Understanding Genetics and the Sire Summaries

"Understanding Genetics and the Sire Summaries", was developed to help individuals learn more about genetics and genetic evaluations. This workbook presents definitions of genetic terms, a basic explanation of official sire summaries, sire comparison, selection exercises, and genetics in the future. More comprehensive information on genetics, genetic measures and sire selection is available from each breed association.

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What Can I Learn From This Workbook?

Genetics is a science that looks at the heredity and biological variation in organisms. There are two sources of genetic variation: chromosomal and gene mutations. This includes duplication, deletion, or rearrangement of chromosome segments. Understanding the basic principles of genetics and dairy cattle breeding is necessary to effectively use sire summaries. Through genetic evaluations, differences in individuals can be measured. Genetic evaluations are important for selecting genetically superior parents and improving characteristics of future generations. Since their introduction in 1935, genetic evaluations have become very complex. Using this information enables us to make decisions that are based on facts.

Use this workbook to gain a basic understanding about genetics as well as the knowledge to help you comprehend genetic evaluations. An awareness and appreciation of dairy cattle genetics can give you the skills necessary to make greater genetic progress in your herd.

Major Factors Influencing Genetic Change

One of the major goals of dairy producers is to maximize profitability. A way to achieve this goal is to have a genetically superior herd. As an important foundation of a profitable herd, genetic change is permanent and accumulates over time. Genetic change is dependent on four major factors and has the following formula:

$$\frac{\text{Accuracy of Selection} \times \text{Selection Intensity} \times \text{Genetic Variation}}{\text{Generation Interval}} = \text{Genetic Change}$$

Accuracy of Selection
Refers to our ability to select animals that truly are genetically superior for a given trait.
It is dependent upon the genetic evaluation techniques used, such as the Animal Model.

Selection Intensity
Is dependent upon the proportion of animals kept as parents for the next generation.
Intensity also includes the superiority of those animals compared to the genetic average of the overall unselected population.

Genetic Variation
Indicates the relative differences among animals that are controlled by genetic factors.
It is measured as the heritability of the trait.

Generation Interval
Is the average age of a parent when offspring are born.

To achieve rapid genetic change, accuracy of selection must be high. Parents must be genetically superior when compared to the average population. In addition, more progress will be achieved with more highly heritable traits and shorter generation intervals. By keeping these four factors in mind, genetic progress can be maximized.

Definitions of Genetic Terms

Cell
A cell is the smallest structural unit of an organism that is capable of independent functioning. All animals are made up of thousands of cells. Genetic material is located in the nucleus of each body cell.

Chromosomes
Chromosomes are the structures that contain the genes. In dairy cattle, 30 pairs of chromosomes are located in each cell's nucleus. The number of chromosomes varies among animals. Humans have 23 pairs of chromosomes.

DNA
Chromosomes are chemically composed of DNA (deoxyribonucleic acid). DNA is a nucleic acid arranged in a double helical structure. Contained within each DNA molecule are genes which are part of a larger element, the chromosome.

Genes
Genes are hereditary units that determine a portion of the animals appearance, performance, behavior and other characteristics. They influence the expression of specific traits and are known as the chemical building blocks of DNA.

Locus
The locus is the region of the chromosome where a particular gene is located.

Allele
An allele is one component of the gene pair which is located at a given locus or position on the chromosome.

Meiosis
Sperm and eggs are created by a process called meiosis, or cell division. The number of chromosomes in the sperm and egg are half of that found in all other cells. One chromosome of each pair is passed to the sperm or egg. A random sample of one allele from each locus is found in the sperm and eggs. The sperm and egg unite to form a zygote, or fertilized egg. The resulting zygote contains an equal number of chromosomes from each parent.

Mendelian segregation is the random process which occurs during meiosis and determines which allele of each gene is contained in a given sperm or egg. Variation among individuals, including offspring of a given animal, results from this process.

Phenotype
The phenotype of the cow is what you observe or measure. It is the individual's actual performance, such as a 305-day record or a classification score.

Genotype
Genotype is the actual genes that the animal possesses for a given trait. In qualitative traits, the genotype identifies the exact alleles that an animal has for a specific trait. In quantitative traits, the genotype is expressed as the breeding value, which is an accumulation of the effects of all genes.
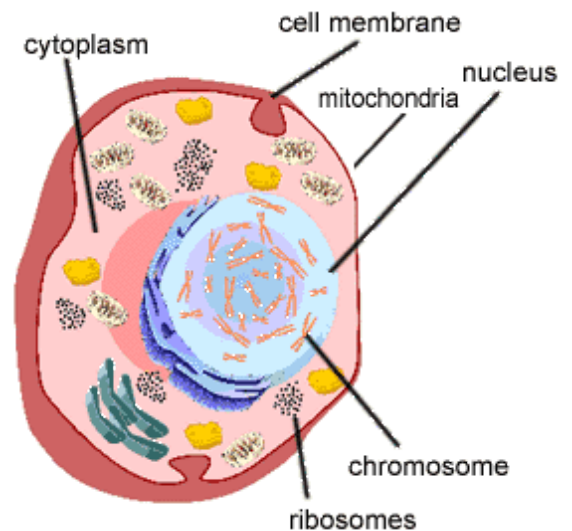
Dominant - Recessive

At each locus there are two alleles for a specific trait, one from each parent. In some cases, one allele is dominant over the other allele in determining the trait.

For example, a single gene controls coat color in Holsteins. Cattle are either red-and-white or black-and-white. The black gene is dominant and the red gene is recessive. Genes are expressed as **"B"** (big B) for the dominant black gene and **"b"** (little b) for the recessive red gene. The combination from the parents will determine if the offspring will be black-and-white or red-and-white.

The three possible genotypes for coat color are: **BB, Bb,** and **bb**; with one gene coming from each parent. Since **B** is dominant over **b**, the presence of at least one **B** allele results in black coat color. Red coat color is only possible with the **bb** genotype.

Differences exist among breeds. In Milking Shorthorn cattle, coat color is expressed differently for each of the three possible genotypes: **RR** - red, **Rr** - roan (red and white mix) and **rr** - white. No dominance is present between the red and white alleles. Therefore, in the **Rr** genotype, the animal is a mix of the two colors.

Heterozygous

An animal is heterozygous for a certain gene when the two alleles at a given locus are not the same. For example, a Holstein's coat color gene may be the heterozygous combination, **Bb**. The animal carries one gene for red coat color and one gene for black.

Homozygous

An animal is homozygous for a certain gene when both alleles at a given locus are the same. For example, if a Holstein's coat color gene is **BB**, it is homozygous for black coat color. A red and white Holstein is homozygous with a genotype of **bb**.

Qualitative Traits

Qualitative traits are generally controlled by one pair of genes. In addition, a given genotype (genetic make-up) will generally result in the same phenotype (actual expression of a trait). Examples of qualitative traits are sex, hair color and horns. Qualitative traits also include undesirable recessives such as Mule-Foot (Syndactylism) in Holsteins and Limber Leg in Jerseys.

Quantitative Traits

Quantitative traits are controlled by many genes, with each gene generally having a relatively small influence on the expression of a trait. Collectively, these genes can have large effects. Examples would include economically important traits such as milk production, fat percentage, and final score. These traits can be significantly influenced by the environment. Research in gene mapping now shows evidence that several "major" genes may have larger effects on traits than do most of the genes influencing the trait.

Environment

The environment that an animal lives in has a large influence on production as well as on other quantitative traits. In fact, environment contributes more to the difference among cows' production than does genetics. Seventy-five percent (75%) of the difference among cows' production is attributed to environment, while only twenty-five percent (25%) is based on genetic merit.

Environmental Variance

Environmental variance is the difference in the performance of animals that is caused by environmental effects. Genetic evaluations are designed to account for differences in production and type due to environmental variance.

Breeding Value

Breeding value is defined as the total genetic ability of an animal for a given trait. An individual receives one-half of their breeding value from each parent. The formula for calculating breeding value is:

Breeding Value = Sire's Transmitting Ability + Dam's Transmitting Ability

Transmitting Ability

Transmitting ability is an estimate of the average genetic merit that will be passed from parent to offspring. This information can be utilized in a breeding program to predict how an animal will produce relative to its herdmates.

Transmitting Ability = 1/2 Breeding Value

Selection Intensity

Selection intensity measures the relative superiority of the group of animals allowed to reproduce. The selection intensity in bulls is high because only a small number of bulls are needed to produce adequate amounts of semen for the U.S. dairy cow population. In cows, however, selection intensity is lower because farmers need to maintain about 75% of their females to produce herd replacements. Higher selection intensity results in more rapid genetic improvement.

Heritability

Heritability is the proportion of variation in a trait that is due to genetic factors. Heritabilities range from 0.0 to 1.0 (zero to 100%). The higher the number, the more heritable the trait will be. By selecting for a high heritability trait, faster genetic progress will be made. Low heritability, less than .10, does not offer much opportunity for rapid improvement in a trait.

When striving to improve a trait, heritability should be considered. For example, Farmer Jones' cow, Charity, needs improvement in both foot angle and teat placement. Heritability for foot angle is .15 and for front teat placement is .26. Given the same selection intensity for both traits, Charity's offspring are expected to improve more rapidly in teat placement than foot angle because the heritability for teat placement is higher.

Generation Interval

The average age of a parent when offspring are born is called the generation interval. Rate of a genetic change increases when the generation interval decreases.

Inbreeding

Inbreeding occurs when two animals that are more closely related than the average population are mated. One form of inbreeding, linebreeding, occurs when progeny are repeatedly mated to ancestors or close relatives. A goal of linebreeding is to increase the frequency of the good genes that are found in the common ancestor.

Several unwanted effects of inbreeding may also occur. Since homozygosity increases, a greater probability of having a homozygous recessive condition for undesirable qualitative traits exists. This concentration of undesirable genes may reduce health, vigor, and growth and increase calf mortality. Production and reproduction are also negatively affected. For each 1% increase in inbreeding, an average decrease of 60 pounds of annual milk production results. Animals that are highly inbred also tend to have a lower conception rate.

Crossbreeding

Crossbreeding occurs when two purebreds from different breeds are mated. Its purpose is to produce a generation that will have greater performance than expected, considering the transmitting abilities of the parents. Crossbreeding generally increases health, vigor and reproductive performance.

Correlated Response

A correlated response occurs when selection for one trait results in genetic changes in other traits. These genetic correlations can be positive or negative. Mathematically, correlations range from -1 to 1. As a correlation value nears -1 or 1, many of the same genes control both traits. A value near 0 indicates that few of the same genes regulate both traits.

Selection for an increase in one trait can result in an increase in the other. A correlation of .40 exists between milk yield and dairy form. Selection only for increased milk yield will generally improve dairy form even though no direct selection was made for dairy form.

In contrast, selection for an increase in one trait can also result in a decrease in another. A correlation of -.35 exists between milk yield and fat percent. Selection for an increase in milk yield will generally result in decreased fat percent.

Variation

Variation, or differences in genetic merit, exists in all animals because of the random sampling of alleles during Mendelian segregation. By graphing the genetic merit or actual performance of all animals in a population, one would observe a normal distribution or a bell-shape curve. A normal distribution is centered on the average measurement for that particular trait. Approximately equal numbers of individuals (50%) are above and below the average. Standard deviation is the number that, when added to and subtracted from the population average, gives a range that includes about two-thirds of the population.

Farmer Jones' 305-day ME
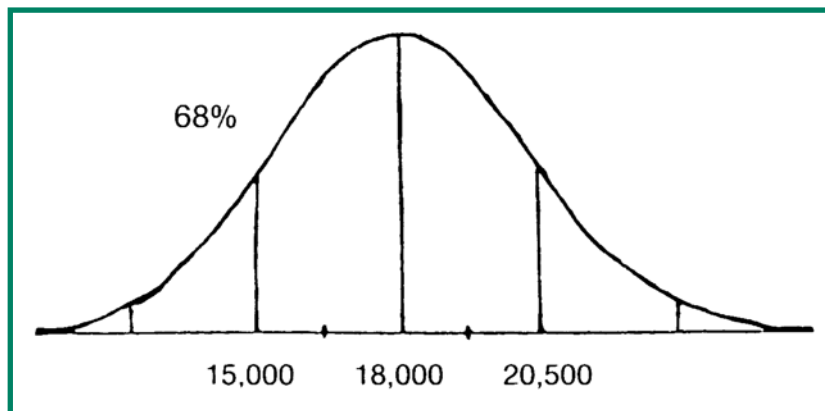
As an example, let's use standard deviation to describe the variation in a herd average. Farmer Jones' herd has a 305-day ME average of 18,000 pounds milk. The standard deviation for 305-day ME average is 2,500 pounds. Sixty-eight percent (68%) of the ME records in this herd are expected to fall into the range of 15,500 to 20,500 pounds. Approximately one in six will fall below 15,500 pounds and one in six will produce over 20,500 pounds.

Undesirable Recessives

Undesirable recessives are defects in cattle that may cause poor health and/or death. These qualitative traits generally are controlled by only one gene. Therefore, if an animal is homozygous for that recessive allele, the undesirable condition is expressed.

Gene Codes			
BD	Bulldog	IS	Imperfect Skin
BL	Bovine Leukouyte Adhesion Deficiency (BLAD)	MF	Mule-Foot
BY	Brachyspina	PO/PP	Polled
CV	Complex Vertebral Malformation (CVM)	PG	Prolonged Gestation
DF	Dwarfism	PT	Pink Tooth (Porphyria)
DP	Deficiency of Uridine Monophosphate Synthase (DUMPS)	RC	Carries gene for Red Hair color
HL	Hairless	B/R	Black/Red hair color

All breed associations recognize undesirable recessives and records the abbreviation for these traits as a part of an animal's name. An example is Ricecrest Emerson - ET *BL. He is a carrier of the recessive gene for BLAD (he is heterozygous for this trait).

Tested Codes			
TL	Tested free of BLAD	TD	Tested free of DUMPS
TY	Tested free of Brachyspina	TM	Tested free of Mulefoot
TV	Tested free of CVM	TR	Tested free of Red Hair Color

If an animal tests free of a trait, that result is also recorded. For example, O-Bee Manfred Justice - ET *TL, tested free of BLAD.

Progeny
Progeny can be defined as an animal's offspring (sons and daughters).

Genetic Evaluations
The United States Department of Agriculture (USDA) and breed associations update their procedures for calculating production and type information as new techniques are developed. As a result, accurate information is available to dairy breeders. The Daughter-Dam Comparison, Herdmate Comparison and Modified Contemporary Comparison all preceded the current Animal Model genetic evaluations. Genetic evaluation calculations account for many environmental and genetic factors which minimize inaccurate and biased proofs. The effects which are used to calculate genetic levels include the following:

Herd Management Effects:
Daughters of bulls are compared directly with their herdmates. The term herdmates can be defined as the daughters of other bulls managed in a herd at the same time. With this comparison, differences due to changes in herd management, such as feeding or housing, are minimized.

Genetic Competition of Herdmates:
The genetic merit of herdmates is used in the evaluation. This accounts for the level of genetic competition within a herd.

Genetic Merit of Mates:

When progeny information is used to evaluate a cow or bull, the genetic merit of the other parent of each offspring is included in the evaluations. When a bull is mated to a non-random group of cows which may include above average or below average genetic merit, the genetic evaluation procedures account for this situation. This eliminates potential sources of bias. When daughter information is used to evaluate cows, the animal model evaluations similarly account for the genetic merit of the daughters' sires.

Environmental/Sire-by-Herd Interaction:

Sometimes a herd manager will manage daughters of certain bulls differently. For example, daughters of a high priced bull may be grouped differently than daughters of lower priced bulls. This potential bias is accounted for in animal model genetic evaluations.

Ancestor Information:

Ancestor information is included in genetic evaluation calculations. As the amount of information from the animal itself or its progeny increases, the weight on ancestor information decreases.

Predicted Transmitting Ability (PTA)

Predicted Transmitting Ability is an estimate of genetic superiority that a bull or cow will transmit to its offspring for a given trait. PTAs are calculated for milk pounds, fat pounds, fat percent, protein pounds, protein percent, somatic cell score, productive life, net merit and final type score. This information can be used to rank bulls and cows by their genetic merit. When using sire summaries, breeders can compare sire PTA values for certain traits to select service sires for their herd. PTAs also are calculated for linear type traits, but then are standardized to simplify interpreting them. A simplified version of the calculation is:

$$w1 \ \times \ \text{progeny} + w2 \ \times \ \text{animal itself} + w3 \ \times \ \text{ancestors} \qquad (w1 + w2 + w3 = 1)$$
$$(w = \text{weight})$$

Genetic Base

A genetic base is a reference point for genetic evaluations. The base is defined by making the average PTA for all cows born in a certain year equal to zero. Evaluations are calculated and expressed relative to the base year. The genetic base has no impact on how animals rank compared to each other. The base changes every five years. The next change will be in 2010.

Standard Transmitting Ability (STA)

Genetic evaluations for linear type traits are expressed as Standard Transmitting Abilities (STAs). Standardized values for linear traits are used because each trait has a different average PTA and the PTA ranges vary within traits. STAs simplify interpreting the linear trait genetic evaluations. As a result, all linear traits have an average of 0. The range of STA values is generally 6 STA units. The midpoint and average are 0. Both extremes for each trait are approximately 3 STA units from the average.

The figure to the right shows the distribution of STA values for a linear trait. This curve is called a normal distribution or a bell-shaped curve. Many biologically important traits in dairy cattle have this distribution. At the average (STA=0), you see the greatest number of bulls. A majority of bulls (68%) are within 1 STA in each direction of the average. As the STA value is farther from the average, fewer bulls will be at that STA. In other words, more bulls will have STAs of low values (0 to 1) than STAs of large values (2 to 3)

3 2 1 0 1 2 3
Distribution of STAs
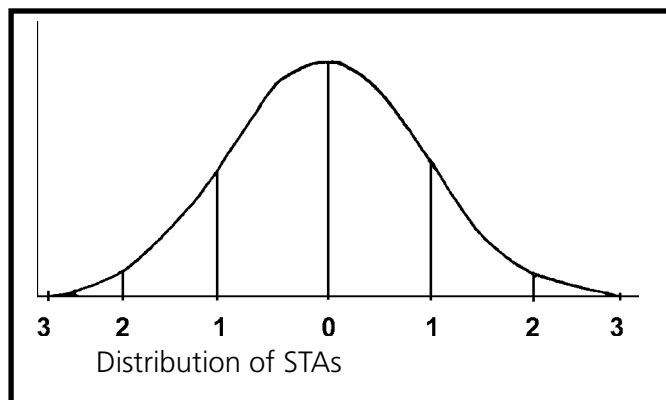
PTA Dollars (PTA$)

This economic index combines relative values of milk and its components; MF$ is an index of milk and fat; MFP$ is an index of milk, fat and protein; CY$ is an index of milk, fat and protein based on cheese yield prices.

Percentile

Percentile values indicate how a bull or cow ranks relative to other individuals. Bulls are ranked on Net Merit. Net Merit is an economic index based on MFP$ and subtracts feed costs, mastitis and milk quality costs associated with somatic cell score and adds the value based on productive life. USDA's Elite Cow list is based on the percentile ranking for MFP$. The highest ranking is 99%. An 85 percentile ranking means the animal is in the top 15% of the population.

Animal Model

The Animal Model was implemented in 1989 by USDA. Animal Model evaluations are based on the animal and its relationship to the other animals being evaluated. Information from the animal itself, its ancestors and its progeny is incorporated, with all records of all female ancestors and descendants used. In Animal Model evaluations, all identified relatives of an animal affect the animal's evaluation. Additionally, each animal influences the evaluation of its relatives. The amount of influence depends on how closely the animals are related. Daughters, sons and parents have more of an impact than less closely related animals.

Linear Composite Indexes

Four linear trait composite indexes are printed in the sire summaries. These indexes are for: Udder (UD), Feet and Legs (FL), Body Form (BD) and Dairy Capacity (D). Linear composite indexes combine linear descriptive type information on several related traits into one number value. The four composites are calculated from genetic evaluations of the following linear type traits:

1. **Udder:** udder depth; front teat placement; udder cleft; rear udder height; rear udder width; fore udder attachment; and rear teat placement.
2. **Feet and Legs:** rear legs - side view; foot angle; rear legs - rear view; and feet and legs score.
3. **Body Size:** stature; body depth; strength; and thurl width.
4. **Dairy Capacity**: dairy form and strength.

Each composite value can be used to identify bulls which are predicted to transmit a desirable combination of the index's traits. For example, if a breeder is aiming to improve a cow's udder he should use a bull with a high udder composite. The desirability values for each trait are weighted according to their economic value and are added together to arrive at the four index values. These composite index values are then standardized in the same manner as the STA values for each linear trait calculated.

When using the standard value, it is not necessary to know the average PTA for a given trait to compare the bull's transmitting ability to the average. The STA indicates the relative magnitude of the bull's transmitting ability. The letter that follows each STA specifies the direction of the trait, or its tendency to one of the extremes. STAs are found in the trait profile blocks of the sire summaries.

For example, consider a bull with an udder cleft STA of 1.83S. This means that his daughters tend to have strong (S) udder cleft. Since the STA is 1.83, we know that this bull has a relatively large transmitting ability for strong udder cleft, almost 2S above average.

Standard Transmitting Abilities can be used in setting herd goals. A breeder can specify a limit that bulls must meet to be included in a semen inventory or, an average STA for a linear trait may be specified as a goal for a herd breeding plan.

Reliability (REL or R)

Reliability is a measure that estimates the accuracy of the Predicted Transmitting Ability. It is based on the amount of information in the evaluation. Information from the animal, parents and progeny are included. As more daughters are included in a bull's proof, more emphasis is placed on progeny information and less is placed on ancestor information. Reliabilities show how much confidence can be placed in the proof. As more daughters are added, the reliability increases.

An example of this is the bull, Jenny-Lou Marshall Toystory-ET. In the February 2006 Sire Summary, he had 76 daughters in his type proof and a Reliability of 86%. In the May 2007 Sire Summary, he had 103 daughters and his Reliability increased to 89%.

Total Performance Index

The acronym TPI was recently changed from Type and Production Index to Total Performance Index to better reflect our balanced breeding objective. Maximum profit is achieved when cows calve with ease, breed back quickly and produce well with a low incidence of mastitis for several lactations. Dairy producers around the world are now putting a priority on selecting for these health traits.

If our cows got a vote in the breeding program, they would approve of the addition of health traits into the TPI formula. The future of the Holstein cow is on the right track. As, breeders continue to focus on the traits that are the most critical to the health and well-being of the cows and the financial security of their owners.

Selecting for Health Traits

Using the TPI formula is an excellent way to improve the health and fertility of Holstein cattle. Its goal is to identify a complete package of top genetics, one that balances improved production along with an outstanding blend of conformation and health characteristics.

The key features of the current TPI formula are as follows:
- 47% emphasis on production (Fat and Protein & part of PTAT)
- 20% emphasis on udder health (SCS, UDC & part of PTAT)
- 19% emphasis on early breeding (DPR, PL & DF)
- 8% emphasis on mobility (Feet & Leg composite & part of PTAT)
- 3% emphasis on calving ability (Daughter Calving Ease & Stillbirth)
- 3% emphasis on body size (part of PTAT)

This formula coincides with the worldwide demand for healthy, fertile and long-lasting dairy cattle. Sires that rank high on Productive Life (PL), Somatic Cell Score (SCS), Daughter Pregnancy Rate (DPR), as well as lower on Calving Ease (Service Sire Calving Ease – SCE and Daughter Calving Ease – DCE) and Stillbirth (Service Sire Stillbirth – SSB and Daughter Stillbirth – DSB) produce cows that are profitable for dairy producers.

Recently Added Traits

Daughter Pregnancy Rate (DPR) is the percentage of nonpregnant cows, past the voluntary waiting period, that become pregnant in a 21-day period. But it can also be looked at as a change in the number of days open and ultimately impacting the number of cows culled for reproductive purposes.

Each increase of 1% in daughter pregnancy rate corresponds to 4 additional days open. Therefore, daughters of the highest and lowest Active AI sires for DPR, representing a difference of 8.6%, would be expected to differ by roughly 34 days open per lactation. An average increase of 34 days open

represents at least one more cycle, with some daughters requiring several more breedings. Some daughters will just simply run out of opportunities to get pregnant and get culled. A bull with an 8.6% lower DPR than another bull would expect to see 11.4% more of his daughters culled for not getting pregnant.

Productive Life (PL) measures the amount of time that a cow is productive, i.e., milking. Cows receive credit for each month of lactation. The amount of credit corresponds to the shape of the lactation curve. The highest credit is given to those months at the peak of lactation and the credits diminish as the cow moves into the tail end of her lactation. First lactations receive less credit than later lactations in proportion to the difference in average production.

Calving Ease and Stillbirth

Calves that die or are born with difficulty reduce dairy farm profit. Calving Ease (CE) measures the ability of a cow to calve easily. CE is scored by the owner, for single births only, on a scale of 1 to 5. A score of 1 meaning no problems encountered or unobserved birth and 5 meaning extreme difficulty.

Two sets of evaluations for Calving Ease are provided. Daughter CE measures the ability of a particular cow (daughter) to calve easily. Service Sire CE measures the tendency of calves from a particular service sire to be born more or less easily.

The CE evaluations are expressed as percent difficult births in first calf heifers, where difficult births are those scored as requiring considerable force or being extremely difficult (4 or 5 on a five point scale). Percent difficult births among first calf Holstein cows is approximately 8%. Listed below is a description of the codes used for scoring this trait as well as their frequency within the Holstein breed.

Calving Ease Codes - description and frequency

Score	Definition	Frequency of Calving Difficulty		
		1st calf	**2nd calf**	**3rd calf**
1	**No problem (or unobserved)**	63%	80%	81%
2	**Slight problem**	15%	10%	9%
3	**Cow needed assistance**	14%	7%	7%
4	**Considerable force used to deliver calf**	5%	2%	2%
5	**Extreme difficult birth**	3%	1%	1%

Stillbirth (SB) is also scored by the farmer on a scale of 1 to 3, 1 meaning the calf was born alive and was alive 48 hours postpartum, 2 meaning the calf was born dead, and 3 indicating the calf was born alive but died within 48 hours postpartum. SB scores of 2 and 3 are combined into a single category for evaluation.

Similar to Calving Ease, two sets of evaluations are provided. Daughter SB measures the ability of a particular cow (daughter) to produce live calves. Service Sire SB measures the tendency of calves from a particular service sire to be stillborn more or less often. The SB evaluations are expressed as percent stillbirths amongst all animals (heifers and cows). Percentage of stillbirths in Holsteins is approximately 8%.

TPI FORMULA

$$\left[\frac{27(\underline{PTAP})}{19.4} + \frac{16(\underline{PTAF})}{23.0} + \frac{10(\underline{PTAT})}{.73} - \frac{1(\underline{DF})}{1.0} + \frac{12(\underline{UDC})}{.8} + \frac{6(\underline{FLC})}{.85} + \frac{9(\underline{PL})}{1.26} - \frac{5(\underline{SCS})}{.13} + \frac{11(\underline{DPR})}{1.0} - \frac{2(\underline{DCE})}{1.0} - \frac{1(\underline{DSB})}{0.9}\right] 3.8 + 1832$$

*The value 1832 adjusts for the periodic base change, allowing TPI values to be compared across time.

Cow Total Performance Index (CTPI)
CTPI is the index for cows, which includes the same factors for calculation as TPI.

Pedigree Total Performance Index (PTPI)
PTPI is the index for young stock, which estimates the ability of the young animal to transmit superior traits. PTPI is calculated by combining the Parent Averages for Protein, Fat, Type, Udder Composite and Feet and Legs Composite in a 3: 1: 1 .65: .35 ratio

How are Composite Indexes Calculated?
The STAs of each linear type trait used in the composite are changed from a value in a range of -5 to 5 (with 99% falling between -3 and 3) to relative desirability values ranging from zero to 100. STAs of least desirability are assigned zero and STAs of highest desirability score 100.

The traits are then weighted according to their economic importance. Traits of high economic importance have larger weighting factors than traits of lower economic importance.

The desirability values are multiplied by the economic weight for each trait to establish the composite index value. Then the composite desirability values are standardized and expressed as STA's (ranging from -3 to 3). The values are based on all bulls in the available bull population.

Modifications to Udder Composite
Using results from a Holstein Association study on herd life, revisions to the weights for the linear traits in the Udder Composite Index have occured. These weights more accurately reflect each udder trait's contribution to increased longevity.

The weights are:

Udder Depth	.35	Rear Udder Width	.12
Fore Udder Attachment	.16	Udder Cleft	.09
Front Teat Placement	.05	Rear Teat Placement	.07
Rear Udder Height	.16		

The Udder Composite is computed as the total of the STAs of the above seven udder traits times their respective relative herd life weight.

UDC = [(UD x .35) + (FU x .16) + (UH x .16) + (UW x .12) + (UC x .09) + (TP x .05) - (RP x .07)]

Progeny Test
The objective of progeny testing bulls is to identify genetically superior sires for economically important traits. A.I. organizations, breed associations, and private breeders conduct progeny tests attempting to obtain a random sample of daughters.

The process begins when bulls are approximately 8 to 10 months-of-age. They are sons of the top A.I. bulls and their dams are among the most outstanding females. Health tests are performed. After passing these tests, semen is collected from the bull.

Semen is distributed and used to breed a random sample of females in many herds. The distribution of semen is carried out quickly, so that a proof is available as soon as possible. The bull is used in many herds to include a variety of environmental conditions. Usually 5 to 10 units of semen are distributed in 80 to 100 herds. The goal is to have about 60 to 75 daughters in 40 to 50 herds.

A proof, or genetic evaluation, is available three to five years after the semen is distributed. This wait includes nine months for pregnancy, two years until daughters calve, and at least six months for milk records to be included in the proof. When the bull receives a proof, the owner has an estimate of the bull's genetic superiority. If the bull is above average, he will be used extensively as a sire.

Genetics Word Search
(find the words below)

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G D M S T E R I S R E
E R A E N M S I Z E D
N I T M E B I R T H Y
E D I E M R U R E T N
S X N N Y G D P M E
T E G A O O G I D D G
I D H N R B L A D E O
A N E V I S S E C E R
R I A L V N G D E R P
T H L P N E O E E B E
R E T L E L E L L A D
C A H C V M L O C U S
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|					
Allele	Birth	BLAD	Legs	Locus	Mating
Breed	Cell	Cloning	Pedigree	Progeny	PTA
CVM	Dam	DNA	Recessive	Red	RHA
DPR	Embryo	Environment	Semen	Sire	Size
Genes	Health	Index	TPI	Traits	Udder

What are Sire Summaries?

Genetic information for production and type traits is published by each specific breed organization. These publications, known as sire summaries, contain sire information on:

a) Production traits: milk, fat and protein;

b) Type traits: final score, linear traits and linear composite indexes;

c) Health and management traits: productive life, somatic cell score, calving ease and daughter pregnancy rate.

The United States Department of Agriculture (USDA) calculates the genetic evaluations for production quarterly in the months of February, May, August and November. Genetic values for type traits are computed by the respective breed association.
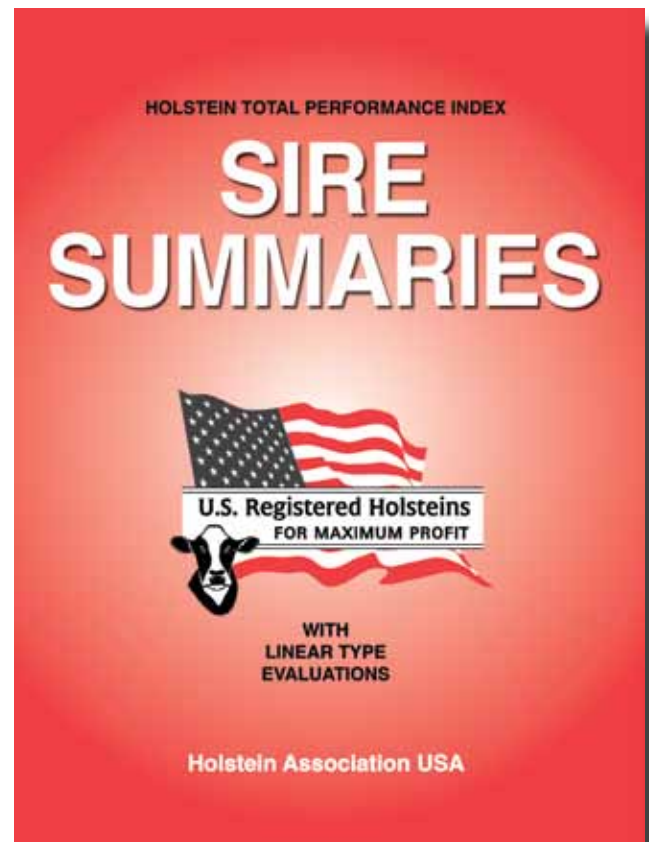
The first sire summary book for Holsteins was published in 1967. Since that time, it has evolved from a two-part book published three times per year, to the 'Red Book' published four times a year. Starting in 2007, the Sire Summaries are only being published three times per year.

PTA values for the production traits somatic cell score, productive life and net merit are calculated by the United States Department of Agriculture's Animal Improvement Programs Laboratory (USDA-AIPL). They have been publishing these values for sires since January 1994 and for cows since July 1995.

Multiple-trait Across Country Evaluations, more commonly known as MACE evaluations, are released by INTERBULL to estimate how sires from other countries might compare to sires with actual proofs in the United States. MACE proofs can assist U.S. producers by expressing proof information from other countries in terms more familiar to U.S. producers. INTERBULL MACE proofs are the official evaluation when it includes both U.S. and foreign daughters. The first INTERBULL evaluations were released in 1995.

Sire summaries provide extensive genetic information on the top Total Performance Index (TPI) bulls in the Holstein breed. They also provide information on other available sires and older sires that were previously marketed through artificial insemination (A.I.) organizations. In the Holstein breed, a bull must have at least ten U.S. daughters contributing production and/or type (classification) data in order for the bull to receive an official U.S. production and/or type sire summary. Dairy producers, A.I. organizations and many others use these summaries to assist them with herd breeding, merchandising and marketing decisions.

This section reviews genetic terms, sire information and explains how to use the values to make breeding decisions. Thoroughly reading the information and performing the exercises will help you know how sire summary information can be used to make breeding decisions.

Parts of the Sire Summaries

Holstein Association USA's Redbooks are published three times per year and are divided into three sections. The book opens with a list of the Top 100 TPI bulls, with minimum U.S. reliabilities of 80% for production and type. Next are the Top 50 Sire Lists for Milk, Fat, Protein, Type, Udder Composite, Feet & Legs Composite, Productive Life, Somatic Cell Score, Net Merit Dollars and Body Composite. To be listed in the Top 50 lists, sires must have a minimum reliability of 75% for type.

Section 1 contains production and type genetic information on the top 400 TPI bulls with semen status active, limited, or foreign. Domestic U.S. reliabilities of at least 65 percent for both production and type are printed in this section. A linear profile and proof block is included for each sire listed. These bulls have semen available and/or are alive and have relatively high genetic rankings. Bull information is printed alphabetically by bull registration name.

Section 2 includes limited genetic information on bulls listed as Active, Limited, or Foreign with PTA values for Production and Type. The genetic information on these bulls is listed in alphabetical order, based on registered name. This section also lists bulls numerically by NAAB (National Association of Animal Breeders) code and by short name.

Section 3 information is similar to that of the first section. It includes the top 100 TPI Inactive Sires with minimum Reliabilities of 95% for Production and Type and the Top 100 TPI Sires with 97% Domestic U.S. Reliabilites for Production and Type. Bulls are ranked according to several possible breeding objectives. Each list represents sires that will help breeders make genetic progress toward the improvement of a specific trait.

Red and Red Carrier Sires ranked by TPI are listed in Section 3 as well. They are Active or Limited sires with PTA values for type and production. The final listing is the Top 100 TPI International Bulls. Reliabilites need to be at least 80% for Production and 80% for type in the country of origin.

How To Read Sire Information

Sire summaries will be more useful if you understand the terms and information provided. These blocks offer answers to nearly every question a breeder may have about a bull. An extensive description of sire information follows:

BLOCK A: IDENTIFICATION PEDIGREE INFORMATION

Line 1: Bull's Registration Name and Total Performance Index (TPI).

John has a TPI of +1619.

Line 2: Nation Code, Registration Number, %RHA, Genetic Test Results, Final Score, Birth Date, and Recognitions.

Nation code is the country of origin for the animal, John. Holstein Juror John is of 100% Registered Holstein Ancestry-North America. Genetic test results determine if individual

```
HOLSTEIN JUROR JOHN-ET                              TPI +1619
    USA   2287161 100%RHA-NA   TV TL        86 06-18-03
Sire:   KED JUROR-ET                                      +1306M
    USA 2124357   100%RHA-NA   TV TL TD      82        GM
Dam:  HOLSTEIN BETTY                                      +1480
    USA 14266198 100%RHA-NA   BL            90 EEEEV  GMD DOM
```

animals carry certain recessive traits. By referring to the suffixes, you can find or avoid a recessive trait carrier. Recessive tested or animals recorded as a carrier of one of the following recessives are identified with these indicated codes.

Genetic Codes:

BD Bulldog[1]
BL Bovine Leukocyte Adhesion Deficiency (BLAD)[1]
TL Tested free of BLAD
BY Brachyspina
TY Tested free of Brachyspina
CV Complex Vertebral Malformation (CVM)[1]
TV Tested free of CVM
DF Dwarfism[1]
DP Deficiency of Uridine Monophosphate Synthase (DUMPS)[1]
TD Tested free of DUMPS

HL Hairless[1]
IS Imperfect Skin[1]
MF Mule-Foot (Syndactylism)[1]
TM Tested free of Mule-Foot
PO Polled[2]
PP Tested Homozygous Polled
PG Prolonged Gestation[1]
PT Pink Tooth (Porphyria)[1]
RC Red Hair Color[1]
B/R Black/Red[1]
TR Tested free of Red Hair Color

[1]Recessive gene carrier   [2]Dominant gene carrier

Parental information may be used to avoid inbreeding or to consider a low reliability bull's genetic potential. John originated in the USA, classified Very Good 86 points, and is born June 18, 1995. Holstein Juror John has a TPI value of +1619.

Line 3: Sire's Name and TPI Value.

John's sire is Ked Juror-ET and has a TPI value of + 1306.

Line 4: Sire's Nation Code, Registration Number, %RHA, Genetic Test Results, Classification Score, Recognitions.

John's sire, Ked Juror-ET is tested 99% free of being a carrier of BLAD (TL), DUMPS (TD) and CVM (TV), scored Good Plus 82 points, and has earned Gold Medal Sire recognition (GM).

Line 5: Dam's Name and CTPI Value.

Cow Total Performance Index (CTPI) combines the Predicted Transmitting Ability for Protein, Fat, Type, Udder Composite, Feet & Legs, Productive Life, and Somatic Cell Score. CTPI ranks cows on their ability to transmit a balance of those seven traits. Holstein Betty has a CTPI value of +1480.

Line 6: Dam's Nation Code, Registration Number; %RHA, Genetic Test Results, Final Score, Classification Breakdowns (Frame, Dairy Character, Body Capacity, Feet & Legs, Udder), and Gold Medal Dam and/or Dam of Merit Recognition.

Betty is classified Excellent 90 with breakdowns of Excellent in Frame, Excellent in Dairy Character, Excellent in Body Capacity, Excellent in Feet & Legs, and Very Good in Udder. She also has earned both Gold Medal Dam and Dam of Merit recognitions.

BLOCK B: PRODUCTION SUMMARY

The production summary gives genetic estimates of the bull's potential to transmit production traits. The milk, fat and protein information can help choose sires to achieve herd production goals.

PRODUCTION		%	%R	SIRE	DAM	DAU	GRP
Milk	+1491		93	+797	+1229	25977	24409
Fat	+47	-.03		+24	+47	953	903
Pro	+37	-.03		+23	+41	773	735
01-2008	181 DAUS	124 HERDS				56 %RIP	100 % US

Line 1: Milk: PTA, % Reliability, Sire's PTA, Dam's PTA, Daughter Averages (ME), and Management Group Average (ME).

This line refers to milk production. The Predicted Transmitting Ability for John is +1491 with 93% reliability. John is exceeding his sire's PTA M of +797 and his dam's PTA M of +1229. Daughters of John average 25,977 lbs. of milk per lactation, while the herdmates of the same age are only producing 24,409 lbs. These values are based on two times per day milking, 305 day lactation on a Mature Equivalent (ME) production level basis. If a bull has an official MACE evaluation, the daughter production averages will be based on the bull's Domestic U.S. evaluation.

Line 2: Fat: PTA, PTA %, Sire's PTA, Dam's PTA, Daughter Averages (ME), and Management Group Average (ME).

This line refers to fat production. The Predicted Transmitting Ability for John is +47 with -.03%. John's sire's PTAF is +24 and his dam has a PTAF of +47. Daughters of John average 953 lbs. of fat per lactation, while the herdmates of the same age are producing 903 lbs. These values are based on Mature Equivalent (ME) production levels.

Line 3: Protein: PTA, PTA %, Sire's PTA, Dam's PTA, Daughter Averages (ME), and Management Group Average (ME).

This line refers to protein production. The Predicted Transmitting Ability for John is +37 with -.03%. John's sire's PTAP is +23 and his dam has a PTAP of +41. Daughters of John average 773 lbs. of protein per lactation, while the herdmates of the same age are producing 735 lb. These values are based on Mature Equivalent (ME) production levels.

Line 4: Evaluation Date, Number of Daughters and Herds, Percentage of Records in Progress (RIP) and Percentage of Daughters in U.S.

This chart is from May 2003 and John had 181 daughters in 124 herds in his production proof. Fifty-six percent of the daughter's records were in progress and all (100%) of the daughters contributing to the sire summary are located in the US.

BLOCK C: ADDITIONAL GENETIC INFORMATION

PL	+3.2	69	+1.0	+1.5	SCE 7%	99 %R
SCS	3.11	81	3.16	3.15	DCE 6%	65 % R
NM$ +454	CM$ +446	FM$ +509			DPR 0.5%	67 %R

Line 1: Productive Life: % Reliability, Sire's PTA, Dam's PTA.

John's PL is +3.2 with 69% Reliability. His sire, Juror, has a PL of + 1.0 and his dam has a PL of +1.5. A high Productive Life PTA is desirable.

Line 2: Somatic Cell Score (SCS): PTA, % Reliability, Sire's PTA, Dam's PTA, Percent Difficult Births in Heifers (%DBH) when they calve for the first time (Calving Ease), and Calving Ease % Reliability.

John's PTA for Somatic Cell Score is +3.11 with a reliability of 81%. Juror's SCS is +3.16 and Betty's is +3.15. A low SCS is desirable. John has a %SCE of 7%, ranking him as a calving ease sire. The reliability is 99%. His %DCE is 6%, with a reliability of 65%. His DPR is 0.5%, with 67% reliabilty.

Line 3: Net Merit ($), Cheese Merit (CM$) and Fluid Merit (FM$).

John's Net Merit is +454, CM$ is +446, and FM$ is +509.

BLOCK D: TYPE SUMMARY

Genetic estimates for type, daughter type information and linear composite indexes are given here. Breeders use these values to select sires that meet herd goals for conformation.

TYPE		%R	SIRE	DAM	DAU SC	AASC
Type	+2.51	84	+1.90	+1.56	77.3	80.4
UDC	+2.39		+2.10	+1.18		
FLC	+.65		-.13	+2.00	BD +1.16	D +2.07
01-2008	57 DAUS	45 HERDS	EFT	D/H 1.6		

Line 1: Type: PTA, % Reliability, Sire's PTA, Dam's PTA, Daughter Averages for Final Score (SC) and Average Age Adjusted Score (AASC).

John has a PTA Type of +2.51 with 84% reliability. Juror has a PTAT of +1.9 and Betty's is +1.56. Daughters of John average 77.3 points, with the age adjusted score of those daughters at 80.4. If a bull has an official MACE evaluation, the average score and AASC, will be based on the bull's Domestic U.S. evaluation.

Line 2: Udder Composite (UDC): Linear Composite Index for Udder (UDC), Sire's UDC and Dam's UDC.

John is +2.39, Juror is +2.10 and Betty is +1.18 for UDC.

Line 3: Feet & Legs Composite (FLC): Linear Composite Index for Feet & Legs (FLC), Sire's FLC, Dam's FLC, Body Size, and Dairy Capacity.

John is +.65, Juror is -.13 and Betty is +2.00 for FLC. John's Body Size PTA is +1.16 and his Dairy Capacity PTA is +2.07.

Line 4: Evaluation Date, Number of Daughters and Herds, and Effective Daughters per Herd (EFT D/H).

In May of 2003, 57 daughters in 45 herds were used for John's linear type evaluations, with 1.6 effective daughters per herd. Effective daughters per herd is an indication of the distribution of daughters across herds. If each daughter were in a separate herd , the effective daughters per herd is 1.7. The lower the value of EFT D/H, the greater the reliability of the proof for a given number of progeny.

BLOCK E: OWNERSHIP INFORMATION

Breeder	Bill & Betty Breeder
Owner	AI Company
Controller	AI Company

Line 1: Name and State of the Bull's Breeder.

The breeder of John is Bill & Betty Breeder.

Line 2: Name and State of the Bull's Owner or Lessee, as Recorded with Holstein Association USA.

The bull's owner is AI Company.

Line 3: Name of the Bull's Controller, as Recorded with NAAB.

AI Company is John's controller and is responsible for submitting his status to NAAB.

BLOCK F: NAAB DATA INFORMATION

ACTIVE
1HO3872/S: 1
JOHN

Line 1: Semen Status.

John's status is recorded as ACTIVE by his controller.

SEMEN STATUS CODES:

C - COLLECTED: Bulls that have had semen collected and/or been assigned an NAAB code but no semen has been released for use.

P - PROGENY TEST SIRE: Semen has been distributed for multiple herd sampling.

F - FOREIGN: Bull has been progeny tested outside the USA and is actively being marketed in the U.S.

A - ACTIVE A.I. SIRE: Bull has been sampled, has a USDA Genetic Evaluation and semen with this NAAB code is routinely available, and for sale.

L - LIMITED: Bull with a USDA published evaluation and semen available in limited amounts.

I - INACTIVE A.I. SIRE.

Line 2: NAAB Number and Sampling Code, Sampler Controller Number.

The NAAB code, 1H03872, is a unique code number for John. It includes three parts. The first portion identifies the source of the semen, the organization that processed the semen. In this case, Artificial Insemination Company 1, AI Company, is the collection center. The next portion contains, HO, the two-letter abbreviation for the breed of the bull. In this case, John is a Holstein bull. The final portion of the NAAB code is the bull's individual code. These numbers are assigned by the semen collection center for each bull. The Sampler Controller Number is separated by a "/" and it indicates the controller of the bull when sampling was initiated. For example, S:100 means controller 1 (AI Company) sampled the bull in a "S" (Standard) sampling program. If a sire has not completed Standard Sampling (semen distributed to at least 40 herds), he is coded "O", for Other Sampling.

Line 3: Short Name.

A bull is given a shortened name from his official registered name for simplified identification.

BLOCK G: TRAIT NAME BLOCK

In this block, twenty-three traits are displayed. These traits include protein, fat, final classification score, productive life and somatic cell score, followed by 18 primary linear descriptive traits. These are the traits for which STA values are graphed.

BLOCK H: STANDARD TRANSMITTING ABILITY (STA)

STAs for each of the twenty-three traits are displayed in this block. STA is a bull's PTA value on a standardized scale. STA values will almost always fall within 3 standard units of 0. Standardizing to a common scale readily allows one to see if a bull is more extreme in one trait than another.

BLOCK I: BIOLOGICAL EXTREMES

This section contains descriptions of the biological extreme for each of the twenty-two traits. When a bull's STA value is 0.85 or greater in either direction, the biological extreme is highlighted and shows that the bull's STA is in the top 20% of the available bull population. These traits are being transmitted by the extreme 20% of the available bull population.

BLOCK J: TRAIT PROFILES

This is a graphic representation of the STA and Confidence Range for each trait. The width of the bar representing each trait is the confidence range of the trait. As reliability increases, the bar width or confidence range decreases. If a trait has a narrow bar, the bull has a fairly high reliability. STA values greater than 2.35 may not show entirely on the scale. These are displayed by a portion of the confidence range, or where no portion of the CR is within the profile, by a (<) or (>) sign at the appropriate end of the scale. The trait profiles give a visual explanation of a bull's transmitting ability for a trait. John is in the upper 20% for many traits (as denoted by the highlighted traits) with Final Score, Rear Udder Width, Udder Cleft and Rear Teat Placement as his strongest transmitting areas, as indicated by the arrow (>) at the end of the STA chart. For these traits, John is in the top 2% of the available population.

Genetics in the Future

What will be the future of genetics? Several processes are being used to accelerate the rate of genetic improvements. Research on new techniques is continuous and could make dramatic changes in years to come.

Embryo Transfer (ET)

Embryo Transfer has become a very important tool in genetic progress. It has increased selection intensity by producing more offspring from the most elite dams. Consequently, fewer offspring are from dams of lower genetic merit. ET results in a shorter generation interval because more offspring are born when the parents are younger. ET work is even being performed on virgin heifers.

The ET process begins when a donor cow of superior breeding is chemically induced to produce an unusually large number of eggs. This process is known as superovulation. She is injected with gonadotropin, which stimulates the ovary to produce a higher number of eggs. On the average, six normal eggs are recovered during a flush. About five days after the injection, the cow is artificially inseminated. Six to eight days later the embryos are recovered nonsurgically. The veterinarian looks at the embryos under a microscope to determine the number and quality of embryos. The embryos are then removed and implanted in recipient cows. Between removal and implantation, the eggs may be frozen in liquid nitrogen to be implanted at a later date, a process known as cryopreservation.

Cloning

Cloning, is another technique that allows the creation of multiple copies of an embryo. The process involves taking an in vitro matured egg or unfertilized egg, and microsurgically removing all its chromosomes. The individual cells of separate embryos are then fused to the oocytes by electrical pulses. After the genetic information has been removed from 32 single-cell eggs, technicians transplant each nucleus of a 32-cell embryo into the de-nucleated eggs. The nuclei and eggs are then fused. The survival rate is approximately 10 percent, therefore about three eggs remain. These embryos are grown to the 32-cell stage and the process is repeated.

Multiple Ovulation and Embryo Transfer (MOET)

MOET, developed in Australia and Great Britain, is yet another process designed to increase genetic improvement. A MOET herd consists of approximately 1,000 animals including heifers, cows, young bulls and possibly recipients. The best females available are purchased, bred to the top AI bulls and superovulated. The progeny are compared for milk production, milk composition, feed intake, milking speed, freedom from disease and type. Environmental bias is reduced because all individuals being compared are in the same herd.
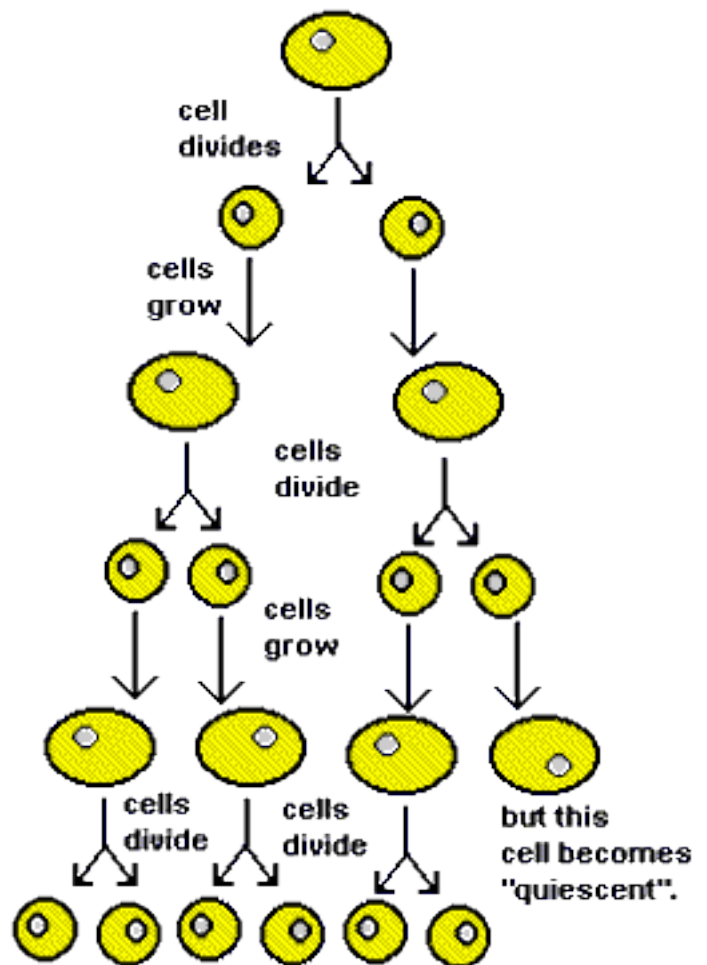
From the progeny comparison, the top five to 10% are selected as dams for the third generation. These cows are bred to the highest ranking A.I. bulls available. This process continues for several generations. Because of the shortened generation interval, as well as the high selection intensity, MOET herds potentially are genetically superior to even progeny-tested bulls. Therefore, more genetic progress may be made by using brothers of the best females as sires for future generations.

Through the use of MOET, the rate of genetic progress could increase. Europe was the first to begin to assemble MOET herds.

Transgenic Animals

Transgenic technology in dairy cattle could prove to be an important factor in genetic improvement. This technology enables parents to be "custom designed." The process involves injecting DNA (genetic material or genes) into one cell embryos. The DNA becomes a part of one of the embryo's chromosomes. The embryos are transferred into an animal. Since all cells contain the same genetic matter, each cell of the body receives the added gene.

An important use of transgenic genetics could be providing an animal with a specific desirable gene from another species. For example, a disease-resistant gene from a zebra could be added to a Holstein embryo. The expected result would be a Holstein resistant to the specific disease.

Genetic Markers

Genetic markers have the potential to become an important tool in selecting animals for breeding purposes. This technology identifies the structural differences in DNA. Examining the DNA from any cell allows scientists to look for specific patterns on the chromosomes. Scientists try to link specific production traits with the patterns.

Kappa casein, a non-whey protein in milk, is one of the first traits to be correlated to DNA structures. Two genes, "A" and "B", can be present for kappa casein. The possible genotypes are AA, AB, and BB. The B gene has been associated with increases in cheese yield and milk production. Therefore, dairy cattle with the genotype BB are most desirable, AB also are desirable.

Research is being conducted to find more genes that are correlated to traits of economic importance. In the process, an extensive gene map of dairy cattle is being developed.

Embryo Sexing

Embryo sexing involves flushing cows for their embryos, followed by a simple lab procedure that takes about two hours. In this procedure, technicians remove a few cells from the embryo and probe DNA in these cells for the presence of a Y-chromosome. The Y-chromosome determines that the embryo is male. Then, the selected embryos are implanted. Lab equipment can be rather expensive, but embryo sexing can pay for itself with increased production because cows will not waste down time carrying bull calves.

Test Your Genetic Knowledge

1.   How many pairs of chromosomes does a cow have?

2.   If a Holstein has a genotype of Bb for coat color, is it black and white or red and white?

3.   In the current U.S. dairy population is selection intensity higher in sires or dams?

4.   Is a 305-day milk record a direct measurement of a cow's phenotype or a genotype?

5.   Udder cleft has a heritability of .24 and udder depth has a heritability of .28. In which trait is more rapid genetic improvement expected?

6.   A genetic correlation of .-30 exists between milk yield and protein percent. When selecting solely for milk yield, will a higher or lower protein percent be expected?

7.   What is the current genetic evaluation method being used by the Holstein Association and USDA?

8.   The standard deviation for 305-day ME milk production is approximately 2,500 pounds. If a herd average is 20,000 pounds, what percent of the herd is expected to produce between 17,500 and 22,500 pounds ME milk?

9.   What value estimates the amount of an animal's genetic superiority or inferiority that is expected to be passed on to offspring?

10.   A decrease in the genetic base increases, decreases, or does not affect the genetic ranking of animals?

11.   If Bull A has a Reliability of 75% and Bull B has a Reliability of 95%, which proof contains more information?

12.   As you decrease the number of genetically superior animals selected as parents for the next generation, selection intensity increases or decreases?

13.   The average ages of the parents of a group of progeny-tested bulls at their birth were 6 years for the dams and 9 years for the sires. How can the generation interval of the next group of progeny-tested bulls be decreased?

14.   What value is used by USDA for percentile ranking based on production traits?

Answers

1. 30   **2.** Black and white   **3.** Sires   **4.** Phenotype   **5.** Udder depth   **6.** Lower   **7.** Animal Model   **8.** 68%
9. Predicted Transmitting Ability   **10.** Does not affect   **11.** Bull B   **12.** Increases   **13.** Select younger sires and/or dams
14. PTA$ Protein

Test Your Sire Summary Knowledge

PASEN MARSH-ET						TPI +1670

```
PASEN MARSH-ET                                                      TPI +1670
  USA 130312332 100%RHA-NA  TR TV TL        07-21-00
Sire:  DIXIE-LEE AARON-ET                                            +1414M
  USA 2265005 100%RHA-NA    TV TL           GM
Dam:  PASEN PRESCOTT MICHELLE-ET                                     +1747
  USA 17205442 100%RHA-NA                91 EEEEE     DOM

PRODUCTION        %     %R    SIRE    DAM    DAU     GRP
  Milk    +1212         89    +682  +1336   26298   25043
  Fat      +53   +.03         -5     +78    972     916
  Pro      +35   -.01         +37    +41    792     754
  05-2006   96 DAUS  71 HERDS             7 %RIP   100 %US
  PL       +0.1         69    -1.2   +1.4  SCE 7%   72 %R
  SCS      2.83         77    3.04   2.58  DCE 8%   61 %R
  NM$ +401  CM$ +399   FM$ +405              DPR -1.7%  62 %R
TYPE              %R    SIRE    DAM   DAU SC  AASC
  Type     +1.78        87    +1.20  +1.26  76.5    80.1
  UDC      +2.09              +1.80  +.75
  FLC      +1.92              +2.37  +1.23  BD +.55  D +1.16
  05-2006   81 DAUS  59 HERDS   EFT D/H 1.8
Breeder    Matthew P. Senita, PA                     LIMITED
Owner      Select Sires, Inc., OH               7HO7011/S: 7
Controller Select Sires, Inc.                        MARSH
```

TRAIT	STA		2	1	0	1	2
Protein	1.80	High					
Fat	2.30	High					
Final Score	2.54	High					
Productive Life	0.11	High					
Somatic Cell Score	2.08	Low					
Stature	0.95	Tall					
Strength	0.09	Frail					
Body Depth	0.05	Deep					
Dairy Form	1.63	Open-Rib					
Rump Angle	0.47	Sloped					
Thurl Width	0.88	Wide					
R Legs-Side View	1.63	Straight					
R Legs-Rear View	1.65	Straight					
Foot Angle	2.07	Steep					
Feet & Legs Score	1.99	High					
Fore Attachment	2.08	Strong					
Rear Udder Height	2.32	High					
Rear Udder Width	2.39	Wide					
Udder Cleft	1.34	Strong					
Udder Depth	2.14	Shallow					
F Teat Placement	2.05	Close					
Teat Length	1.75	Short					

1. What is Marsh's STA for Rear Udder Height?

2. Would Marsh tend to help improve Dairy Form in cows?

3. What is Marsh's PTA Milk?

4. Is Marsh's semen available?

5. What is Marsh's PTA PL?

6. What percent records in progress were used to calculate Marsh's production information?

7. What is Marsh's STA for Body Depth?

8. In Marsh's Production evaluation:

   a. How many daughters were used?

   b. How many different herds were represented?

9. What is Marsh's Linear Composite index for Udder Traits?

10. What does STA stand for?

11. What is the average STA for each Linear Trait in the available bull population?

12. What is Marsh's Linear Composite index for Feet and Legs?

13. What is Marsh's Dam's classification score?

14. When was Marsh born?

15. What is Marsh's Reliability for PTA Type?

16. What is Marsh's TPI?

17. For which Type Trait does Marsh have the most extreme STA?

18. What is Marsh's STA for Final Score?

19. What is Marsh's Reliability for Production evaluations?

20. What is Marsh's sire's TPI?

Answers:
1. 2.32 High   **2.** Yes   **3.** +1212   **4.** Yes, but in limited amounts   **5.** +0.1   **6.** 7%   **7.** 0.05   **8a.** 96   **8b.** 71
9. +2.09   **10.** Standard Transmitting Ability   **11.** 0   **12.** +1.92   **13.** EX-91   **14.** July 21, 2000   **15.** 87%
16. +1670   **17.** Rear Udder Width   **18.** 2.54   **19.** 89%   **20.** +1414

Compare These Bulls

Now that you understand the terms and information given in the sire summaries, let's practice comparing bulls. Answer these questions by indicating A or B.

A.

R-E-W BUCKEYE-ET   TPI +1896
USA 130588960 100%RHA-NA TV TL   12-25-00
Sire: MARA-THON BW MARSHALL-ET   +1701M
USA 2290977 100%RHA-NA TV TL   86   GM
Dam: MAYERLANE RUD BUBBLE-ET   +1795
USA 120536177 100%RHA-NA TV   86 VV+VV GMD DOM

PRODUCTION		%	%R	SIRE	DAM	DAU	GRP
Milk	+1847		88	+1916	+1811	27319	25492
Fat	+49	-.07		+41	+59	984	936
Pro	+53	-.01		+44	+53	832	775
05-2006	90 DAUS	56 HERDS				23 %RIP	100 %US
PL	+1.6		66	+0.1	+1.5	SCE 6%	69 %R
SCS	2.87		75	2.92	3.02	DCE 6%	58 %R
NM$ +541	CM$ +537	FM$ +549				DPR -.3%	58 %R

TYPE			%R	SIRE	DAM	DAU SC	AASC
Type	+2.33		87	+2.00	+1.88	77.5	80.7
UDC	+2.16			+1.94	+.99		
FLC	+2.06			+2.35	+1.06	BD +1.52	D +1.50
05-2006	78 DAUS	54 HERDS		EFT D/H 1.7			

Breeder R-E-W Farm, CT
Owner The Semex Alliance, CAN   ACTIVE
Controller Semex Alliance   200HO4779/S: 200
   BUCKEYE

TRAIT	STA	2	1	0	1	2
Protein	2.73 High					
Fat	2.13 High					
Final Score	3.33 High					
Productive Life	1.78 High					
Somatic Cell Score	1.77 Low					
Stature	1.92 Tall					
Strength	1.14 Strong					
Body Depth	1.21 Deep					
Dairy Form	0.91 Open Rib					
Rump Angle	0.49 Sloped					
Thurl Width	0.90 Wide					
R Legs-Side View	1.54 Straight					
R Legs-Rear View	2.52 Straight					
Foot Angle	1.45 Steep					
Feet & Legs Score	2.26 High					
Fore Attachment	2.32 Strong					
Rear Udder Height	2.93 High					
Rear Udder Width	2.35 Wide					
Udder Cleft	2.52 Strong					
Udder Depth	1.98 Shallow					
F Teat Placement	1.17 Close					
Teat Length	0.25 Short					

B.

PURSUIT SEPTEMBER STORM-ET   TPI +1580M
CAN 6820564 100%RHA-NA RC TV TL   09-03-97
Sire: MAUGHLIN STORM-ET   +1463M
CAN 5457798 100%RHA-NA B/R TV TL   GM
Dam: GLEN DRUMMOND SHIMMER-ET   +1210C
CAN 6185591 100%RHA-NA RC

MACE PRODUCTION		%	%R	SIRE	DAM	DAU	GRP
Milk	+433		95	+245	-455	25704	25258
Fat	+56	+.16		+40	+17	991	936
Pro	+9	-.01		+8	-13	767	758
05-2006	577 DAUS	431 HERDS				56 %RIP	37 %US
PL	+0.7		77	+0.7	+0.3	SCE 9%	98 %R
SCS	2.78		91	2.76	2.94	DCE 10%	80 %R
NM$ +284	CM$ +277	FM$ +298				DPR -1.2%	64 %R

MACE TYPE			%R	SIRE	DAM	DAU SC	AASC
Type	+2.31		89	+1.67	+1.45	81.4	84.1
UDC	+1.57			+1.57	+1.22		
FLC	+2.91			+1.68	+1.39	BD +2.19	D +2.03
05-2006	278 DAUS	209 HERDS		EFT D/H 2.6			

Breeder Pursuit Partners, CAN
Owner The Semex Alliance, CAN   ACTIVE
Controller Semex Alliance   200HO3067/200
   SEPTEMBER STORM

TRAIT	STA	2	1	0	1	2
Protein	0.46 High					
Fat	2.43 High					
Final Score	3.30 High					
Productive Life	0.78 High					
Somatic Cell Score	2.46 Low					
Stature	2.73 Tall					
Strength	1.59 Strong					
Body Depth	1.78 Deep					
Dairy Form	1.36 Open Rib					
Rump Angle	0.44 High Pins					
Thurl Width	1.56 Wide					
R Legs-Side View	1.96 Straight					
R Legs-Rear View	4.18 Straight					
Foot Angle	2.73 Steep					
Feet & Legs Score	2.66 High					
Fore Attachment	2.36 Strong					
Rear Udder Height	2.01 High					
Rear Udder Width	1.91 Wide					
Udder Cleft	0.12 Weak					
Udder Depth	1.48 Shallow					
F Teat Placement	1.32 Close					
Teat Length	0.52 Long					

1. Which bull would more likely improve rear udder height?
2. Which bull has the higher udder composite index?
3. Which bull was bred in Canada?
4. Which bull has semen available?
5. Which bull has a higher PTA Milk?
6. Which bull has more classified daughters used in his genetic evaluations?
7. Which bull has a higher PTA PL?
8. Which bull has a higher reliability for genetic information?
9. Which bull would have a greater tendency to improve low foot angle?
10. Which bull is younger?
11. Which sire has the higher PTA for Type?
12. Has either bull been identified as a recessive trait carrier?
13. Which bull's sire has a higher TPI?
14. Which bull is more likely to transmit high fat yield?
15. Which bull carries the gene for red hair color?

Answers:
1. A   **2.** A   **3.** B   **4.** A&B   **5.** A   **6.** B   **7.** A   **8.** B   **9.** B   **10.** A   **11.** A   **12.** B   **13.** A   **14.** B   **15.** B

Select A Mating

The purpose of sire summaries is to aid in choosing sires that meet your breeding criteria. Individual sire information also may be used to determine a specific mating sire. The following exercise requires you to select a mating sire for a given cow.

Sires in Herd's Semen Inventory:

JENNY-LOU MARSHALL P149-ET — TPI +1782

USA 122274798 100%RHA-NA TV TL 88 05-06-01
Sire: MARA-THON BW MARSHALL-ET
USA 2290977 100%RHA-NA TV TL 86 GM +1701M
Dam: JENNY-LOU PATRON TOYANE +1544
USA 17313307 100%RHA-NA 89 VEEEV GMD DOM

PRODUCTION		%	%R	SIRE	DAM	DAU	GRP
Milk	+1449		88	+1916	+485	27874	26380
Fat	+34	-.07		+41	+38	1010	977
Pro	+38	-.02		+44	+24	836	791
05-2006	99 DAUS		71 HERDS			82 %RIP	100 %US
PL	+1.1		57	+0.1	+1.3	SCE 9%	75 %R
SCS	3.10		72	2.92	3.05	DCE 7%	57 %R
NM$ +369	CM$ +359	FM$ +387				DPR -.4%	57 %R

TYPE		%R	SIRE	DAM	DAU SC	AASC
Type	+3.17	85	+2.00	+1.69	78.0	81.1
UDC	+2.97		+1.94	+1.56		
FLC	+1.92		+2.35	+.85	BD +2.70	D +2.69
05-2006	69 DAUS	50 HERDS	EFT D/H 1.9			

Breeder Mystic Valley Dairy LLC, WI
Owner Select Sires, Inc., OH ACTIVE 7HO7359/S: 7
Controller Select Sires, Inc. LOU

TRAIT	STA	2	1	0	1	2
Protein	1.96	High				
Fat	1.48	High				
Final Score	4.53	High				
Productive Life	1.22	High				
Somatic Cell Score	0.00					
Stature	3.20	Tall				
Strength	1.74	Strong				
Body Depth	2.29	Deep				
Dairy Form	3.11	Open Rib				
Rump Angle	1.11	Sloped				
Thurl Width	3.23	Wide				
R Legs-Side View	1.14	Curved				
R Legs-Rear View	2.41	Straight				
Foot Angle	1.78	Steep				
Feet & Legs Score	2.26	High				
Fore Attachment	3.16	Strong				
Rear Udder Height	2.72	High				
Rear Udder Width	3.52	Wide				
Udder Cleft	3.70	Strong				
Udder Depth	2.69	Shallow				
F Teat Placement	2.71	Close				
Teat Length	2.04	Long				

SANDY-VALLEY BOLTON-ET — TPI +1949

USA 131823833 100%RHA-NA TV TL 80 09-11-01
Sire: LEXVOLD LUKE HERSHEL-ET
USA 2294436 100%RHA-NA TV TL GM +1371M
Dam: SANDY-VALLEY BLESSING-ET +1973
USA 128824973 100%RHA-NA TV 88 VVVVE

PRODUCTION		%	%R	SIRE	DAM	DAU	GRP
Milk	+2339		85	+1576	+2484	28688	26265
Fat	+92	+.03		+24	+108	1058	958
Pro	+63	-.02		+37	+76	870	803
05-2006	84 DAUS		58 HERDS			99 %RIP	100 %US
PL	+0.3		53	+0.3	-0.8	SCE 11%	81 %R
SCS	2.92		68	3.01	2.96	DCE 10%	57 %R
NM$ +584	CM$ +570	FM$ +608				DPR -2.6%	50 %R

TYPE		%R	SIRE	DAM	DAU SC	AASC
Type	+2.14	81	+.06	+1.79	76.8	80.3
UDC	+2.52		+.08	+1.54		
FLC	+1.88		+1.23	+1.90	BD +1.37	D +1.87
05-2006	49 DAUS	32 HERDS	EFT D/H 2.1			

Breeder David, Patrick, Frank, Jr. & Gregory Bauer, WI
Owner ABS Global, Inc., WI ACTIVE 29HO11111/S: 29
Controller ABS Global, Inc. BOLTON

TRAIT	STA	2	1	0	1	2
Protein	3.25	High				
Fat	4.00	High				
Final Score	3.06	High				
Productive Life	0.33	High				
Somatic Cell Score	1.38	Low				
Stature	1.91	Tall				
Strength	0.82	Strong				
Body Depth	0.95	Deep				
Dairy Form	2.08	Open Rib				
Rump Angle	0.98	Sloped				
Thurl Width	0.63	Wide				
R Legs-Side View	0.11	Curved				
R Legs-Rear View	2.17	Straight				
Foot Angle	1.87	Steep				
Feet & Legs Score	2.08	High				
Fore Attachment	3.05	Strong				
Rear Udder Height	2.64	High				
Rear Udder Width	2.63	Wide				
Udder Cleft	2.26	Strong				
Udder Depth	2.64	Shallow				
F Teat Placement	1.73	Close				
Teat Length	0.40	Long				

SAVAGE-LEIGH MR LEVEL-ET — TPI +1757

USA 60046232 100%RHA-NA CV 86 06-22-00
Sire: WA-DEL CONVINCER-ET
USA 2249055 100%RHA-NA CV TL 95 +1310M
Dam: SAVAGE-LEIGH BELLWOOD LINDA +1770
USA 17121835 100%RHA-NA TV TL 92 EEEEE GMD DOM

PRODUCTION		%	%R	SIRE	DAM	DAU	GRP
Milk	+1274		87	+942	+1444	26732	25465
Fat	+112	+.24		+46	+98	1077	959
Pro	+44	+.02		+25	+37	836	784
05-2006	69 DAUS		38 HERDS			4 %RIP	100 %US
PL	-0.3		67	-1.6	+0.7	SCE 7%	55 %R
SCS	3.03		75	3.13	2.76	DCE 7%	56 %R
NM$ +504	CM$ +515	FM$ +484				DPR -.8%	61 %R

TYPE		%R	SIRE	DAM	DAU SC	AASC
Type	+1.20	82	+.43	+1.88	77.0	80.3
UDC	+.88		+.53	+.62		
FLC	+.93		+.55	+1.16	BD +1.54	D +2.08
05-2006	52 DAUS	30 HERDS	EFT D/H 2.5			

Breeder Christopher Wayne Savage, MD
Owner Taurus Service, Inc., PA ACTIVE 76HO278/S: 2022
Controller Taurus Service, Inc. MR LEVEL *CV

TRAIT	STA	2	1	0	1	2
Protein	2.27	High				
Fat	4.87	High				
Final Score	1.71	High				
Productive Life	0.33	Low				
Somatic Cell Score	0.54	Low				
Stature	1.59	Tall				
Strength	1.41	Strong				
Body Depth	1.92	Deep				
Dairy Form	1.84	Open Rib				
Rump Angle	1.26	High Pins				
Thurl Width	1.08	Wide				
R Legs-Side View	0.14	Straight				
R Legs-Rear View	1.56	Straight				
Foot Angle	1.31	Steep				
Feet & Legs Score	0.63	High				
Fore Attachment	1.54	Strong				
Rear Udder Height	0.69	High				
Rear Udder Width	0.84	Wide				
Udder Cleft	0.39	Strong				
Udder Depth	0.54	Shallow				
F Teat Placement	1.40	Close				
Teat Length	0.58	Long				

ERBACRES DAMION — TPI +1509M

USA 130263722 100%RHA-NA TR TV TL 93 07-23-00
Sire: REGANCREST ELTON DURHAM-ET
USA 2250783 100%RHA-NA TR CV TL 90 GM +1593M
Dam: REGANCREST ENCORE DALHIA-ET +1106
USA 124287356 100%RHA-NA 89 EEEEV

MACE PRODUCTION		%	%R	SIRE	DAM	DAU	GRP
Milk	+1		96	+104	-561	25807	25851
Fat	-30	-.12		-21	-34	916	944
Pro	+14	+.05		+21	-6	790	777
05-2006	351 DAUS		220 HERDS			34 %RIP	91 %US
PL	+0.5		79	+1.5	-0.7	SCE 7%	94 %R
SCS	2.87		90	2.82	3.18	DCE 6%	69 %R
NM$ +149	CM$ +175	FM$ +101				DPR 1.2%	76 %R

TYPE		%R	SIRE	DAM	DAU SC	AASC
Type	+3.21	92	+2.69	+2.10	78.6	81.7
UDC	+2.44		+2.74	+1.39		
FLC	+2.67		+2.18	+1.96	BD +2.71	D +2.72
05-2006	159 DAUS	101 HERDS	EFT D/H 2.5			

Breeder John Paul F. & Anjie Erbsen, IL
Owner Select Sires, Inc., OH ACTIVE 7HO7004/S: 7
Controller Select Sires, Inc. DAMION

TRAIT	STA	2	1	0	1	2
Protein	0.72	High				
Fat	1.30	Low				
Final Score	4.59	High				
Productive Life	0.56	High				
Somatic Cell Score	1.77	Low				
Stature	2.74	Tall				
Strength	2.53	Strong				
Body Depth	2.86	Deep				
Dairy Form	2.19	Open Rib				
Rump Angle	0.05	Sloped				
Thurl Width	2.79	Wide				
R Legs-Side View	1.29	Straight				
R Legs-Rear View	3.20	Straight				
Foot Angle	2.39	Steep				
Feet & Legs Score	2.81	High				
Fore Attachment	3.07	Strong				
Rear Udder Height	3.09	High				
Rear Udder Width	2.98	Wide				
Udder Cleft	2.83	Strong				
Udder Depth	1.74	Shallow				
F Teat Placement	1.85	Close				
Teat Length	0.26	Long				

Select a Mating:

Morning-View Lief Jordan

Classification:	Good Plus - 81
Production:	2-01 18,940M 3.2%F 615F 2.9%P 544P
Composites:	UD 1.13 FL 1.12 BD -0.03 D 1.21
Dam:	Morning-View Converse Jade VG 88
Sire:	Blok-Bros AS Lief EX 93

Jordan is housed in a free-stall operation. Her owner would like to select a sire to improve the following traits. These traits are ranked in order of importance to the producer.

1. Udder traits (especially udder cleft)
2. Fat yield
3. Protein yield
4. Strength

Recommendation #1 - Explain:

_____

_____

_____

_____

Recommendation #2 - Explain:

_____

_____

_____

_____

NOTE: Depending on your breeding goals and what you want to emphasize, each bull could be a logical mating sire.

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