15 mm | D4 |
| | < 4 mm | B1 | | |
| Marbling | Absent | B1 | | |
| | Traces | A | | |
| | Slight | AA | | |
| | Small | AAA | | |
| | ≥ Sl. Abund. | Prime | | |
| Gender | Bull | E | | |

[a] Indicates carcass eligible for the four youthful, "high" quality grades: A, AA, AAA, Canada Prime. Other grades assigned on the basis of quality defects.

Further information available from the Canadian Beef Export Federation at: http://www.cbef.com

# APPENDIX 5.1, NATIONAL CATTLE EVALUATION

## Animal Model for a Maternally Influenced Trait

In matrix notation the model is:

$$y = Xb + Z_d u_d + Z_m u_m + Z_{pe} u_{pe} + e$$

where X and Z's are incidence matrices relating the fixed effects (b) and the random factors ($u_d$, direct breeding values; $u_m$, maternal breeding values and $u_{pe}$, maternal permanent environmental effects) to the vector of records, y.

The variance-covariance matrix for the random effects in the model is:

$$V\begin{bmatrix} u_d \\ u_m \\ u_{pe} \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & A\sigma_{am} & 0 & 0 \\ A\sigma_{am} & A\sigma_m^2 & 0 & 0 \\ 0 & 0 & I\sigma_{pe}^2 & 0 \\ 0 & 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

where

A = Wright's numerator relationship matrix,
$\sigma_a^2$ = additive direct genetic variance,
$\sigma_m^2$ = additive maternal genetic variance,
$\sigma_{am}$ = genetic covariance between additive direct and maternal effects,
$\sigma_{pe}^2$ = maternal permanent environmental variance, and
$\sigma_e^2$ = remaining (residual) environmental variance.

The following occurs because $u_d$ and $u_m$ include the same animals.

$V\begin{bmatrix} u_d \\ u_m \end{bmatrix} = \begin{bmatrix} \sigma_a^2 & \sigma_{am} \\ \sigma_{am} & \sigma_m^2 \end{bmatrix} \otimes A = G_o$ where $\otimes$ represents the direct product.

Taking the inverse of $G_o$ and multiplying by $\sigma_e^2$ gives the following:

$$\begin{bmatrix} \alpha_1 & \alpha_2 \\ \alpha_2 & \alpha_3 \end{bmatrix} = \begin{bmatrix} \sigma_a^2 & \sigma_{am} \\ \sigma_{am} & \sigma_m^2 \end{bmatrix}^{-1} \sigma_e^2 = G_o^{-1}\sigma_e^2$$

With $\alpha_4 = \frac{\sigma_e^2}{\sigma_{pe}^2}$,

the mixed animal model equations for a maternally influenced trait after multiplying both sides of the equations by $\sigma_e^2$ are:

$$\begin{bmatrix} X'X & X'Z_d & X'Z_m & X'Z_{pe} \\ Z_d'X & Z_d'Z_d + A^{-1}\alpha_1 & Z_d'Z_m + A^{-1}\alpha_2 & Z_d'Z_{pe} \\ Z_m'X & Z_m'Z_d + A^{-1}\alpha_2 & Z_m'Z_m + A^{-1}\alpha_3 & Z_m'Z_{pe} \\ Z_{pe}'X & Z_{pe}'Z_d & Z_{pe}'Z_m & Z_{pe}'Z_{pe} + I\alpha_4 \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{u}_d \\ \hat{u}_m \\ \hat{u}_{pe} \end{bmatrix} = \begin{bmatrix} X'y \\ Z_d'y \\ Z_m'y \\ Z_{pe}'y \end{bmatrix}.$$

**Reduced Animal Model**

The number of equations resulting from the application of the animal model can be extremely large, exceeding the number of animals in the population. The reduced animal model (RAM) provides the same solutions (breeding values) as the animal model but reduces the overall number of equations to be solved. The reduction in number of equations is accomplished by absorbing the equations for non-parents into the equations for parents. Thus the number of equations in RAM is a function of the number of parents, which is considerably less than the total number of animals in the population. The animal model equations for a maternally influenced trait can be reduced in number as shown by Quaas and Pollak (1980; J. Anim. Sci. 51:1277). Bertrand et al. (1985; BIF Meeting Proceedings) provide a discussion of how to build the RAM equations for a maternally influenced trait.

**Multiple-Trait Models**

The following multiple-trait model is for a maternally influenced trait such as weaning weight and a second trait such as postweaning gain:

$$\begin{bmatrix} y_w \\ y_g \end{bmatrix} = \begin{bmatrix} X_w & O \\ O & X_g \end{bmatrix} \begin{bmatrix} b_w \\ b_g \end{bmatrix} + \begin{bmatrix} Z_w & O & Z_m & Z_{pe} \\ O & Z_g & O & O \end{bmatrix} \begin{bmatrix} u_w \\ u_m \\ u_g \\ u_{pe} \end{bmatrix} + \begin{bmatrix} e_w \\ e_g \end{bmatrix}$$

where $y_w$ and $y_g$ are vectors of weaning weight and postweaning gain records. The X's, b's, Z's, u's and e's are the same as previously defined with the subscripts w and g indicating weaning weight and postweaning gain.

The variance-covariance matrix for the random effects in this model is:

$$V\begin{bmatrix} u_w \\ u_m \\ u_g \\ u_{pe} \\ e_w \\ e_g \end{bmatrix} = \begin{bmatrix} g_{11}A & g_{12}A & g_{13}A & 0 & 0 & 0 \\ g_{12}A & g_{22}A & g_{23}A & 0 & 0 & 0 \\ g_{13}A & g_{23}A & g_{33}A & 0 & 0 & 0 \\ 0 & 0 & 0 & g_{44}I & 0 & 0 \\ 0 & 0 & 0 & 0 & \sigma^2_{ew}I & \sigma_{ew,eg}I \\ 0 & 0 & 0 & 0 & \sigma_{ew,eg}I & \sigma^2_{eg}I \end{bmatrix}$$

where

$g_{11} = \sigma^2_{aw}$ = additive direct genetic variance for weaning weight,
$g_{22} = \sigma^2_{m}$ = additive maternal genetic variance for weaning weight,
$g_{33} = \sigma^2_{ag}$ = additive genetic variance for postweaning gain,
$g_{12} = \sigma_{aw,m}$ = additive covariance between direct and maternal genetic effects for weaning weight,
$g_{13} = \sigma_{aw,g}$ = additive genetic covariance between weaning direct and postweaning gain,
$g_{23} = \sigma_{m,ag}$ = additive genetic covariance between maternal ability for weaning weight and postweaning gain,
$g_{44} = \sigma^2_{pe}$ = maternal permanent environmental variance for weaning weight.

With $\sigma^2_{ew}$ and $\sigma^2_{eg}$, the residual variances, and $\sigma_{ew,eg}$, the residual covariance:

$$R^{-1} = \begin{bmatrix} R^{11} & R^{12} \\ R^{21} & R^{22} \end{bmatrix} = \begin{bmatrix} I\sigma^2_{ew} & I\sigma_{ew,eg} \\ I\sigma_{ew,eg} & I\sigma^2_{eg} \end{bmatrix}^{-1}$$

and

$$G_o^{-1} = \begin{bmatrix} g^{11} & g^{12} & g^{13} \\ g^{21} & g^{22} & g^{23} \\ g^{31} & g^{32} & g^{33} \end{bmatrix} = \begin{bmatrix} \sigma^2_{aw} & \sigma_{aw,m} & \sigma_{aw,ag} \\ \sigma_{aw,m} & \sigma^2_{m} & \sigma_{m,ag} \\ \sigma_{aw,ag} & \sigma_{m,ag} & \sigma^2_{ag} \end{bmatrix}^{-1}$$

The full mixed-model equations assuming no missing observations for each trait are:

$$\begin{bmatrix}
X_w'R^{11}X_w & X_w'R^{12}X_g & X_w'R^{11}Z_w & X_w'R^{11}Z_m & X_w'R^{12}Z_g & X_w'R^{11}Z_{pe} \\
X_g'R^{12}X_w & X_g'R^{22}X_g & X_g'R^{21}Z_w & X_g'R^{21}Z_m & X_g'R^{22}Z_g & X_g'R^{21}Z_{pe} \\
Z_w'R^{11}X_w & Z_w'R^{21}X_g & Z_w'R^{11}Z_w + A^{-1}g^{11} & Z_w'R^{11}Z_m + A^{-1}g^{12} & Z_w'R^{12}Z_g + A^{-1}g^{13} & Z_w'R^{11}Z_{pe} \\
Z_m'R^{11}X_w & Z_m'R^{21}X_g & Z_m'R^{11}Z_w + A^{-1}g^{12} & Z_m'R^{11}Z_m + A^{-1}g^{22} & Z_m'R^{12}Z_g + A^{-1}g^{23} & Z_m'R^{11}Z_{pe} \\
Z_g'R^{12}X_w & Z_g'R^{22}X_g & Z_g'R^{12}Z_w + A^{-1}g^{13} & Z_g'R^{12}Z_m + A^{-1}g^{23} & Z_g'R^{22}Z_g + A^{-1}g^{33} & Z_g'R^{21}Z_{pe} \\
Z_{pe}'R^{11}X_w & Z_{pe}'R^{21}X_g & Z_{pe}'R^{11}Z_w & Z_{pe}'R^{11}Z_m & Z_{pe}'R^{21}Z_g & Z_{pe}'R^{11}Z_{pe} + Ig_{44}^{-1}
\end{bmatrix}$$

$$X \begin{bmatrix} \hat{b}_w \\ \hat{b}_g \\ \hat{u}_w \\ \hat{u}_m \\ \hat{u}_g \\ \hat{u}_{pe} \end{bmatrix} = \begin{bmatrix}
X_w'R^{11}y_w + X_w'R^{12}y_g \\
X_g'R^{22}y_g + X_g'R^{21}y_w \\
Z_w'R^{11}y_w + Z_w'R^{12}y_g \\
Z_m'R^{11}y_w + Z_m'R^{12}y_g \\
Z_g'R^{22}y_g + Z_g'R^{21}y_w \\
Z_{pe}'R^{11}y_w + Z_{pe}'R^{12}y_g
\end{bmatrix}$$

Quaas and Pollak (1980; J. Anim. Sci. 51:1277) show the multiple-trait mixed model equations for the full animal model.

The structure of $R_n$ and $R_n^{-1}$ changes for animals with missing records. Quaas and Pollak (1980; J. Anim. Sci. 51:1277) present the multiple-trait animal and reduced animal mixed model equations when some do not have all traits measured.

The reduced animal model for the multiple-trait case as with the single trait model takes advantage of representing a non-parent record as the average of parental breeding values plus a Mendelian sampling effect.

**Solution Methods**

Generally, a variant of the Gauss-Seidel method, such as successive-over-relaxation or block iteration, is used to solve the mixed model equations. Some variants include bumping factors or other "tricks" to improve convergence rates. Absorption of fixed effects will decrease the number of rounds required to converge, but absorption can

increase the number of non-zero elements and increase computer requirements for setting up the equations and for input of the coefficients for each round of iteration.

Threshold and survival models are iteratively solved using either Newton-Raphson iteration or an expectation maximization (EM) method. Newton's method usually requires fewer total rounds of iteration on the right hand sides but the EM approach requires less computation for each round.

Computing the solutions to mixed model equations is not as problematic as it was due to the availability of large computer servers. This additional computing power has also improved the ability to achieve more complete convergence of large systems of equations. Because the round-by-round convergence rates and criteria that are typically published in the literature may not adequately account for slow convergence rates that are often observed in multiple trait analyses, it may be prudent to iterate the system of equations thousands of rounds to insure convergence and(or) to establish when convergence occurs for use in future analyses.

## Interim EPDs

**Forming adjusted deviations to compute interim EPDs.** Using the animal's own record and information regarding its contemporaries, an adjusted within-group deviation is obtained for each available trait. The adjusted deviations for birth weight, weaning weight, and yearling weight are shown in Table 1. The contemporary group mean is adjusted for the average EPD of the sires and dams represented in the group. For weaning weight and yearling weight, the contemporary group is adjusted for the average maternal environment ($2*EPD_{mmk}$ + PE) provided by the dams in the group. The calf's deviation from its adjusted group mean is then adjusted for the expected contribution of its parents. The adjusted deviation for each trait represents what cannot be explained by the contemporary group and the parents' expected contribution to the calf's performance. See the table for an outline for computing adjusted deviations for interim EPDs.

**Computing single-trait interim EPDs.** The single-trait interim EPD can be represented as follows:

$$EPD_i = 0 .5\ EPD_{s,i} + 0.5\ EPD_{d,i} + 0.5\ b_i\ D_i$$

where $EPD_{s,i}$ and $EPD_{d,i}$ are the sire and dam EPDs for the $i^{th}$ trait, $b_i$ is the regression coefficient for the $i^{th}$ trait and $D_i$ is the adjusted deviation for the $i^{th}$ trait. For each trait, a value for $b_i$ is calculated for each parent combination: Known Parents, Known Sire and Unknown Dam, Unknown Sire and Known Dam, and Unknown Parents. In the case where a calf does not have a record for a particular trait, the interim EPD for that trait will be the average of the parents' EPDs or the pedigree index.

Ignoring the potential genetic and environmental covariances between the traits in the evaluations, the regression coefficients (b) can be easily calculated and stored for use during processing. If the covariance between direct and maternal effects for weaning weight is assumed to be zero, the interim maternal EPD will be the pedigree index if both parents are known or where the sire is unknown and the dam is known. In the case of a known sire and an unknown dam or the case of unknown parents, the calf's weaning deviation will have an influence on the interim maternal EPD. The $b_i$s are shown in the table of regression coefficients for each trait and parent combination (Table 2).

**Multiple-trait interim EPDs.** Procedures here are analogous to computations for "back-solving" to get the solutions for a "non-parent" in a reduced animal model analysis. Interim EPDs are computed as:

$\mathbf{EPD}_I = 0.5 \times (\mathbf{EPD}_S + \mathbf{EPD}_D) + 0.5\mathbf{B}_{ij} \times \delta$ where $\mathbf{EPD}_X = .5\hat{\mathbf{u}}_X$; $\mathbf{u}_X$ = vector of breeding values for X = individual, sire, dam, respectively; $\delta$ is a vector of residuals (Table 1) and $\mathbf{B}_{ij}$ is a matrix of partial regression coefficients of $\mathbf{u}_I$ on $\delta$. $\mathbf{B}_{ij}\delta$ predicts Mendelian sampling deviations for each evaluated trait using all available information; it is halved to go from breeding value (BV) to EPD.

With a multiple-trait model for BW, WW (direct and maternal), and YW, there are five combinations (models) of known parents required to compute interim EPDs. In Table 3, the required design matrices are shown. Each design matrix describes the influence of the sire (S), dam (D), and individual calf (I) on the calf's own performance record for each trait. The breeding values are ordered, within S, D and I, BW (b), WW-direct (w), YW (y), and WW-maternal (m). The dam's permanent environmental effect for weaning weight is in the last column ($D_p$). The first design matrix $\mathbf{Z}_f$ is for the full animal model for an animal with a record, pedigree information, and no progeny data. The following design matrices are for a non-parent model with known parents ($\mathbf{Z}_1$), a known sire and unknown dam ($\mathbf{Z}_2$), an unknown sire and known dam ($\mathbf{Z}_3$), and the case where both parents are unknown ($\mathbf{Z}_4$). Each $\mathbf{Z}_i$ is a 3×15 matrix

Full Model: $\mathbf{y} = \mathbf{X}\beta + \mathbf{Z}_f\mathbf{u} + e \Rightarrow$ $\mathbf{R}_f = var(\mathbf{e}) = \mathbf{V} - \mathbf{Z}_f\mathbf{G}\mathbf{Z}_f^T$

Reduced Model: $\mathbf{y} = \mathbf{X}\beta + \mathbf{Z}_i\mathbf{u} + \left[(\mathbf{Z}_f - \mathbf{Z}_i)\mathbf{u} + \mathbf{e}\right] \Rightarrow$ $\mathbf{R}_i = var\left\{(\mathbf{Z}_f - \mathbf{Z}_i)\mathbf{u} + \mathbf{e}\right\} = \mathbf{V} - \mathbf{Z}_i\mathbf{G}\mathbf{Z}_i^T$

where $\mathbf{u} = [\mathbf{u}_S, \mathbf{u}_D, \mathbf{u}_I]$, $\mathbf{V}$ is the phenotypic covariance matrix, $\mathbf{Z}_{ij}$ denotes $\mathbf{Z}_i$ with the rows corresponding to traits missing in the $j^{th}$ combination of traits set to zero and

$$\mathbf{G} = \text{var}\begin{pmatrix} \mathbf{u}_S \\ \mathbf{u}_D \\ \mathbf{u}_I \\ pe \end{pmatrix} = \begin{pmatrix} \mathbf{G}_0 & 0 & .5\mathbf{G}_0 & 0 \\ 0 & \mathbf{G}_0 & .5\mathbf{G}_0 & 0 \\ .5\mathbf{G}_0 & .5\mathbf{G}_0 & \mathbf{G}_0 & 0 \\ 0 & 0 & 0 & \sigma_p^2 \end{pmatrix} \quad \text{where } \mathbf{G}_0 = \begin{bmatrix} \sigma_b^2 & \sigma_{bw} & \sigma_{by} & \sigma_{bm} \\ \sigma_{bw} & \sigma_w^2 & \sigma_{wy} & \sigma_{wm} \\ \sigma_{by} & \sigma_{wy} & \sigma_y^2 & \sigma_{ym} \\ \sigma_{bm} & \sigma_{wm} & \sigma_{ym} & \sigma_m^2 \end{bmatrix}$$

There are four possible non-parent models and, for BW, WW, and YW, five possible combinations of traits recorded for a particular calf (assuming YW without WW eliminated because both are needed to compute post-weaning gain). Thus there are 20 different $\mathbf{B}_{ij}$.

$$\mathbf{B}_{ij} = cov\left\{\mathbf{u}_I, \left(\left[\mathbf{Z}_{fj}-\mathbf{Z}_{ij}\right]\mathbf{u}+\mathbf{e}\right)^T\right\}\left\{var\left(\left[\mathbf{Z}_{fj}-\mathbf{Z}_{ij}\right]\mathbf{u}+\mathbf{e}\right)\right\}^{-1} = \left(\left[\mathbf{G}_{IS}, \mathbf{G}_{ID}, \mathbf{G}_{II}, \mathbf{0}\right]\left[\mathbf{Z}_{fj}-\mathbf{Z}_{ij}\right]^T\right)\times\mathbf{R}_{ij}^{-1}$$

.

where $R_{ij}^{-1}$ shown in Table 4 depend on traits measured.

**Interim EPD accuracy.** A single-trait approximation for an interim EPD accuracy is:

$$ACC_I \approx 1-\sqrt{W+W^2\left[\left(1-ACC_S\right)^2+\left(1-ACC_D\right)^2\right]}$$

where $W=\frac{\alpha}{1+2\alpha}, \alpha=\frac{1-r-.75h_d^2}{h_d^2}$, r = repeatability of the trait and $h_d^2$ = direct heritability. With no genetic nor environmental maternal effects, $\alpha=\left(1-h_d^2\right)/h_d^2$. For maternal EPDs or if the calf has no record for the trait, W = 0.5, which yields the accuracy of a pedigree index.

**Appendix 5.1, Table 1. Adjusted Deviations for Interim EPDs**

Birth Weight

$$BW_{DEV} = \left(BW - EPD_S - EPD_D\right) - \left(CG_{BW} - \overline{EPD_S} - \overline{EPD_D}\right)$$

$CG_{BW}$ = contemporary group average: $EPD_s$ ($EPD_d$) = sire's (dam's) EPD.

Weaning Weight

$$WW_{DEV} = \left(WW - EPD_S - PPA_D\right) - \left(CG_{BW} - \overline{EPD_S} - \overline{PPA_D}\right)$$

$CG_{WW}$ = contemporary group average;

$EPD_s$ = sire's EPD;

$PPA_d$ = dam's predicted producing ability ($EPD_{WW} + 2\times EPD_{MMK} + PE$);

$EPD_{WW}$ = dam's weaning weight EPD:

$EPD_{mmk}$ = dam's maternal milk EPD; and

PE = dam's permanent environmental effect for weaning weight.

Yearling Weight

$$YW_{DEV} = \left(YW - EPD_S - EPD_D - 2\times EPD_{mmk} + PE\right) - \left(CG_{YW} - \overline{EPD_S} - \overline{EPD_D} - 2\times\overline{EPD_{mmk}} + \overline{PE}\right)$$

$CG_{yw}$ = contemporary group average;

$EPD_s$ = sire's EPD; $EPD_d$ = dam's EPD;

$EPD_{mmk}$ = dam's maternal milk EPD; and

PE = dam's permanent environmental effect for weaning weight.

Note: In the above, BW, WW and YW are assumed to be adjusted for any fixed effects not included in CG, e.g., age of calf, age of dam, sex of calf where applicable.

**Appendix 5.1, Table 2. Regression Coefficients for Single-Trait Interim EPDs**

| Birth Wt. | Weaning Wt. | Yearling Wt. |
|---|---|---|
| Known Parents: | Known Parents: | Known Parents: |
| $b = .5\sigma_a^2/(.5\sigma_a^2 + \sigma_e^2)$ | $b_d = .5\sigma_a^2/(.5\sigma_a^2 + \sigma_e^2)$<br>$b_m = .5\sigma_{am}/(.5\sigma_a^2 + \sigma_e^2)$ | $b = .5\sigma_a^2/(.5\sigma_a^2 + \sigma_e^2)$ |
| Known Sire, Unknown Dam: | Known Sire, Unknown Dam: | Known Sire, Unknown Dam: |
| $b = .75\sigma_a^2/(.75\sigma_a^2 + \sigma_e^2)$ | $b_d = (.75\sigma_a^2 + .75\sigma_{am})/(.5\sigma_a^2 + \sigma_{am} + \sigma_m^2 + \sigma_{pe}^2 + \sigma_e^2)$<br>$b_m = (.5\sigma_a^2 + .75\sigma_{am})/(.75\sigma_a^2 + \sigma_{am} + \sigma_m^2 + \sigma_{pe}^2 + \sigma_e^2)$ | $b = .75\sigma_a^2/(.75\sigma_a^2 + \sigma_m^2 + \sigma_{pe}^2 + \sigma_e^2)$ |
| Unknown Sire, Known Dam: | Unknown Sire, Known Dam: | Unknown Sire, Known Dam: |
| $b = .75\sigma_a^2/(.75\sigma_a^2 + \sigma_e^2)$ | $b_d = .75\sigma_a^2/(.75\sigma_a^2 + \sigma_e^2)$<br>$b_m = .75\sigma_{am}/(.75\sigma_a^2 + \sigma_e^2)$ | $b = .75\sigma_a^2/(.75\sigma_a^2 + \sigma_e^2)$ |
| Unknown Parents: | Unknown Parents: | Unknown Parents: |
| $b = \sigma_a^2/(\sigma_a^2 + \sigma_e^2)$ | $b_d = (\sigma_a^2 + .5\sigma_{am})/(\sigma_a^2 + \sigma_{am} + \sigma_{pe}^2 + \sigma_e^2)$<br>$b_m = (.5\sigma_a^2 + \sigma_{am})/(\sigma_a^2 + \sigma_{am} + \sigma_{pe}^2 + \sigma_e^2)$ | $b = \sigma_a^2/(\sigma_a^2 + \sigma_m^2 + \sigma_{pe}^2 + \sigma_e^2)$ |

**Appendix 5.1, Table 3. Design Matrices for Multiple-Trait Interim EPDs**

| Trait | $S_b$ | $S_w$ | $S_y$ | $S_m$ | $D_b$ | $D_w$ | $D_y$ | $D_m$ | $I_b$ | $I_w$ | $I_y$ | $I_m$ | $D_p$ |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| $\mathbf{Z}_f$: Full Model - Sire, Dam, Individual | | | | | | | | | | | | | |
| BW | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| WW | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 |
| YW | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| $\mathbf{Z}_1$: Non-parent Model with Known Parents | | | | | | | | | | | | | |
| BW | 0.5 | 0 | 0 | 0 | 0.5 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| WW | 0 | 0.5 | 0 | 0 | 0 | 0.5 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| YW | 0 | 0 | 0.5 | 0 | 0 | 0 | 0.5 | 1 | 0 | 0 | 0 | 0 | 1 |
| $\mathbf{Z}_2$: Non-parent Model with Known Sire and Unknown Dam | | | | | | | | | | | | | |
| BW | 0.5 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| WW | 0 | 0.5 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| YW | 0 | 0 | 0.5 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| $\mathbf{Z}_3$: Non-parent Model with Unknown Sire and Known Dam | | | | | | | | | | | | | |
| BW | 0 | 0 | 0 | 0 | 0.5 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| WW | 0 | 0 | 0 | 0 | 0 | 0.5 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| YW | 0 | 0 | 0 | 0 | 0 | 0 | 0.5 | 1 | 0 | 0 | 0 | 0 | 1 |
| $\mathbf{Z}_4$: Non-parent Model with Unknown Sire and Dam | | | | | | | | | | | | | |
| BW | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| WW | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| YW | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

## Appendix 5.1, Table 4. Inverses of the Residual (Co)Variance Matrices for Multiple-Trait Interim EPDs

$$\mathbf{R}_{i1}^{-1} = \begin{pmatrix} r_{11}^{-1} & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \qquad \mathbf{R}_{i2}^{-1} = \begin{pmatrix} 0 & 0 & 0 \\ 0 & r_{22}^{-1} & 0 \\ 0 & 0 & 0 \end{pmatrix}$$

$$\mathbf{R}_{i3}^{-1} = \begin{pmatrix} \begin{pmatrix} r_{11} & r_{12} \\ r_{21} & r_{22} \end{pmatrix}^{-1} & 0 \\ 0 \quad 0 & 0 \end{pmatrix} \qquad \mathbf{R}_{i4}^{-1} = \begin{pmatrix} 0 & 0 & 0 \\ 0 & \begin{pmatrix} r_{22} & r_{23} \\ r_{32} & r_{33} \end{pmatrix}^{-1} \\ 0 & \end{pmatrix}$$

$$\mathbf{R}_{i5}^{-1} = \begin{pmatrix} r_{11} & r_{12} & r_{13} \\ r_{21} & r_{22} & r_{23} \\ r_{31} & r_{32} & r_{33} \end{pmatrix}^{-1}$$

**Analytical Models for Across-Breed Factors**

To estimate direct effects of sire breeds for birth weight, 205-day weight, and yearling weight, data on topcross progeny should be analyzed to remove significant effects of location, year, season of birth, sex, age of dam, breed group of dam, and of all significant interactions among fixed effects. Two analyses are required:

1) The first analysis with a mixed model must include sire breed as a fixed effect and should include random effects for sires within breed, dams within dam breed, and progeny in sire and dam (residual). This analysis estimates breed of sire differences, $Y_j$ for breed j, and appropriate error variances for differences among breeds.

2) The model for the second analysis should delete sires as random effects but dams should be included as random effects to account for dams having more than one progeny. Inclusion of sire EPD as a covariate provides an estimate of the regression coefficient (b) to use to adjust for sire sampling and genetic change to a recent birth year.

Means from 1) should be adjusted to the chosen ith birth year for the jth sire breed as follows:

$$Y_{ij} \text{ (adjusted)} = Y_j + b[E_{ij} - E_j(EXP)]$$

where,

$Y_{ij}$ (adjusted) is the estimate for the jth breed of sire adjusted to the ith year of birth (corresponding to birth year providing most recent 365-day weights for intra-breed calculation of EPDs),

$Y_j$ is the estimate of jth breed of sire effect in the experimental herd(s) from mixed-model analysis (analysis 1),

b is the pooled, within-breed regression coefficient of calf performance on the EPD of its sire for the respective trait (lb of calf/lb EPD, from the analysis including EPD as covariate). This regression coefficient is expected to have a value of 1.0 for each trait, but if b deviates from 1.0, b is used to adjust estimates of sire breed differences for different scaling of performance of progeny in the experimental or industry herds where topcrosses are produced, compared to data used in the calculation of within-breed EPDs,

$E_{ij}$ is the mean EPD of non-parents for animals of breed j born in year i, and

$E_j(EXP)$ is the mean EPD of sires used to produce topcross progeny in experimental herds

with each sire's EPD weighted by number of topcross progeny which contribute to $Y_j$ in the analysis of data from experimental and industry herds. If locations are included in the analytical model as fixed effects, the mean EPD of sires would be weighted by progeny within location, but unweighted across locations (i.e., locations weighted equally).

For maternal traits, data on progeny of topcross daughters should be analyzed with a model that accounts for important fixed effects including location, year, season of birth, sex, age of dam, breed of maternal grandam, breed of maternal grandsire of the progeny, and all significant interactions. Sire breed of progeny of the topcross dams must also be accounted for in the model if more than one sire breed is involved. Again, two analyses are required:

1) The first analysis should use a mixed model including maternal grandsire, dam within maternal grandsire, and residual as random effects. This analysis is needed to obtain estimates of breed of maternal grandsire differences, $TOTMAT_j$, and appropriate prediction error variances.

2) The model for the second analysis should include as covariates both the milk and direct weaning weight EPDs of the maternal grandsire. In the second model, maternal grandsires should be deleted as random effects, but dams should still be included as random effects to account properly for dams with more than one progeny.

The following equation should be used to adjust total maternal weaning weight of each maternal grandsire breed (jth) in experimental or industry herds for sire sampling and genetic trend to the same base year as for birth, weaning, and yearling weight:

$$TOTMAT_{ij}\ (\text{adjusted}) = TOTMAT_j + b_{WW}[WNWT\ E_{ij} - WNWT\ E_j(EXP)]$$

$$+ b_{Milk}\ [MILK\ E_{ij} - MILK\ E_j(EXP)]$$

where,

$TOTMAT_{ij}$ (adjusted) is the estimated mean total maternal weaning weight of the jth breed of maternal grandsire adjusted to the ith year of birth (corresponding to birth year providing most recent 365-day weights for intra-breed EPDs),

$TOTMAT_j$ is the estimate of total maternal weaning weight for the jth maternal grandsire breed in the experimental herd(s) from mixed model analysis,

$b_{WW}$ = pooled, intra-breed regression coefficient of calf weaning weight on the direct weaning weight EPD of the maternal grandsire (lb/lb) (estimates of $b_{WW}$ are expected from theory to be 0.5),

$WNWT\ E_{ij}$ is the mean for non-parent EPD for the ith year for the jth breed,

WNWT $E_j$(EXP) is the mean EPD for direct weaning weight of sires with daughters used to estimate total maternal weaning weight, weighted by the number of grandprogeny contributing to the estimate of $TOTMAT_x$ in the analysis of data from experimental and industry herds. If locations are included in the analytical model as fixed effects, the mean EPD of sires should be weighted by number of progeny within location, but unweighted across locations (i.e., locations weighted equally),

$b_{Milk}$ = pooled, intra-breed regression coefficient of calf weaning weight on the milk EPD of the maternal grandsire (lb/lb) (the value expected for $b_{Milk}$ is 1.0),

MILK $E_{ij}$ is the mean EPD for milk of non-parents born in year i for the jth breed, and

MILK $E_j$(EXP) is the mean milk EPD for sires with daughters used to estimate total maternal weaning weight, weighted by the number of topcross daughters contributing to the estimate of $TOTMAT_j$, in the analysis of data from experimental and industry herds. If locations are included in the analytical model as fixed effects, the mean milk EPD of sires should be weighted by progeny within location, but unweighted across locations (i.e., locations weighted equally).

Breed means for "MILK" can then be estimated by an indirect procedure by subtracting out one-half of the adjusted breed of sire estimates for direct weaning weight as:

$$MILK_{ij} \text{ (adjusted)} = [TOTMAT_{ij}(adj.) - TOTMAT_{i.}(adj.)] - (2)[Y_{ij}(adj.) - Y_{i.}(adj.)]$$

where,

$TOTMAT_{ij}$ (adj.) and $TOTMAT_{i.}$ (adj.) are the means for the jth breed of maternal grandsire and over all breeds for maternal weaning weight, respectively, both adjusted to the ith birth year,

$Y_{ij}$(adj.) and $Y_{i.}$(adj.) are the estimated means for the jth breed and over all breeds for direct weaning weight (direct, breed of sire), respectively, both adjusted to the ith year.

**Across-Breed EPDs.** Across-breed adjustment factors can be calculated as follows:

$$A_j = (M_{ij} - M_{ib}) - (E_{ij} - E_{ib})$$

where,

$M_{ij}$ = estimate for jth breed of sire (or maternal grandsire) adjusted to ith birth year [corresponding to $Y_{ij}$ (adjusted) or to $Milk_{ij}$ (adjusted)].

$M_{ib}$ = estimate for the base breed, b,

$E_{ij}$ = Average EPD for non-parents born in year i for jth breed, and

$E_{ib}$ = Average EPD for non-parents born in year i for the base breed, b.

The first part of the equation ($M_{ij}$ - $M_{ib}$) provides an estimate of current differences between breeds j and b for year i. The second part of the equation ($E_{ij}$ - $E_{ib}$) accounts for differences in the base year EPD for breeds j and b. The adjustment is necessary because the base for the genetic evaluations varies from one breed to another. This adjustment would not be necessary if all breeds used a fixed base set to the same year. In recent applications, the Angus breed was chosen as the base breed because they are one of the largest breeds. Any other breed or average of all breeds could be chosen as the base. However, it is important to settle on a fixed base that does not change over time so that cattlemen can use across-breed EPDs to identify optimal EPD limits and ranges for their herd and environment.

Across-breed EPDs are computed as follows:

$A_j$ + EPD of individual animal of jth breed.

All across-breed EPDs computed for animals in this manner are made relative to EPDs of 0 in the base breed. For example, if Angus is chosen as the base breed, all across-breed EPDs are relative to Angus with an EPD = 0. The adjustment factors are useful only for adjusting EPDs to a common breed base. The adjustment factors alone cannot be used to compare breeds, because the bases for EPDs for different breeds are fixed at different points in time.

## Appendix 5.2, Heritabilities and Selected Genetic Correlations Used in NCE Programs for Several US Breed Associations

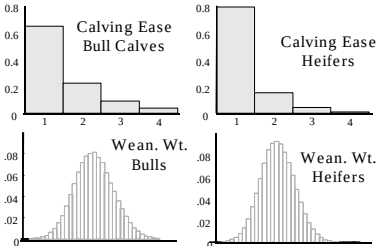
| | Birth Wt. | | 205-day Weaning Wt. | | | 160-day Gain | |
|---|---|---|---|---|---|---|---|
| Breed | $h^2_A$ | $h^2_M$ | $h^2_A$ | $h^2_M$ | $r_{AM}$ | $h^2_A$ | $r_{AW,\ AG}$ |
| Angus | .33 | .0 | .20 | .14 | .0 | .20 | .15 |
| Blonde d'Aquitaine | .30 | .0 | .35 | .15 | .0 | .24 | .20 |
| Beefmaster | .14 | .26 | .18 | .19 | -.29 | .28 | .35 |
| Brahman | .25 | .14 | .18 | .12 | .0 | .26 | .35 |
| Brangus | .28 | .12 | .28 | .20 | -.29 | .20 | .30 |
| Braford | .47 | .21 | .23 | .13 | .0 | .22 | .55 |
| Braunvieh | .50 | .0 | .41 | .09 | .0 | .40 | .58 |
| Charolais[a] | .42 | .14 | .23 | .27 | -.26 | .22 | .39 |
| Gelbvieh | .42 | .12 | .23 | .10 | -.21 | .19 | .40 |
| Hereford[b] | .40 | .08 | .19 | .15 | .0 | .25 | .70 |
| Limousin[c] | .42 | .18 | .23[a] | .19[a] | .0 | .20 | .28 |
| Red Angus | .47 | .21 | .23 | .12 | .0 | .22 | .55 |
| Red Brangus | .47 | .21 | .23 | .13 | .0 | .22 | .55 |
| Romagnola | .47 | .0 | .23 | .13 | .0 | .22 | .55 |
| Salers | .40 | .12 | .38 | .15 | .0 | .27 | .35 |
| Santa Gertrudis | .38 | .0 | .22 | .16 | .0 | .26 | .35 |
| Senepol | .41 | .18 | .25 | .20 | -.18 | .20 | .30 |
| Shorthorn[b] | .22 | .13 | .19 | .21 | -.09 | .29 | .85 |
| Simmental (M)[a,d] | .39 | .0 | .28 | .16 | -.32 | .26 | .51 |
| Simmental (F)[a,d] | .45 | .0 | .33 | .15 | -.32 | .32 | .51 |
| Tarentaise | .69 | .0 | .44 | .04 | .0 | .30 | .07 |

[a]Estimates from U.S. and Canada joint analyses.
[b]Parameters for Hereford and Shorthorn are for 365-d weight rather than postweaning 160-d gain.
[c]Parameters for Limousin are for 205-day preweaning gain.
[d]M = male calves and F = female calves for Simbrah, Chianina,and Maine Anjou as well as Simmental.

# APPENDIX 5.3, THRESHOLD TRAITS

Threshold traits are discrete; they have just a few possible phenotypes. Often they are binary traits with only two outcomes, e.g., dead / alive or pregnant / open. Sometimes there are several **ordered** categories, e.g., scores for calving difficulty (1, 2, 3, 4). The distribution of threshold traits is in sharp contrast to a continuous trait such as weaning weight whose distribution is the typical bell-shaped ("normal") curve (Fig. 1). For analysis of traits such as calving ease, a "threshold model" is often appropriate. In a threshold model, an underlying, continuously distributed but unobservable phenotype is assumed. The categorical phenotypes we observe ('realized" phenotypes) arise from truncating the underlying phenotypes into categories with a series of "thresholds" as in Fig. 2. In this model there is a heritability for the underlying phenotype but also for the observed phenotype. The latter will depend upon the number of observed categories but more importantly on whether one category predominates, especially if that category is one of the extremes. Figure 3 illustrates this for calving ease. As the frequency of category 1 (unassisted calving, on the X axis) increases, which corresponds to moving the thresholds to the right, frequencies of categories 2 through 4 also change. Note that the 'very hard' category steadily decreases but the 'easy' category actually increases for a while before also decreasing. The realized heritability (on the underlying scale) is maximum when there is a substantial incidence of each score. This corresponds to a frequency of ~0.1 to 0.2 in category 1.

**Fig. 1 Threshold vs. Continuous Traits**



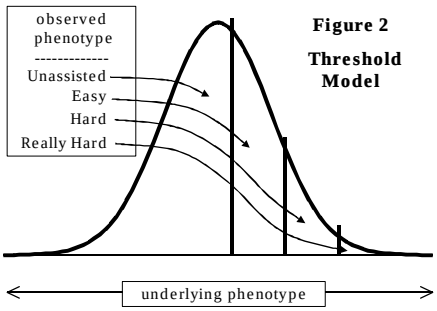




**Figure 2**
**Threshold Model**

**Figure 3. Realized vs. Underlying $h^2$**

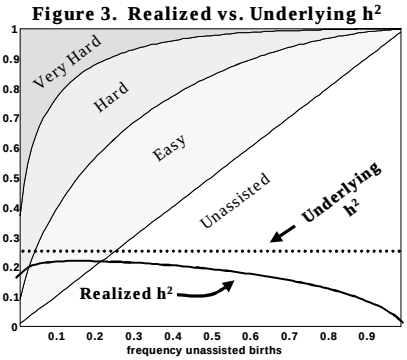
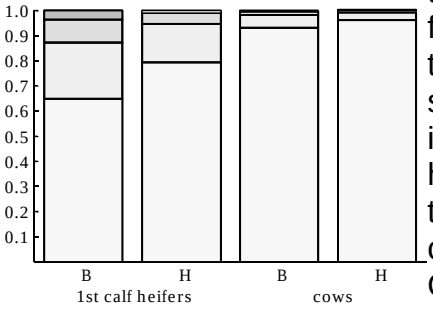
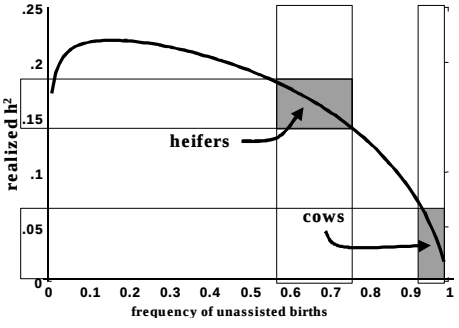



**Fig. 4 Distribution of Calving Ease Scores**




Of course this does not actually occur with calving ease scores. Most births are unassisted, especially for female births and most especially for any calf out of a later parity dam (Fig. 4). The impact this has on realized $h^2$ is demonstrated in the Fig. 5. If all calves are born unassisted, there cannot be much difference among sires. Thus for cows the realized $h^2$ is very low leading some to conclude that only scores from first-calf heifer calvings should be used for genetic evaluation of calving ease. The counter-argument is that the lion's share of data come from cow calvings and, in some breeds at least, young bulls are "tried out" on cows before being used on heifers. The threshold model allows all information to be combined in a valid manner, taking

**Figure 5. CE $h^2$: 1st calf heifers vs. cows**



into account differences between heifers and bull calves, first calf heifers, and cows. In such cases, the joint analysis of calving ease with an indicator trait – birth wt. – may be appropriate. Finally it should be noted, however, that linear analyses (BLUP) of the raw scores tend to produce similar rankings, especially if only scores from first calf heifer calvings are used.

## Technical Details for a Threshold Model

**MAP** (maximum *a posteriori*) **estimator** of $\theta^T = \left(\beta^T \quad \mathbf{u}^T\right)$

$Y_1 = k$ if $t_{k-1} < y_1 \le t_k$ = realized phenotype, e.g., observed CE score

$y_1$ = latent (unobservable) continuous CE phenotype

$y_2$ = birth weight (continuous)

$$\begin{matrix}\text{latent CE phenotype} \rightarrow \\ \text{birth wt. phenotype} \rightarrow\end{matrix}\begin{pmatrix}\mathbf{y}_1 \\ \mathbf{y}_2\end{pmatrix} = \begin{pmatrix}\mathbf{W}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{W}_2\end{pmatrix}\begin{pmatrix}\boldsymbol{\theta}_1 \\ \boldsymbol{\theta}_2\end{pmatrix} + \begin{pmatrix}\mathbf{e}_1 \\ \mathbf{e}_2\end{pmatrix}$$

Assume $\mathbf{y}_1$ & $\mathbf{y}_2$ jointly normal. Maximize w.r.t $\theta^T = \left(\beta^T \quad \mathbf{u}^T\right)$**:**

$$ln\, p\left(\boldsymbol{\theta}\middle|\mathbf{y}_2, \mathbf{Y}_1\right) = const + ln\, p\left(\mathbf{Y}_1\middle|\mathbf{y}_2, \boldsymbol{\theta}\right) + ln\, p\left(\mathbf{y}_2\middle|\boldsymbol{\theta}\right) + ln\, p\left(\boldsymbol{\theta}\right)$$

$p\left(\mathbf{Y}_2\middle|\mathbf{y}_2, \boldsymbol{\theta}\right)$: multinomial (or binomial)
$p\left(\mathbf{y}_2\middle|\boldsymbol{\theta}\right)$: normal
$p\left(\boldsymbol{\theta}\right)$: normal ("random effects")

$\hat{\boldsymbol{\theta}}$ = joint posterior mode

**Caveats & Quirks**: If there is a fixed effect level that contains only extreme scores, the solution will be $\pm\infty$. Those data provide no information regarding any of other effects; effectively, these data are deleted. Also computers do not like infinities. A common instance of this is a contemporary group with all unassisted births. An easy (and reasonable?) fix is to treat the effect, e.g. contemporary group, as random by assuming a normal prior with null mean and large but finite variance.

Not all parameters are identifiable. The computing formulas are functions of

$$x = \left(t_k - \mu\right)/\sigma = \kappa\left(\left\lfloor t_k + \delta\right\rfloor - \left\lfloor \mu + \delta\right\rfloor\right)/\left(\kappa\sigma\right)$$

which is unchanged by adding a constant $\delta$ to all the thresholds and all levels of a fixed effect. Typically one threshold is set to zero. (With binary data this removes the threshold from all computations.) Likewise, x is invariant to multiplication of both **t** and $\theta$ by a constant $\kappa$. The typical constraint is the residual variance for the threshold trait ($r_{11}$) = 1.

Another numerical difficulty can arise with

$$\lambda = -\frac{\phi(x_R) - \phi(x_L)}{\Phi(x_R) - \Phi(x_L)}$$

if $x_L$ or $x_R \to \pm$BIG causes computed denominator (and numerator) to be operationally zero. This might happen, .e.g., for a heifer calf out of a mature dam with a CE score of 4. In large data sets extremely unlikely events will happen and the code must handle them. $\Phi$ is especially difficult to approximate for large x, say >4. In such cases an easy approximation is to use the limit of the expectation of a doubly truncated normal:

$$\lambda = \begin{cases} x_L & \text{if } x_L > \text{ BIG} \\ x_R & \text{if } x_R < -\text{BIG} \end{cases}$$

**Fitting model: EM Algorithm $\hat{\theta} \mid \mathbf{t}$**

We cannot estimate **t** with EM algorithm; see Newton's method below. In routine NCE the thresholds (**t**) will be fixed just as are the variances and covariances in a routine BLUP analysis. The EM algorithm for $\hat{\theta} \mid \mathbf{t}$ is quite similar to a usual BLUP analysis. The LHS is a typical coefficient matrix and need be formed only once but the RHS depends on current solutions and must be updated each round. The inverse of LHS does **not** yield accuracies (It gives the PEVs assuming $\mathbf{y}_2$ observed). The EM algorithm probably requires more rounds to converge but because it is so much like typical MME it is easily incorporated into multiple-trait continuous analysis.

For the EM update $\hat{\theta} \mid \mathbf{t}$, a typical MM analysis is repeatedly performed given $\tilde{\mathbf{y}}_1 = E(\mathbf{y}_1 | \mathbf{y}_2, \theta, \mathbf{t}) \& \mathbf{y}_2$, i.e.,

$$\left[ \begin{pmatrix} \mathbf{W}_1^T \mathbf{R}^{11} \mathbf{W}_1 & \mathbf{W}_1^T \mathbf{R}^{12} \mathbf{W}_2 \\ \mathbf{W}_2^T \mathbf{R}^{21} \mathbf{W}_1 & \mathbf{W}_1^T \mathbf{R}^{22} \mathbf{W}_2 \end{pmatrix} + \mathbf{G}^* \right] \begin{bmatrix} \hat{\boldsymbol{\beta}} \\ \hat{\mathbf{u}} \end{bmatrix} = \begin{bmatrix} \mathbf{W}_1^T \left( \mathbf{R}^{11} \tilde{\mathbf{y}}_1 + \mathbf{R}^{12} \mathbf{y}_2 \right) \\ \mathbf{W}_2^T \left( \mathbf{R}^{21} \tilde{\mathbf{y}}_1 + \mathbf{R}^{22} \mathbf{y}_2 \right) \end{bmatrix}$$

where $\mathbf{G}^*$ is the inverse of the (prior) covariance matrix of the "random effects" interspersed with zeros in rows & columns pertaining to "fixed effects." The LHS is exactly as in a usual MM analysis. However $\tilde{\mathbf{y}}$ in the RHS must be recomputed each round. For observed score = k, $\tilde{\mathbf{y}}_1 = \mu + \sigma\lambda$ where

$$\mu = \begin{cases} \mathbf{w}_1^T \hat{\mathbf{e}} + b_e \left( \mathbf{y}_2 - \mathbf{w}_2^T \hat{\mathbf{e}} \right) & \text{if BW} \\ \mathbf{w}_1^T \hat{\mathbf{e}} & \text{otherwise} \end{cases} \qquad \sigma^2 = \begin{cases} 1 - r_{12}^2 / r_{22} & \text{if BW} \\ 1 & \text{otherwise} \end{cases}$$

$$b_e = r_{12} / r_{22}; \ \lambda = -\left[ \phi(x_R) - \phi(x_L) \right] / P$$

$$x_L = (t_{k-1} - \mu)/\sigma; \ x_R = (t_k - \mu)/\sigma$$

$$P = \Phi(x_R) - \Phi(x_L)$$

**Fitting the model: Newton's Method** for $\hat{\theta} | \mathbf{t}, \hat{\mathbf{t}} | \theta$ or $\hat{\theta} \& \hat{\mathbf{t}}$

Newton's method is prefered to Fisher Scoring for a joint threshold/continuous analysis because many fewer computations are required to accumulate the Hessian.

Again the updating equations for $(\hat{\boldsymbol{\theta}}\,|\,\mathbf{t})$ will look like MME but both RHS & LHS depend on current solutions and must be re-formed each round though the LHS might be re-formed less frequently. The LHS are 2nd derivatives and the inverse of LHS approximates PEVs (accuracies).

Though fixed for routine NCE, the thresholds (**t**) do have to be estimated at some point. It is possible to simultaneously solve for **t** and θ using Newton's method. Here a cyclic two step procedure is suggested in which **t** and then θ alternatively are fixed, i.e.,

$$\text{Update: } \boldsymbol{\theta}^1\big|\mathbf{t}^0 \rightarrow \mathbf{t}^1\big|\boldsymbol{\theta}^1 \rightarrow \boldsymbol{\theta}^2\big|\mathbf{t}^2 \rightarrow \mathbf{t}^2\big|\boldsymbol{\theta}^2 \rightarrow \text{etc.}$$

Newton's method for **t**, given everything else

$$\mathrm{t}^{\ell+1} = \mathrm{t}^{\ell} - \mathbf{H}^{-1}\nabla$$

where $\nabla$ is the vector of first partial derivatives (gradient) and **H** is the (tridiagonal) matrix of second derivatives (Hessian). $\nabla$ and **H** can be formed by reading the data file one record at a time accumulating the following quantities. For record w/ CE score k, calculate $x_L, x_R$ & P as above and accumulate:

$$\left.\begin{array}{ll} \mathrm{DL} = -\phi(x_L)/(P\sigma) \rightarrow \nabla_{k-1} & \text{if } k>1 \\ \mathrm{DR} = \phi(x_R)/(P\sigma) \rightarrow \nabla_{k} & \text{if } k<m \end{array}\right\} \text{ gradient}$$

$$\left.\begin{array}{ll} \mathrm{DLL} = -[\mathrm{DL}\times\mathrm{DL} + x_L \times \mathrm{DL}/\sigma] \rightarrow \mathbf{H}_{k-1,k-1} & \text{if } k>1 \\ \mathrm{DLR} = -[\mathrm{DL}\times\mathrm{DR}] \rightarrow \mathbf{H}_{k-1,k} \;\&\; \mathbf{H}_{k,k-1} & \text{if } 1<k<m \\ \mathrm{DRR} = -[\mathrm{DR}\times\mathrm{DR} + x_R \times \mathrm{DR}/\sigma] \rightarrow \mathbf{H}_{k,k} & \text{if } k<m \end{array}\right\} \text{ Hessian}$$

Updating **θ|t**: To get the Newton update, 1st & 2nd partial derivatives (for gradient & Hessian, respectively) of

$$\mathrm{L} = \sum_i ln\,p(y_{1i}\,|\,y_{2i},\boldsymbol{\theta}) + ln\,p(y_{2i},\boldsymbol{\theta}) + ln\,p(\boldsymbol{\theta})$$

are needed. The first is multinomial; the last 2 are normals. (Because of the odds that this will be printed error-free, a more detailed derivation is included that allows a reader to check, especially the ±signs.) The subscript i is dropped with the understanding that, e.g., $P_k$ = probability of the score observed - k - for ith animal (conditional on θ and a BW if recorded).

$$P_k = \Phi\left\{\frac{t_k - \mu}{\sigma}\right\} - \Phi\left\{\frac{t_{k-1} - \mu}{\sigma}\right\};\quad Q_k = ln\,P_k$$

$$\partial P_k/\partial \boldsymbol{\theta} = \phi\left\{\frac{t_k - \mu}{\sigma}\right\}\frac{\partial}{\partial \boldsymbol{\theta}}\left\{\frac{t_k - \mu}{\sigma}\right\} - \phi\left\{\frac{t_{k-1} - \mu}{\sigma}\right\}\frac{\partial}{\partial \boldsymbol{\theta}}\left\{\frac{t_{k-1} - \mu}{\sigma}\right\}$$

$$= \frac{-\phi\left\{\frac{t_k - \mu}{\sigma}\right\} + \phi\left\{\frac{t_{k-1} - \mu}{\sigma}\right\}}{\sigma}\frac{\partial \mu}{\partial \boldsymbol{\theta}} = \mathbf{w}\left(-\phi\left\{\frac{t_k - \mu}{\sigma}\right\} + \phi\left\{\frac{t_{k-1} - \mu}{\sigma}\right\}\Big/\sigma\right);$$

$$\mu = b_e y_2 + \mathbf{w}^{\mathrm{T}}\boldsymbol{\theta};\qquad \mathbf{w}^{\mathrm{T}} = \left[\mathbf{w}_1^{\mathrm{T}} : -b_e \mathbf{w}_2^{\mathrm{T}}\right]$$

$$\partial Q_k/\partial \grave{\mathbf{e}} = \frac{\partial P_k/\partial \grave{\mathbf{e}}}{P_k} = \mathbf{w}\left(\frac{-\phi\left\{\frac{t_k-\mu}{\sigma}\right\}+\phi\left\{\frac{t_{k-1}-\mu}{\sigma}\right\}}{P_k\sigma}\right) = \mathbf{w}(-DR-DL) = \mathbf{w}(-\delta)$$

$$\partial^2 P_k/\partial \grave{\mathbf{e}}\,\partial \grave{\mathbf{e}}^T = \mathbf{w}\left(\frac{-\partial\phi\left\{\frac{t_k-\mu}{\sigma}\right\}\Big/\partial\theta^T+\partial\phi\left\{\frac{t_{k-1}-\mu}{\sigma}\right\}\Big/\partial\theta^T}{\sigma}\right)$$

$$= \mathbf{w}\left(\frac{-\phi\left\{\frac{t_k-\mu}{\sigma}\right\}}{\sigma}\times\frac{t_k-\mu}{\sigma}+\frac{\phi\left\{\frac{t_{k-1}-\mu}{\sigma}\right\}}{\sigma}\times\frac{t_{k-1}-\mu}{\sigma}\right)\mathbf{w}^T$$

$$\partial^2 Q_k/\partial \grave{\mathbf{e}}\,\partial \grave{\mathbf{e}}^T = \frac{\partial^2 P_k/\partial \grave{\mathbf{e}}\,\partial \grave{\mathbf{e}}^T}{P_k} - \frac{\left(\partial P_k/\partial \grave{\mathbf{e}}\right)\left(\partial P_k/\partial \grave{\mathbf{e}}^T\right)}{P_k^2}$$

$$= \mathbf{w}\left(\frac{-\phi\left\{\frac{t_k-\mu}{\sigma}\right\}}{P_k\sigma}\times\frac{t_k-\mu}{\sigma}+\frac{\phi\left\{\frac{t_{k-1}-\mu}{\sigma}\right\}}{P_k\sigma}\times\frac{t_{k-1}-\mu}{\sigma}\right)\mathbf{w}^T - \mathbf{w}\left(\frac{-\phi\left\{\frac{t_k-\mu}{\sigma}\right\}+\phi\left\{\frac{t_{k-1}-\mu}{\sigma}\right\}}{P_k\sigma}\right)^2\mathbf{w}^T$$

$$= -\tilde{a}\mathbf{w}\mathbf{w}^T$$

where

$$\tilde{a} = \frac{\phi\left\{\frac{t_k-\mu}{\sigma}\right\}}{P_k\sigma}\times\frac{t_k-\mu}{\sigma}+\frac{-\phi\left\{\frac{t_{k-1}-\mu}{\sigma}\right\}}{P_k\sigma}\times\frac{t_{k-1}-\mu}{\sigma}+\left(\left[\phi\left\{\frac{t_k-\mu}{\sigma}\right\}\Big/P_k\sigma\right]+\left[-\phi\left\{\frac{t_{k-1}-\mu}{\sigma}\right\}\Big/P_k\sigma\right]\right)^2$$

$$= (DR\times x_R + DL\times x_L)+(DR+DL)^2$$

Now the second term:

$$ln\,p(y_{2i}|\theta_2) = \text{const} - \tfrac{1}{2}r_{22}^{-1}(y_{2i}-\mathbf{w}_{2i}^T\theta)^2 \Rightarrow \begin{cases}\dfrac{\partial}{\partial\theta_2}ln\,p(y_2|\theta_2) = \mathbf{w}_{2i}r_{22}^{-1}(y_2-\mathbf{w}_2^T\theta)\\ \dfrac{\partial^2}{\partial\theta_2\partial\theta_2^T}ln\,p(y_2|\theta_2) = -\mathbf{w}_{2i}r_{22}^{-1}\mathbf{w}_{2i}^T\end{cases}$$

Combining these with the previous,

1. "Likelihood" contributions to $\nabla$: $\begin{bmatrix}\mathbf{w}_1(-\ddot{a})\\ \mathbf{w}_2(b_e\ddot{a}+r_{22}^{-1}[y_2-\mathbf{w}_2^T\theta])\end{bmatrix}$

2. "Likelihood" contributions to **H**: $` - \begin{pmatrix} \mathbf{w}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{w}_2 \end{pmatrix} \begin{pmatrix} \gamma & -b_e\gamma \\ -b_e\gamma & b_e^2\gamma + r_{22}^{-1} \end{pmatrix} \begin{pmatrix} \mathbf{w}_1^T & \mathbf{0} \\ \mathbf{0} & \mathbf{w}_2^T \end{pmatrix}$

Note the latter is very similar to the "least squares" contributions to "usual" MME except that each individual has its own residual covariance matrix (inverse) that depends, through $\gamma$, on its CE score, BW and the current value of $\theta$. The final term of the log posterior comes from the priors for $\theta$**;** assumed flat for "fixed effects" and normals for "random effects."

$$ln\,p(\theta) = \text{const} - \tfrac{1}{2}\theta^T\mathbf{G}^*\theta \Rightarrow \begin{cases} \dfrac{\partial}{\partial\theta_2} ln\,p(\theta) = -\mathbf{G}^*\theta \\ \dfrac{\partial^2}{\partial\theta_2\partial\theta_2^T} ln\,p(\theta) = -\mathbf{G}^* \end{cases}$$

where **G*** is the the same as in EM. Note that in this straight implementation of Newton's method **G*** gets into the RHS as well as the LHS. It is possible to formulate the updating equations to look more like 'usual' MME. The updating equations are:

$$\theta^{\ell+1} = \theta^{\ell 1} - \left[-\left(\mathbf{W}^T\tilde{\mathbf{R}}^{-1}\mathbf{W} + \mathbf{G}^*\right)\right]^{-1}\left[\mathbf{W}^T\mathbf{z}^\ell - \mathbf{G}^*\theta^\ell\right]$$

$$\Updownarrow$$

$$\left[\mathbf{W}^T\tilde{\mathbf{R}}^{-1}\mathbf{W} + \mathbf{G}^*\right]\theta^{\ell+1} = \left[\mathbf{W}^T\tilde{\mathbf{R}}^{-1}\mathbf{W} + \mathbf{G}^*\right]\theta^\ell + \mathbf{W}^T\tilde{\mathbf{R}}^{-1}\tilde{\mathbf{R}}\mathbf{z}^\ell - \mathbf{G}^*\theta^\ell$$

$$\Updownarrow$$

$$\left[\mathbf{W}^T\tilde{\mathbf{R}}^{-1}\mathbf{W} + \mathbf{G}^*\right]\theta^{\ell+1} = \mathbf{W}^T\tilde{\mathbf{R}}^{-1}\left(\tilde{\mathbf{R}}\mathbf{z}^\ell + \mathbf{W}\theta^\ell\right) + \mathbf{G}^*\theta^\ell - \mathbf{G}^*\theta^\ell$$

$\tilde{\mathbf{R}}$ is block diagonal and for a typical animal:

$$\begin{pmatrix} \tilde{r}_{11} & \tilde{r}_{12} \\ \tilde{r}_{21} & \tilde{r}_{22} \end{pmatrix}^{-1} = \begin{pmatrix} \gamma & -b_e\gamma \\ -b_e\gamma & b_e^2\gamma + r_{22}^{-1} \end{pmatrix} \Leftrightarrow \begin{pmatrix} \tilde{r}_{11} & \tilde{r}_{12} \\ \tilde{r}_{21} & \tilde{r}_{22} \end{pmatrix} = \begin{pmatrix} \gamma^{-1} + b_e^2 r_{22} & r_{12} \\ r_{21} & r_{22} \end{pmatrix}$$

$$\tilde{\mathbf{R}}\mathbf{z} = \begin{bmatrix} \gamma^{-1} + b_e^2 r_{22} & r_{12} \\ r_{21} & r_{22} \end{bmatrix} \begin{bmatrix} -\delta \\ b_e\delta + r_{22}^{-1}\left(y_2 - \mathbf{w}_2^T\theta\right) \end{bmatrix} = \begin{bmatrix} b_e\left(y_2 - \mathbf{w}_2^T\theta\right) - \gamma^{-1}\delta \\ \left(y_2 - \mathbf{w}_2^T\theta\right) \end{bmatrix}$$

$$\tilde{\mathbf{R}}\mathbf{z} + \mathbf{w}^T\theta == \begin{bmatrix} \mathbf{w}_1^T\theta + b_e\left(y_2 - \mathbf{w}_2^T\theta\right) - \gamma^{-1}\delta \\ \left(y_2 - \mathbf{w}_2^T\theta\right) + \mathbf{w}_2^T\theta \end{bmatrix} = \begin{bmatrix} \mu - \gamma^{-1}\delta \\ y_2 \end{bmatrix} = \begin{bmatrix} \hat{y}_1 \\ y_2 \end{bmatrix}$$

Thus yielding

$$\left[\begin{pmatrix} \mathbf{W}_1^T\tilde{\mathbf{R}}^{11}\mathbf{W}_1 & \mathbf{W}_1^T\tilde{\mathbf{R}}^{12}\mathbf{W}_2 \\ \mathbf{W}_2^T\tilde{\mathbf{R}}^{21}\mathbf{W}_1 & \mathbf{W}_1^T\tilde{\mathbf{R}}^{22}\mathbf{W}_2 \end{pmatrix} + \mathbf{G}^*\right]\begin{bmatrix} \hat{\mathbf{a}} \\ \hat{\mathbf{u}} \end{bmatrix} = \begin{bmatrix} \mathbf{W}_1^T\left(\tilde{\mathbf{R}}^{11}\hat{\mathbf{y}}_1 + \tilde{\mathbf{R}}^{12}\mathbf{y}_2\right) \\ w_2^T\left(\tilde{\mathbf{R}}^{21}\hat{\mathbf{y}}_1 + \tilde{\mathbf{R}}^{22}\mathbf{y}_2\right) \end{bmatrix}$$

Note that $\hat{\mathbf{y}}_1 \neq \tilde{\mathbf{y}}_1$ used in EM. Both LHS & RHS need be formed anew each round.

**Brief bibliography of joint analysis of threshold and continuous traits.**

Hoeschele I., Tier B. and Graser H.U. 1995 Multiple-trait genetic evaluation for one polychotomous trait and several continuous traits with missing data and unequal models. J Anim Sci. 73:1609.

Janss, L.L.G. and J.L. Foulley. 1993. Bivariate analysis for one continuous and one dichotomous trait with unequal design matrices and an application to birth weight and calving difficulty. Livestock Prod. Sci. 33:183.

Wang, C.S., R.L. Quaas and E.J. Pollak. 1997. Bayesian analysis of calving ease scores and birth weights. Genetics Selection Evolution 29:117.

# APPENDIX 5.4, GENETIC EVALUATION OF SURVIVAL TRAITS

A survival trait can be broadly defined as the length of time between two events. A typical survival trait is productive life. Length of productive life is the length of time, measured in years, between the start of production until the end of the productive life of the animal. Traits which are measured in days, months, or years pose a number of issues which must be addressed before they can be included in a genetic evaluation program. First, the endpoints of the interval must be defined. Second, how will records be handled when the animal leaves the herd? Third, how will incomplete records be handled when evaluation takes place before an animal's second endpoint has been observed? Fourth, how will effects be modeled that occur between the two endpoints? Fifth, how should estimates of the genetic effects be presented to users?

This discussion will describe the use of the Weibull family of survival functions for genetic evaluation. While survival analysis can be used for a number of traits, this guideline will focus on length of productive life.

**Definitions**. The failure time, $T$, is the length of time until the animal fails. The survival function, $S(t;h)$, is the probability that the animal with a risk level $h$ will survive until time $t$. The risk level is the sum of effects of factors affecting survival on a log time scale. The median survival, $m$, is the time by which 50% of animals of a given class are expected to have failed. In the case of length of productive life, failure would be when a cow is no longer producing.

**Hazard function**. Models for survival functions are typically constructed from a hazard function. A hazard function describes the instantaneous failure rate:

$$l(t;h) = \lim_{\Delta t \to 0} \frac{\Pr(T < t + \Delta t \mid T > t)}{\Delta t}.$$

For short periods of time, $\Delta t$, the probability that an animal fails is approximately equal to $l(t;h)\Delta t$. Four typical shapes for the hazard function are constant, increasing, decreasing, and bowl shaped. With a constant hazard function, the probability that an animal survives an additional year is the same for an animal's first year and n$^{th}$ year. The resulting model for a constant hazard function is the exponential. The exponential survival function is give by

$$S(t;h) = e^{-\exp(\ln(t)+h)}$$

which depends on time $t$, and a risk level $h$.

The Weibull model is a generalization of the exponential family, which allows the hazard function to either increase or decrease over time. The Weibull model includes an additional rate parameter, $r$. The rate parameter is less than one when the hazard function decreases the longer an animal is in the herd and is greater than one when the

hazard function increases the longer an animal is in the herd. The survival function for the Weibull model is given by

$$S(t;h) = e^{-\exp(r\ln(t)+h)}.$$

The impact of different rate parameters on survival can be seen in Figure 1. The three curves all have the same median survival time of five years. With a rate parameter of less than one, $r = .5$, there are a relatively large number of animals with a very short productive life or a very long productive life. When the rate parameter is greater than one, $r = 2$, there are a relatively small number of animals with a very short or a very long productive life.

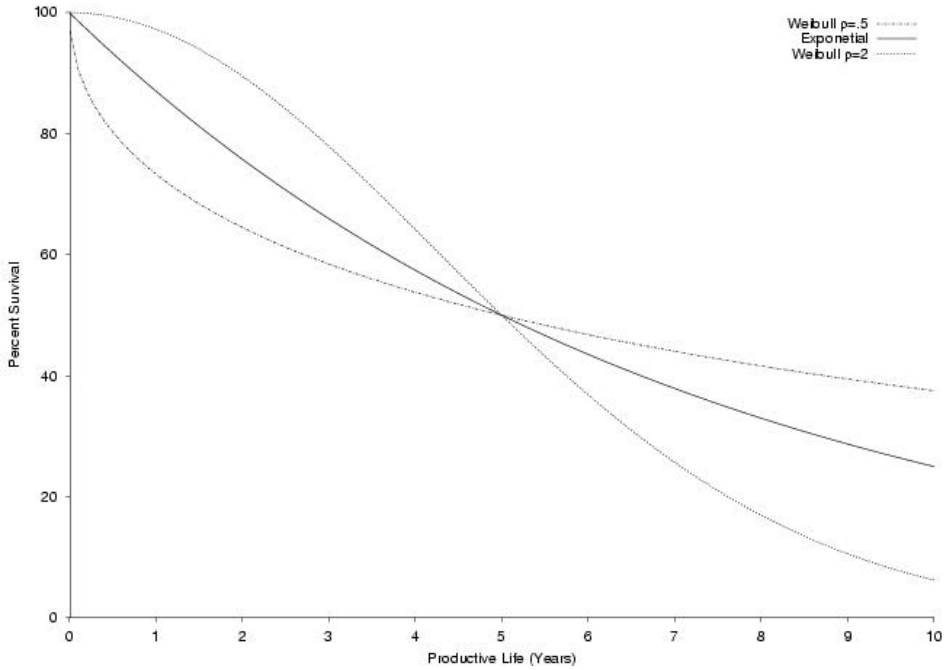



**Figure 1. Weibull survival function for 3 rate parameters and 5 year median productive life.**

In addition to the Weibull model, there are a number of other models for survival which will not be discussed here.

**Risk level**. The risk of an animal failing is influenced by genetic, random environmental, and managerial factors. The risk level of an animal can be modeled as the sum of the genetic, environmental, and management effects as

$$h = G + E + M,$$

where $G$ is the genetic risk, $E$ is the environmental risk, and $M$ is the contemporary group risk. For the risks to be additive, changes in management factors or environment must not change factors affecting survival. This assumption might not be reasonable, as for example, if culling practices in one herd depend on calf performance and in another herd depend on the reproductive performance of the cow.

Median survival time is one way to gauge the impact of changes in an animal's risk level. For the Weibull distribution, the median survival time for animals at risk level $h$, is given by

$$m(h) = [-\ln(0.5)]^{-1/r} e^{-h/r}.$$

The impact of a change in the genetic risk of $\Delta$ on median survival time is given by

$$\frac{m(h+\Delta) - m(h)}{m(h)} = e^{-\Delta/r} - 1.$$

The expected percentage changes in median survival time are shown in **Table 1**.

**Table 1. Expected changes in median survival time.**

| Scaled GeneticRisk ($\Delta / r$) | Change in Median Survival (%) | Impact when Median Survival is 5 Years (yr) | Median Survival when Risk is Increased by $\Delta$ (yr) |
|---|---|---|---|
| -.5 | 64.9 | +3.25 | 8.25 |
| -.4 | 49.2 | +2.46 | 7.46 |
| -.3 | 35.0 | +1.75 | 6.75 |
| -.2 | 22.1 | +1.11 | 6.11 |
| -.1 | 10.5 | +0.53 | 5.53 |
| .0 | 0.0 | 0.00 | 5.00 |
| .1 | -9.5 | -0.48 | 4.52 |
| .2 | -18.1 | -0.91 | 4.09 |
| .3 | -25.9 | -1.30 | 3.70 |
| .4 | -33.0 | -1.65 | 3.35 |
| .5 | -39.3 | -1.97 | 3.03 |

**Censoring**. Unlike traits such as weaning weight, survival traits are often censored. A record is censored for length of productive life when it is known that a cow's length of productive life is at least a certain number of years. Typical causes for a censored record are if the cow was still in production when the final data were collected for analysis or if the animal left the herd for non-production reasons. If censoring is not taken into account, then the genetic evaluations for young sires, which could have a large percentage of daughters with censored records, would be biased upwards.

**Issues**. A number of issues need to be addressed before a survival trait can become an effective part of a genetic evaluation program. First, survival must be defined in a biologically meaningful manner. The definition must also make sense across a variety production environments. Second, selection goals are needed. For example, is the goal to have cows with very long production lives or to have cows that are not likely to be culled early? Third, how should sires with a large number of progeny with censored records be handled? The method to be described for handling censoring works well when less than 20% of the records are censored. However, young sires are likely to have a larger proportion of progeny with censored records.

## Technical Detail for Genetic Evaluation of Survival Traits

**Data.** Two measurements of survival for a cow need to be recorded: a survival time and a censoring indicator. Survival time $(T_i)$ will be either the actual survival time or the time when the record was censored. The censoring indicator $(W_i)$ will be one if the record is uncensored and zero if it is censored. That is, $W_i = 0$ when the animal is still alive when the record is collected.

**Model.** Survival can be modeled using a generalized linear mixed model. Two components to be modeled are the risk level $(h_i)$ and the rate parameter $(r_i)$ for each animal. The risk level for an animal can be modeled as a linear function of fixed and random effects as with other traits

$$h = X_h b_h + Z_h u_h ,$$

where $b_h$ is the vector of fixed effects for risk level (e.g. contemporary groups), $u_h \sim N(0, G_h)$ is the vector of random effects for risk level (e.g. breeding values), $G_h$ is the covariance matrix for the $u_h$, and $X_h$ and $Z_h$ are incidence matrices. The rate parameter for an animal can also be modeled as a linear function of fixed and random effects

$$r = X_r b_r + Z_r u_r ,$$

where $b_r$ is the vector of fixed effects for the rate parameter, $u_r \sim N(0, G_r)$ is the vector of random effects for the rate parameter, $G_r$ is the covariance matrix for $u_r$, and

$X_r$ and $Z_r$ are incidence matrices. Typically the rate parameter is assumed to be the same for all animals with $X_r = 1$ and $Z_r = 0$.

The (MAP) maximum a posteriori estimates are obtained by solving

$$\begin{pmatrix} X'RX & X'RZ \\ Z'RX & Z'RZ + G^{-1} \end{pmatrix} \begin{pmatrix} \hat{b} \\ \hat{u} \end{pmatrix} = \begin{pmatrix} X'y^* \\ Z'y^* \end{pmatrix},$$

with $X = \begin{pmatrix} X_h & X_r \end{pmatrix}$, $Z = \begin{pmatrix} Z_h & Z_r \end{pmatrix}$, $\hat{b} = \begin{pmatrix} \hat{b}_h \\ \hat{b}_r \end{pmatrix}$, $\hat{u} = \begin{pmatrix} \hat{u}_h \\ \hat{u}_r \end{pmatrix}$, $u \sim N(0, G)$, $R = \begin{pmatrix} R_h & R_{hr} \\ R'_{hr} & R_r \end{pmatrix}$,

$y^* = \begin{pmatrix} y^*_h \\ y^*_r \end{pmatrix}$, $R_h = Diag(e^{r_i \ln(T_i) + h_i})$, $R_r = Diag(e^{r_i \ln(T_i) + h_i} \ln(T_i)^2) + \frac{1}{r_i^2}$,

$R_{h,r} = Diag(e^{r_i \ln(T_i) + h_i} \ln(T_i))$, $y^*_h = \{W_i - e^{r_i \ln(T_i) + h_i}\}_i + R_h h + R_{h,r} r$, and

$y^*_r = \{W_i - e^{r_i \ln(T_i) + h_i} \ln(T_i)\}_i + R'_{h,r} h + R_r r$. The $h$ and $r$ are the estimates from the previous iteration.

Simultaneous estimation of the risk factor and rate parameter can lead to convergence problems. Frequently such problems can be dealt with by initially fixing the rate parameter until estimates of the risk factor have stabilized. During routine genetic evaluation, the rate parameter can be assumed to be known. Similar to problems encountered with the analysis of threshold traits, estimates of the risk factors can become infinite. One way of handing this is to provide bounds for the risk factors. In practice, bounds for the quantity $r \ln(T_i) + h_i$ of –7 and 2.5 have worked well.

**Additional information**. A general introduction to survival analysis can be found in Miller et al. (1981). Recent overviews of the analysis of survival traits from an animal breeding perspective can be found in Ducrocq and Cassella (1996), Kachman (1999), and Vukasinovic (1999).

Ducrocq, V., and G. Cassella. 1996. A Bayesian analysis of mixed survival analysis. Genet. Sel. Evol. 28:505-529.

Kachman, S. D. 1999. Applications in survival analysis. J. Anim. Sci. 77, Suppl. 2:147-153.

Miller, R. G., Jr., G. Gong, and A. Muñoz. 1981. Survival Analysis. Wiley Series in Probability and Mathematical Statistics. John Wiley & Sons inc., New York, NY.

Vukasinoviv, N. 1999. Application of survival analysis in breeding for longevity. In: Proc. of the Workshop on Genetic Improvement of Functional Traits in Cattle- Longevity, May 1999, Jouy-en-Josas, France. Interbull Bulletin. 21:3-10.

# APPENDIX 6.1, GUIDELINES FOR THE BULL BREEDING SOUNDNESS EVALUATION AS RECOMMENDED BY THE SOCIETY FOR THERIOGENOLOGY

Examination of bulls for breeding soundness has become a commonly accepted practice by seedstock producers offering young bulls for sale and by commercial cow-calf producers as a pre-breeding evaluation of their existing herd sires. There are several essential components of a standardized Breeding Soundness Examination which should conform to recommendations that have been set forth by the Society for Theriogenology. Adherence to these recommendations should allow uniformity in the interpretation of results based upon published scientific information and avoidance of incomplete, inaccurate, or misleading results that may lead to disagreement in the classification of bulls.

1. A veterinarian or allied professional that is experienced and competent should conduct the examination.
2. A general evaluation of the bull should be conducted, including historical information and observation of locomotion in the unrestrained bull.
3. The bull's external reproductive genitalia should be thoroughly examined, and scrotal circumference should be recorded.
4. A seminal ejaculate should be collected and evaluated.
5. A signed report should be prepared defining the standard results.

**Conducting the examination.** The Breeding Soundness Examination should be conducted by a trained and experienced professional in order to obtain reliable and repeatable results. Interpretation of findings requires knowledge of the animal's health and physical status, a careful evaluation of the reproductive system, and an examination of semen.

**History and physical examination.** The bull should be carefully observed for any structural or physical defects that might interfere with natural mating. Conditions that should be noted include defects in vision, foot and leg problems preventing normal locomotion, and general abnormalities that may adversely alter spermatogenesis. A detailed examination of the reproductive organs will permit detection of abnormalities of the accessory glands, testis, scrotum, prepuce, or penis. All findings should be noted on the report.

**Scrotal circumference.** Positive correlations between scrotal circumference and semen production, and negative correlations between scrotal circumference and age at puberty, have been demonstrated in young sires. A mild negative correlation has been reported between scrotal circumference and proportion of sperm with normal morphology. Measurement of scrotal circumference should be done by experienced personnel. Optimum value is realized from these measurements when they are accurately collected in young bulls of known age, weight, and condition. Measurements are routinely reported in millimeters or centimeters.

**Semen collection and evaluation.** Semen samples can be collected by rectal massage, the use of an artificial vagina, or by electro-ejaculation. The last method is most commonly utilized and should be conducted with good restraint and minimal stress to the animal. This is accomplished in the majority of cases with experienced personnel and modern equipment.

A properly conducted semen evaluation provides important information relative to a bull's potential fertility. Accurate and repeatable results are highly dependant on the collection and handling of a quality sample of semen. Adverse effects on quality are often the result of sample contamination by water, urine, or preputial fluid or by a failure to maintain optimum temperature of the ejaculate between collection and evaluation. Adequate penile extension during electro-ejaculation will reduce contamination of semen with preputial fluid.

The most important information obtained from semen evaluation is the assessment of sperm viability and morphology. Additional information may be obtained by observation of a properly collected sample for abnormal cellular material, such as from an inflammatory process involving the reproductive tract. Although prediction of the degree of fertility is not possible from a semen evaluation, it does provide reliable indicators of future performance based upon the animal's seminal characteristics.

**Classification of bulls.** Bulls are classified into three possible outcomes following the breeding soundness examination. The **Satisfactory** category is used for bulls that meet or surpass the minimum recommended thresholds for scrotal circumference, sperm motility, and sperm morphology, and which have no abnormal physical traits or reasons that could compromise their breeding performance. **Unsatisfactory** bulls are those that fail to meet the recommended thresholds in one or more traits and are unlikely to ever improve their status. This category also would include bulls with genetic defects or irrevocable problems that would compromise their use as a breeding animal. The last classification, **Deferred,** describes any bull that does not fit into the previously defined categories. This classification is recommended for bulls that are immature or suffering from a transient problem that prevents a satisfactory classification at the time of examination but indicates the bull is likely to improve with age or convalescent time. This category is also utilized for bulls that could not be accurately classified because of problems in collection and for bulls that nearly meet the standard thresholds but may be in below average condition or demonstrate seminal characteristics that may improve at subsequent collection dates.

**The breeding soundness examination report.** A proper breeding soundness examination should be followed by a completed report containing the following information for future use and documentation of the examination:

- Owner's name, address, and location
- The date of examination, and identification of any repeat examinations
- Unique permanent animal identification, breed, age, and alternate identification

- Animal history, weight, condition score, and results of previous tests
- Results of physical examination with explanation of findings if necessary
- Results of scrotal circumference measurements
- Results of semen motility estimate
- Results of semen morphology (percent normal cells if **Satisfactory**/or the morphologic defect(s) resulting in **Deferred or Unsatisfactory** status)
- Signature and address of veterinarian or person performing the examination.

**Reference.** Guidelines for The Bull Breeding Soundness Evaluation - Society for Theriogenology / American College of Theriogenologists. Revised 1993.

## Reference Tables for Evaluation of Scrotal Circumference and Spermiogram

### Minimum Recommended Scrotal Circumference

| Age | SC (cm) |
|---|---|
| * ≤ 15 MO | 30 |
| > 15 ≤ 18 MO | 31 |
| > 18 ≤ 21 MO | 32 |
| > 21 ≤ 24 MO | 33 |
| > 24 MO | 34 |

### Minimum Recommended Motility is: 30% or Fair (F)

| **Mass Activity (Gross)** | **Rating** | **Individual** |
|---|---|---|
| Rapid Swirling | Very Good (VG) | ≥ 70% |
| Slower Swirling | Good (G) | 50 - 69% |
| Generalized Oscillation | Fair (F) | 30 - 49% |
| Sporadic Oscillation | Poor (P) | < 30% |

## Sperm Morphology

Minimum Recommended Morphology is 70% Normal Cells

Primary Sperm Abnormalities
- Underdeveloped
- Double forms
- Acrosome defect (e.g. knobbed acrosome)
- Narrow heads
- Crater/Diadem defect
- Pear-shaped defect
- Abnormal contour
- Small abnormal heads
- Free abnormal heads
- Abnormal midpiece
- Proximal droplet
- Strongly folded or coiled tail
- Accessory tails

Secondary Sperm Abnormalities
- Small normal heads
- Giant and short broad heads
- Free normal heads
- Detached, Folded, Loose acrosomal membranes
- Abaxial implantation
- Distal droplet
- Simple bent tail
- Terminally coiled tail

Other Cells
- Epithelial cells
- Erythrocytes
- Medusa formation
- Sperm precursor cells
- Round cells
- White blood cells

For more information on sperm morphology refer to:
Abnormal Morphology of Bovine Spermatozoa
A.D. Barth and R.J. Oko. 1989. Iowa State University Press, Ames, Iowa

To be classified a Satisfactory Potential Breeder requires a satisfactory Physical Examination and minimum values for Scrotal Circumference, Motility and Morphology. Any bull not meeting minimums is either classified as an Unsatisfactory Potential Breeder or classification may be Deferred at the discretion of the evaluator.

* It should be noted that it is common for yearling bulls, due to immaturity, to require a second fertility examination to achieve satisfactory potential breeder status.

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