NATIONAL COOPERATIVE DAIRY HERD IMPROVEMENT PROGRAM

HANDBOOK

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• Dairy producers • Breed associations • AI organizations • Cooperative Extension • USDA—Extension Service — Agricultural Research Service

Sire Evaluation Procedures for Yield Traits

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Dairy bulls are evaluated genetically for their ability to transmit to their offspring. Currently, evaluations are calculated regularly for milk yield (volume and composition), calving ease (see Fact Sheet H-6) and a number of conformation traits. However, yield traits are of greatest economic importance to dairy producers, and procedures in this fact sheet describe only those traits.

When sire proving began in the United States, daughter-dam comparisons were used. In these comparisons, the yield of a bull's daughters was compared with the yield of their dams. However, this procedure was ineffective because feeding and management practices differed each year (dams' yields were from earlier years than the daughters'), and yearly fluctuation impacts milk yield more than does genetics of sire or dam. Therefore, procedures proposed in 1954 to compare a sire's daughters with their contemporaries[1] or with their herdmates[2] had major advantages over the daughter-dam methods. Sire evaluations using the Herdmate Comparison (HC) were implemented in United States Department of Agriculture-Dairy Herd Improvement Association (USDA-DHIA) Sire Summaries in 1961. Since 1961, advances in methodology and other improvements have made current sire evaluations highly effective for identifying bulls that are genetically superior. The accuracy of current evaluations contrasts with the low accuracy of sire evaluations before 1960.

Genetic improvement began to accelerate in the late 1960's (see Figure 1) as a result of the increased use of genetically superior bulls made possible by cooperation between various segments of the dairy cattle industry. Availability of production data through National Cooperative Dairy Herd Improvement Program (NCDHIP) increased, and computer capabilities for handling large quantities of data became more efficient. More young bulls were sampled by artificial insemination (AI) organizations, and culling of sires intensified for those proven to be inferior or average. The dairy industry accepted the new genetic evaluation techniques and was willing to capitalize on them. Today's advancements in computer technology make possible the incorporation of most identified improvements in sire evaluation methods.

One negative consequence of the rapid genetic progress caused by use of the Herdmate Comparison was a deterioration of the procedure itself. Genetic progress caused some basic assumptions underlying the Herdmate Comparison methods to become unacceptable. Additional improvements were needed again to increase the accuracy of U.S. sire evaluation methods.

Modified Contemporary Comparison

In the fall of 1974, USDA made many improvements to the procedures for calculating USDA-DHIA Sire Summaries. Instead of comparing each daughter's lactation yield with the yield of herdmates of all ages as before, each was compared primarily with the yield of her sire-identified contemporaries; that is, sire-identified herdmates in the same lactation group (first lactation or later lactation) as the daughter. Comparing daughters with contemporaries instead of herdmates minimizes the effects of individual herd-age responses that deviate from the age responses for the entire population. Any paternal half-sisters are excluded when calculating averages of contemporaries. Contemporaries with complete records receive more weight in calculating contemporary averages than do those with partial records (see Fact Sheet G-2). The sum of all sire-identified herdmates not in the daughter's lactation group is limited to the equivalent of a single additional contemporary. Results of a 1973 study showed that, on the average, 23 percent of a

[1] Robertson, A. and J.M. Rendel. 1954. *The performance of heifers got by artificial insemination.* **J. Agric. Sci.** 44:184.

[2] Henderson, C.R., H.W. Carter and J.T. Godfrey. 1954. *Use of the contemporary herd average in appraising progeny tests of dairy bulls.* **J. Anim. Sci.** 13:949.

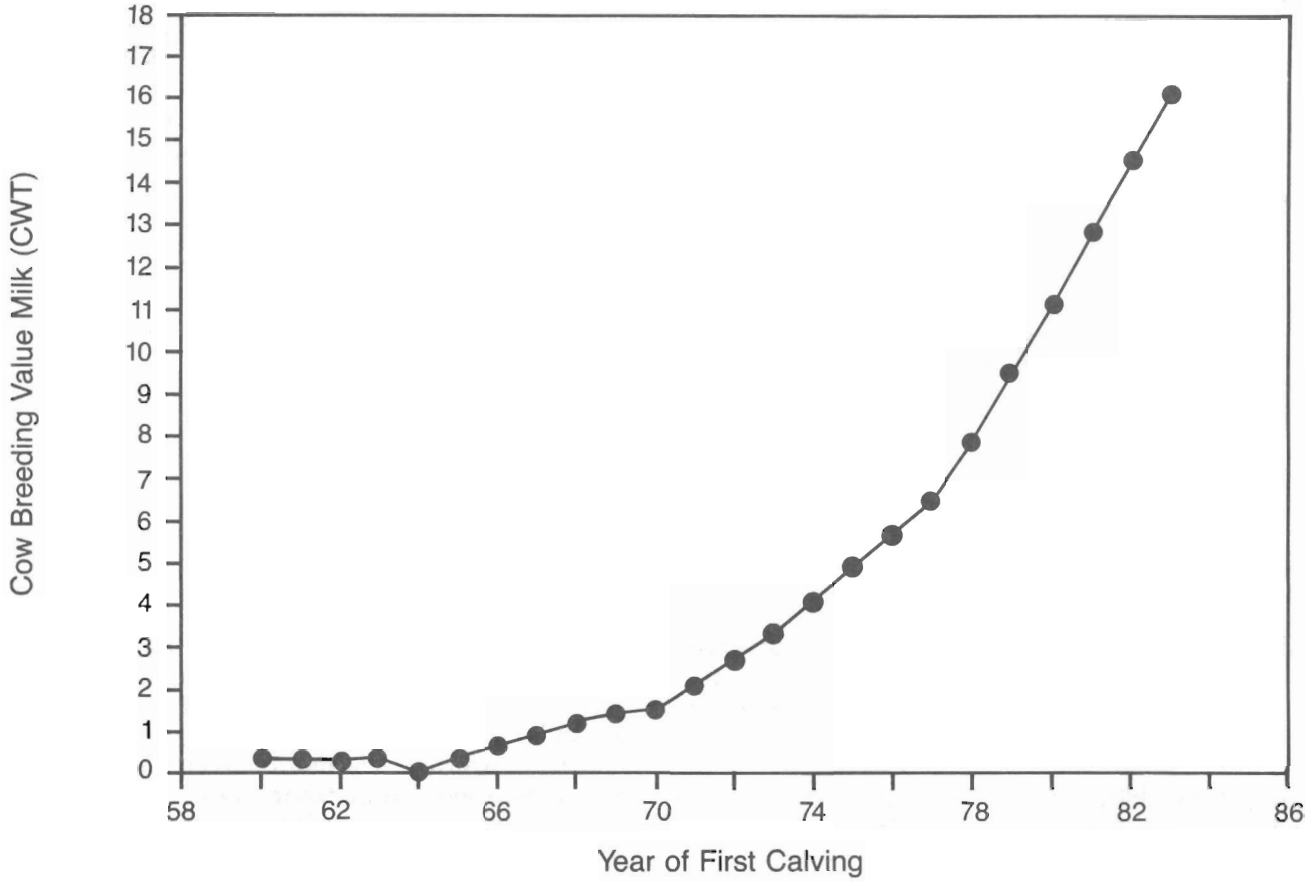

Figure 1. Rate of genetic improvement for milk yield of dairy cattle in the United States.

bull's daughters for some breeds did not contribute to his evaluation if contemporaries were restricted to "true" contemporaries and the traditional herd-year-season approach was applied to first-lactation records.[3] When the average for herdmates not in the daughter's lactation group is combined with the contemporary average of the daughter's lactation group, an adjustment is used to account for the average selection bias from culling for yield after first lactation.[4] Combining the contemporary average and the average of herdmates from the other lactation group results in a Modified Contemporary Average (MCA) for each lactation of every daughter. To be considered as a contemporary, a herdmate must calve in the 5-month period around the daughter's calving month (from 2 months before to 2 months after). As long as herd sizes remain small and every herd is managed differently, all seasonal effects can never be removed from genetic evaluations. Nevertheless, monthly bias usually is smaller from a rolling rather than fixed herd-year-season.

The sire evaluation procedure implemented in 1974 was defined as the Modified Contemporary Comparison (MCC) and used the following formula:

$$PD74 = R(MCD) + (1 - R)GA$$

where PD74 = Predicted Difference (PD) under the 1974 genetic base; R = Repeatability, an indication of the accuracy of the progeny information; MCD = Modified Contemporary Deviation, an indication of daughter yield compared with MCA adjusted for the average genetic merit of the contemporaries' sires; and GA = group average MCD of bulls with similar pedigree indexes. Other scientists have shown that the formula for obtaining best linear unbiased prediction properties through an iterative approach is PD = R (daughter average yield − contemporary average yield + average evaluation of contemporaries' sires) + (1 − R) (average evaluation of other sires in the group). This is similar to the basic MCC formula.[5]

In July 1983, GA was replaced with a prediction of GA called ancestor merit (AM) because AM gave a better indication of daughter performance.[6] The

[3] McDaniel, B.T., H.D. Norman and F.N. Dickinson. 1973. *Herdmate versus contemporaries for evaluating progeny tests of dairy bulls.* **J. Dairy Sci.** 56:1545.

[4] Dickinson, F.N., H.D. Norman, R.L. Powell, L.G. Waite and B.T. McDaniel. 1976. *Procedures used to calculate the USDA-DHIA Modified Contemporary Comparison.* **The USDA-DHIA Modified Contemporary Comparison,** USDA Prod. Res. Rpt. No. 165, p. 18.

[5] Quaas, R.L. and E.J. Pollak. 1981. *Modified equations for sire models with groups.* **J. Dairy Sci.** 64:1868.

[6] Wiggans, G.R. and R.L. Powell. 1984. *Increasing pedigree contribution to dairy sire evaluation.* **J. Dairy Sci.** 67:893.

AM procedure was modified in July 1985 to include protein, to account for genetic trend for bulls without a pedigree index (PI), and to eliminate the assumption that the specific trend estimated in the past will continue.[7] For more detailed information on calculation of AM, see Appendix A.

At present, the MCC PD is calculated with

$$PD82 = R(MCD) + (1 - R)AM$$

where PD82 = PD under the 1982 genetic base and $MCD = D - MCA + PD_{smc}$ (where D = daughter yield, MCA = modified contemporary average, and PD_{smc} = average PD of the modified contemporaries' sires). For young bulls, PD82 is AM because no daughter information is available. As Repeatability in the MCC equation approaches one (that is, 100 percent), the contribution from the pedigree effectively is eliminated. At this point, PD is nearly the same as MCD.

The Genetic Base

A stepwise genetic base is used in the MCC. A stepwise genetic base (that is, a fixed base for a specified number of years) is a compromise between a fixed and a moving base. Maintaining a fixed (or constant) base over a long period minimizes any problems with comparing bulls over time. A fixed base permits the appropriate adjustment for sires of contemporaries because all bulls are evaluated to the same base within breed. Therefore, all Sire Summaries with the same base are directly comparable regardless of the evaluation date. When the base was changed in January 1984, all bulls with Sire Summaries that had been released were reevaluated. The weighted average PD of sires of first-lactation cows calving in 1982 was defined as zero for the present MCC genetic base for each trait and breed. Having all estimates of genetic merit with the same base increases the accuracy of PD's, Cow Indexes (CI's) and pedigree evaluations. Comparability of these genetic tools increases genetic gain because bulls and cows are selected on the basis of progeny performance as well as pedigree potential. Problems are encountered with a moving base if evaluations from different runs are compared.

Innovations of MCC

The term "modified" in MCC also refers to the following innovations, each a significant improvement, that make the procedure superior to a traditional contemporary comparison: (1) adjustment of each daughter-contemporary difference by the genetic merit of the contemporaries' sires, (2) regression of daughter information on each bull evaluated to his population based on his pedigree merit, and (3) weighting of daughter information according to its accuracy.

Adjustment of daughter-contemporary difference for genetic merit of contemporaries' sires. If all the sires and dams of contemporaries associated with each daughter in a sire evaluation were a random sample of one single genetic population for each breed, complex sire evaluation techniques would not be needed. Each cow would need to be compared only with her contemporary average, and the common effects of herd environment (feeding and management) and genetics of contemporaries would be removed. The deviation of each daughter would serve as a direct reflection of the superiority her sire was capable of transmitting.

This assumption of no genetic differences among contemporary averages was made for HC. Although this assumption was not absolutely true for HC (even in the beginning), its shortcomings did not prohibit an acceleration of genetic improvement. However, as the rate of genetic improvement increased, some biases in HC resulted from differences in genetic merit of herdmates with which a bull's daughters were compared.[8] Three of these problems were (1) overevaluation of older bulls, (2) overevaluation of non-AI bulls, and (3) misranking of bulls from different segments of the population (for example, from AI organizations).

Research showed that if the contemporaries of an individual bull's daughter were sired by better than average bulls, the superiority of contemporaries' sires biased (in the opposite direction) differences of the daughter from contemporary average.[9] Elimination of this bias permits comparisons of bulls across time regardless of where or when progeny testing occurred. A direct measure of the genetic merit of contemporaries' sires is included in the MCC through the PD of each individual contemporary's sire. The average PD of contemporaries' sires is added to each daughter's deviation from her contemporaries; thus, each daughter is credited for any nonrandomness in the genetic merit of her competition, both within and across time periods. A sire evaluation procedure that includes such an adjustment is not dependent on the assumption that sires of contemporaries are a random sample from a single genetic population.

For the MCC, the genetic equality of dams of both daughters and contemporaries within herd-year of calving is assumed, and no consideration is given to adjustment for differences. Recent findings showed only small differences in merit of dams ("merit of mates").[10]

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[7] Wiggans, G.R. 1986. *Revision of computation of ancestor merit for Modified Contemporary Comparison sire Evaluations.* **J. Dairy Sci.** (submitted).

[8] McDaniel, B.T., H.D. Norman and F.N. Dickinson. 1974. *Variation in genetic merit of sires of herdmates of first lactation cows.* **J. Dairy Sci.** 57:1234.

[9] Norman, H.D., B.T. McDaniel and F.N. Dickinson. 1972. *Regression of daughter and herdmate milk yield on genetic value of the herdmates' sires.* **J. Dairy Sci.** 55:1735.

[10] Norman,H.D., R.L. Powell and J.R. Wright. 1986. *Influence of genetic differences in merit of mates on sire evaluation.* **J. Dairy Sci.** (submitted.)

Assumption that each bull evaluated is from a unique population based on pedigree. Including pedigree information was one of the most valuable improvements in the MCC and yet was one of its most controversial aspects. Previous Sire Summaries had ignored ancestor information that could have been valuable in predicting breeding value. The previous practice of not using pedigree information as soon as any progeny data became available was unjustified. Ironically, information from relatives other than daughters had been included in cow evaluations for many years. The genetic grouping and ancestor merit procedures make use of pedigree information in a manner similar to selection index procedures.

The emphasis on pedigree information varies inversely with the amount of progeny information available. A bull's pedigree information can be the equivalent of information from up to nine daughters each in a different herd. Pedigree information can aid in selection of bulls to progeny test and can increase accuracy of Sire Summaries with low Repeatability. Pedigree information should be weighted with progeny information according to the value of each source. The MCC was designed to use information on the genetic transmitting ability of a bull's sire and maternal grandsire in addition to the yield of his daughters. Results show that pedigree information is a worthwhile addition even for bulls with moderate to high Repeatabilities.[11] The regression of bull's daughter yield on pedigree index based on the MCC procedure averaged nearly one, with a correlation close to the expected value.[12] Before MCC, pedigree information consistently was less effective (50 percent on the average) than theory would suggest, undoubtedly because evaluations were calculated from procedures without a fixed base, without multiple-population grouping, and with no accounting for genetic merit of herdmate sires.

Weighting of daughter and contemporary information according to its accuracy. Each record is weighted according to days in milk, number of contemporaries, and number and average Repeatability of contemporaries' sires. This weighting is more accurate than if all records were assumed to be equal in length and to have an infinite number of herdmates. The statistical procedure for weighting daughter and contemporary information in the calculation of MCC Sire Summaries is quite complex.[4,13] Each cow's records are combined and weighted by the inverse of their expected variances, thus using the appropriate accuracy for each. Following this, daughter averages also are combined within and across herds by the inverse of their respective variances. Repeatability is calculated by a formula that accounts for variation within and between herds in the present dairy cattle population.

The MCC procedure combines daughter information by weighting for daughter distribution over herds in the presence of residual environmental correlations. This recognizes that a bull's daughters in the same herd are more alike than they are expected to be just from having a common sire. This technique limits the influence of daughter information from any single herd and thus produces more reliable combined information from all herds. Repeatability increases faster with new daughters in new herds than with additional daughters or records in a herd that already has daughters. Thus, the influence of a herd with a high proportion of a bull's daughters is limited considerably. MCC is one of the few sire evaluation procedures in use with this capability. In most countries, release of evaluations is delayed by requiring a bull to have daughters in a large number of herds. This requirement minimizes the problems that result from ignoring a bull's residual environmental correlations.

The weighting procedure is a key reason that USDA-DHIA Sire Summaries for bulls with daughters in only a few herds have greater accuracy than do evaluations calculated with other methods used throughout the world. This reliability was documented for 192 bulls that entered AI service based on information from natural service daughters in a few herds.[14] Estimated transmitting abilities before entering AI were compared with those estimated after each bull had hundreds of daughters in a large number of herds. Average PD milk decreased by 2 pounds; average PD fat remained the same. Any losses incurred by use of individual bulls with evaluations that decline will be compensated for by use of other bulls with evaluations that increase.

Protein and Solids-Not-Fat Evaluations

Evaluation procedures for protein and solids-not-fat (SNF) were initiated in the fall of 1977. A mixed model sire evaluation procedure with best linear unbiased prediction properties was used. The description of the original procedure for calculation of protein and SNF sire evaluations was published in 1979.[15]

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[11] Norman, H.D., R.L. Powell and F.N. Dickinson. 1976. *Modified contemporary and herdmate comparisons in sire summary.* **J. Dairy Sci.** 59:2155.

[12] Powell, R.L., H.D. Norman and F.N. Dickinson. 1977. *Relationships between bulls' pedigree indexes and daughter performance in the modified contemporary comparison.* **J. Dairy Sci.** 60:961.

[13] Norman, H.D. 1976. *Theoretical background for the USDA-DHIA Modified Contemporary Comparison Sire Summary procedure.* **The USDA-DHIA Modified Contemporary Comparison,** USDA Prod. Res. Rpt. No. 165, p. 8.

[14] Norman, H.D., R.L. Powell and J.R. Wright. 1985. *Changes in evaluation for natural-service sampled bulls brought into artificial insemination service.* **J. Dairy Sci.** 68:1513.

[15] Norman, H.D. and B.G. Cassell. 1979. *The USDA-DHIA sire evaluation procedure for protein and solids-not-fat. USDA-DHIA Milk Components Sire Summary,* USDA Prod. Res. Rpt. No. 178, p. 6.

In the late 1970's, only limited numbers of cows were tested for these components through NCDHIP. The amount of protein information has grown rapidly since 1980 and now is available for most cows tested for fat.

Effective with the January 1984 Sire Summary, many changes were made in the procedure for calculating PD's for protein ($PD82_{protein}$) and SNF ($PD82_{SNF}$) yields. Beginning with the July 1985 genetic evaluations, $PD82_{protein}$ was calculated with MCC procedures because of increasing cost and the need for CI's for protein. The procedure for calculating $PD82_{SNF}$ remains the same as that implemented in 1977. For more detailed information on calculating $PD82_{protein}$, see Appendix B.

Calculation of PD for protein and SNF percentages. Breed averages (BA's) used in calculating PD for protein percentage ($PD\%_{protein}$) and SNF percentage ($PD\%_{SNF}$) are in Table 1. Averages for milk and fat on a 305-day, two-times-a-day milking, mature-equivalent basis are for first-lactation, sire-identified cows calving in 1982. Averages in pounds for protein and SNF are the product of 1982 BA_{milk} and the corresponding average sample percentage for cows with protein and SNF available. The $PD\%_{protein}$ is calculated by

$$PD\%_{protein} = [(PD_{protein_{subset}} + BA_{protein})/(PD_{milk_{subset}} + BA_{milk}) - (BA_{protein}/BA_{milk})] \times 100$$

where subset refers to daughter records with protein information. The $PD\%_{SNF}$ is calculated similarly.

Calculation of Economic Indexes for Yield

For purposes of ranking bulls and cows, economic indexes combining the relative value of milk and fat have been included in USDA-DHIA Sire Summaries and CI's since 1971. These indexes—PD dollars (PD$) and CI dollars (CI$)—were developed because the product value of most milk produced was dependent on both quantity and fat content. In 1977, economic indexes that also included economic value of protein and SNF were developed.

Each year these economic values are updated. For example, economic values used to calculate PD$ and CI$ for 1986 were $11.70 per hundredweight for milk with 3.5 percent fat and a differential of $.164 for each .1 percent change from the 3.5 percent base. These prices were determined from 1985 average prices for the nation as reported by USDA's Economic Research Service (ERS).[16] Average blend price for all milk sold to plants was estimated to be $12.73 per hundredweight for milk with 3.67 percent butterfat. Average price for 3.5 percent milk was calculated to be $12.45 per hundredweight. A hauling assessment of $.45 per hundredweight was subtracted and the price reduced by $.275 for the Commodity Credit Corporation assessment and promotion, which resulted in a price of $11.725 per hundredweight. This was rounded to $11.70 per hundredweight.

The PD$ for milk and fat was calculated by

$$PD\$ = \$.0596 \times PD_{milk} + \$1.64 \times PD_{fat}$$

where $\$.0596 = \$.1170 - .035 \times \$1.64$.

Genetic evaluations for protein and SNF in 1986 used PD$ derived from a base test of 3.2 percent for protein and 8.5 percent for SNF. Differentials were $.114 per .1 percent deviation for protein and $.080 per .1 percent deviation for SNF (95 percent of the wholesale, nonfat, dry milk price). Average powder price reported by ERS was $.8406 per pound for 1985. The protein differential was determined from the SNF differential by dividing the SNF differential by .7 (the ratio of the value of SNF to the value of protein).

The higher differential for protein evaluations is used because (1) protein is the most valuable part of SNF for cheese production; (2) as SNF yield increases 1 pound, protein yield increases considerably less than 1 pound; and (3) the ratio of the

[16] USDA, Econ. Res. Serv. *Dairy Outlook & Situation*, DS-403. 1985

Table 1. Yield averages[1] used in calculating Predicted Difference component percentages for fat, protein and solids-not-fat (SNF) by breed.

Breed	Milk	Fat	Fat	Protein	Protein	SNF	SNF
	Pounds	Percentage	Pounds	Percentage	Pounds	Percentage	Pounds
Ayrshire	12,843	3.88	499	3.29	423	8.88	1,140
Guernsey	11,558	4.63	535	3.56	412	9.13	1,055
Holstein	17,378	3.60	625	3.15	548	8.58	1,491
Jersey	11,584	4.78	553	3.79	439	9.42	1,091
Brown Swiss	14,293	4.00	571	3.49	499	9.13	1,305
Milking Shorthorn	11,912	3.69	440	3.25	387	8.70	1,036
Red and White	15,840	3.69	585	3.18	504	8.60	1,362

[1] Standardized yield from first lactation calvings in 1982.

differentials used for protein and SNF produces approximately the same $PD\$_{protein}$ and $PD\$_{SNF}$ distribution, which allows for more interchange of protein and SNF evaluations. Therefore, dairy producers receiving payment for protein can select with some confidence among bulls with high $PD\$_{SNF}$ and vice versa.

The $PD\$_{protein}$ was calculated by

$$PD\$_{protein} = \$.02312 \times PD_{milk} + \$1.64 \times PD_{fat} + \$1.14 \times PD_{protein}$$

where
$\$.02312 = \$.1170 - .035 \times \$1.64 - .032 \times \$1.14.$

The $PD\$_{SNF}$ was calculated by

$$PD\$_{SNF} = -\$.0084 \times PD_{milk} + \$1.64 - PD_{fat} + \$.80 \times PD_{SNF}$$

where
$-\$.0084 = \$.1170 - .035 \times \$1.64 - .085 \times \$.80.$

A PD for cheese dollars (PD$ cheese) was added to the Sire Summary in 1984 (see Appendix C). To calculate PD$ cheese, two pricing formulas were needed, depending on whether or not the milk had an excess of fat to be removed before making cheese.[17] For breeds with milk above or equal to the critical ratio of .64 for ratio of casein to fat (Ayrshire, Holstein, Brown Swiss, Milking Shorthorn, and Red and White) and using 1985 average milk prices,

$$PD\$ \text{ cheese} = -\$.00211 \times PD_{milk} + \$1.899 \times PD_{fat} + \$1.646 \times PD_{protein}$$

For breeds with milk below the critical ratio of casein to fat (Guernsey and Jersey),

$$PD\$ \text{ cheese} = -\$.00211 \times PD_{milk} + \$1.64 \times PD_{fat} + \$1.961 \times PD_{protein}$$

For both formulas, total weight of milk is deducted.

Dollar Percentile

Genetic progress has been occurring at an impressive rate. Average PD milk for active AI bulls has continued to increase more than 100 pounds per year. A weakness of evaluations from a fixed genetic base is that they do not reflect how each bull compares with the current average bull. In other words, an evaluation by itself does not indicate whether a specific bull is above or below average for the current "bull battery". For example, in the early 1970's, bulls that were +1,000 pounds for PD milk were some of the best bulls available. However, before the base changed in January 1984, a bull with +1,000 pounds for PD milk was a candidate for culling.

Dollar percentiles were added to the USDA-DHIA Sire Summary to indicate how bulls compare with active AI bulls at any time. Percentiles provide information about the ranking of each bull for PD$ relative to the PD$ of active AI bulls of that breed. Specifically, a bull's percentile shows the percentage of all active AI bulls that the bull exceeds for PD$. Information for active AI bulls for each breed is sorted by PD$ from high to low. Bulls in the top 1 percent are in percentile 99; this means that their PD$ is better than the PD$ of 99 percent of all active AI bulls. Bulls in the bottom 1 percent are in percentile 0, their PD$ exceed fewer than 1 percent of all active AI bulls.

Recently percentiles based on $PD\$_{cheese}$ also were added to USDA-DHIA Sire Summaries. In addition, percentiles for CI$ and $CI\$_{cheese}$ have been implemented.

Competition within and across breeds continues to be intense. Therefore, breeders cannot afford to use bulls with PD milk lower than that of the average active AI bull unless those bulls have outstanding PD's for fat or protein. Only bulls that are above percentile 50 should be used extensively; those below percentile 50 should receive little use. Matings currently being made to bulls below percentile 50 should be made instead to young bulls with high pedigree indexes for sampling. Not only will the daughters of the young bulls be more productive, but the top AI bulls for the next generation will be easier to identify. Use of percentile rankings can help breeders put active AI bulls in their proper perspective both before and after updates of the genetic base.

See Fact Sheet H-3 for data sources and requirements for evaluation of yield traits.

Appendix A: Calculation of Ancestor Merit

To compute ancestor merit (AM), bulls are assigned to groups based on breed, birth year and pedigree information available (sire and maternal grandsire (MGS), sire only or none). Bulls with only MGS information are included with the group of bulls with no pedigree information available.

Bulls with pedigree information available are grouped by bull's birth year. In addition, Holstein bulls with sire information only (no MGS information) are grouped separately. For other breeds, an MGS evaluation is estimated from average Cow Indexes (CI's) of dams of contemporaries, which are the adjustments to CI's for genetic merit of contemporaries' dams. This estimate is combined with the known sire evaluation so that these bulls can be included with those that have both sire and MGS pedigree information. Holstein and Jersey

[17] E.P. Barton, H.D. Norman and R.L. Powell. 1983. *Correlations of Predicted Differences for milk, fat, and protein yields and percentages to economic indexes appropriate for different markets.* Handout P69, 78th Amer. Dairy Sci. Assoc. meeting, Madison, WI.

bulls with both sire and MGS information (including Jersey bulls with estimated MGS evaluations) are categorized further by the type of sampling program. The sampling programs would include natural service (NS) or artificial insemination (AI).

Bulls with no pedigree information available are grouped by average year of daughter birth for the bull's first evaluation with five or more daughters. For bulls with less than five daughters, birth year from the bull's latest evaluation is used. If the birth date is known for a bull with no pedigree information, average birth year of daughters is constrained to be no more than 3 years after the bull's birth year.

Difference between Modified Contemporary Deviation (MCD) and pedigree index (PI) is computed individually for all bulls. Then means of differences weighted by Repeatability are computed for each breed, yield trait (milk, fat or protein), birth year and pedigree category. These means are smoothed by regression over 9 consecutive years with the estimate for the middle year retained. Some examples of the smoothed means for January 1986 USDA-DHIA genetic evaluations are in Table A1 for Holsteins and Jerseys. Means for recent years are calculated from regression coefficients from the last complete set of 9 years.

After calculation of means, AM is calculated by

$$AM = \text{mean} + \text{bull's PI}$$

Table A1. Smoothed average differences between all-lactation Modified Contemporary Deviation and pedigree index for computing January 1986 genetic evaluations of Holsteins and Jerseys for selected birth years by pedigree category, type of sampling program [natural service (NS) or artificial insemination (AI)], and yield trait[1].

	Pedigree information available											
	Sire and maternal grandsire											
Birth	NS-sampled			AI-sampled			Sire only			None[3]		
year[2]	Milk	Fat	Protein	Milk	Fat	Protein	Milk	Fat	Protein	Milk	Fat	Protein
						Holstein						
1960	−409	−14	−12	−397	−13	−12	−533	−17	−16	−1,162	−38	−34
1965	−405	−14	−12	−321	−11	−10	−777	−26	−23	−1,406	−46	−42
1970	−395	−15	− 9	−336	−13	− 5	−719	−26	−14	−1,246	−40	−37
1975	−324	−13	− 7	−243	−10	− 4	−641	−23	−14	− 884	−29	−19
1980	−242	−10	− 8	−153	− 7	− 5	−583	−22	−14	− 590	−19	−18
1981	−226	− 9	− 8	−134	− 7	− 5	−565	−21	−14	− 540	−17	−18
1982	−210	− 9	− 8	−115	− 6	− 5	−547	−21	−14	− 490	−15	−18
1983	−193	− 8	− 8	− 97	− 5	− 5	−528	−20	−14	− 440	−13	−18
1984	−177	− 8	− 8	− 78	− 4	− 5	−510	−19	−14	− 390	−11	−18
1985	−160	− 7	− 8	− 59	− 4	− 5	−492	−19	−14	− 340	− 9	−18
						Jersey[4]						
1960	−371	−15	−13	−282	−11	− 9				−1,047	−37	−34
1965	−356	−15	−12	−215	− 9	− 7				−1,143	−41	−38
1970	−239	−11	− 7	− 87	− 4	− 2				−1,074	−39	−35
1975	−153	− 7	− 9	39	1	− 2				− 889	−31	−28
1980	− 64	− 3	−10	161	7	− 3				− 681	−26	−30
1981	− 45	− 2	−10	187	8	− 3				− 638	−25	−30
1982	− 26	− 1	−10	214	9	− 3				− 595	−24	−30
1983	− 8	0	−10	240	10	− 3				− 551	−23	−30
1984	11	1	−10	266	12	− 3				− 508	−21	−30
1985	30	2	−10	293	13	− 3				− 465	−20	−30

[1]Milk and fat differences calculated from records of all lactations; protein differences calculated from subset of records with protein information.

[2]For bulls with no pedigree information available, birth year was average year of daughter birth for bull's first evaluation with five or more daughters, with the constraint that average birth year of daughters was no more than 3 years after bull's birth year if known. For bulls with pedigree information, birth year was bull's birth year.

[3]Includes bulls with only maternal grandsire pedigree information available.

[4]Maternal grandsire evaluation estimated for bulls with only sire pedigree information available.

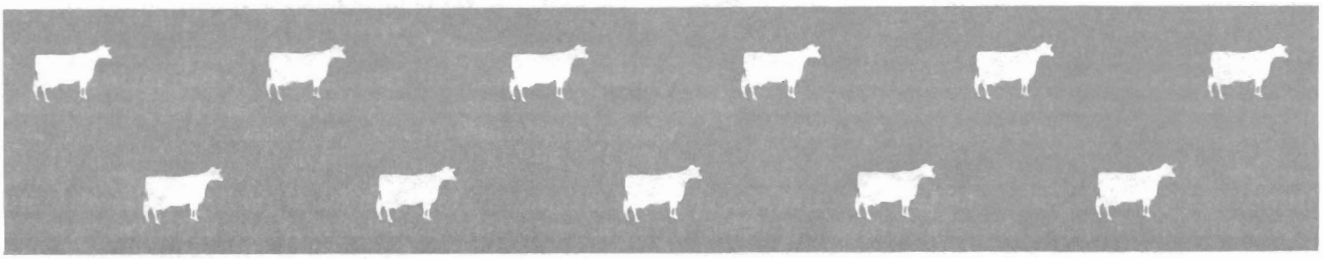


Table B1. Coefficients (b's) for predicting protein and solids-not-fat (SNF) by breed

Component	Breed	Intercept[1]	b_1	b_2
Protein	Ayrshire	14.15	.0233814	.215052
	Guernsey	10.44	.0226375	.256000
	Holstein	19.58	.0236162	.185246
	Jersey	24.27	.0252764	.213545
	Brown Swiss	16.34	.0222398	.285633
	Milking Shorthorn	17.09	.0200552	.292116
	Red and White	7.11	.0224831	.239944
SNF	Ayrshire	22.68	.0765184	.267184
	Guernsey	12.82	.0794981	.229118
	Holstein	12.66	.0742099	.304047
	Jersey	.93	.0812947	.256132
	Brown Swiss	− 1.76	.0789940	.309003
	Milking Shorthorn	− 16.40	.0706282	.570832
	Red and White	−116.57	.0851449	.222717

[1] Should not be used for predicting deviation.

Appendix B: Calculation of Predicted Differences (1982 Genetic Base) for Protein and Solids-Not-Fat Yields

With protein data collected through NCDHIP, new equations were developed for predicting protein yield of cows without actual data from their milk and fat yields:

$$\text{estimated protein yield} = \text{intercept} + b_1 \times \text{milk yield} + b_2 \times \text{fat yield}$$

where the intercept and the b's (regression coefficients are in Table B1. For example, an Ayrshire with 13,000 pounds of milk and 520 pounds of fat would have an estimated protein yield of

$$14.15 + .0233814 \times 13{,}000 + .215052 \times 520$$

or 429.94 pounds. A similar procedure was used to estimate solids-not-fat (SNF) yields, and the SNF coefficients also are in Table B1 by breed.

These prediction equations are used in several ways throughout the procedures to calculate genetic evaluations for protein and SNF. They were used to set the 1982 genetic bases for protein and SNF for each breed. Many of the cows that were tested for milk and fat were not tested for protein or SNF; therefore these prediction equations provided a way to make the bases equivalent for all component traits. Records from all first-lactation, sire-identified cows calving in 1982 were included in setting the genetic bases for milk and fat. The base was set for protein evaluations by forcing the average Predicted Difference (PD) for protein for bulls evaluated using only daughters with protein records (subset) to equal the average estimated $PD_{protein}$ for those same bulls evaluated using all daughters with milk and fat records. This estimated $PD_{protein}$ was calculated by

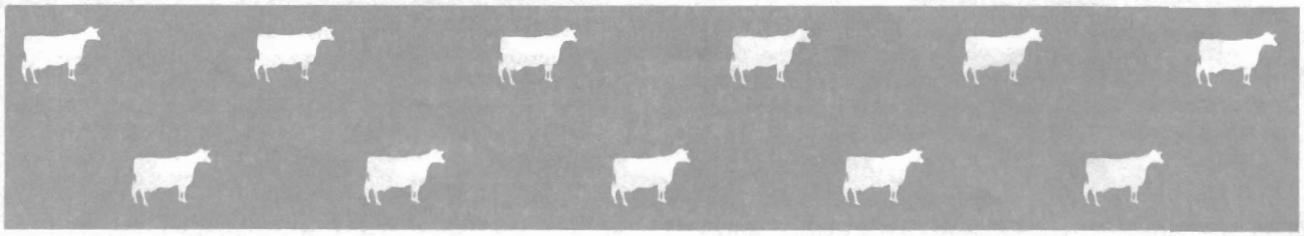
$$\text{estimated } PD_{protein} = b_1 \times PD_{milk} + b_2 \times PD_{fat}$$

where the b's again are the regression coefficients in Table B1 for predicting protein yield. The intercept is not included because PD's are defined as the deviations from breed averages and the intercepts cancel out.

These regression equations also were used directly in calculation of PD protein:

$$PD_{protein_{released}} = PD_{protein_{subset}} + b_1 \times (PD_{milk_{all}} - PD_{milk_{subset}}) + b_2 \times (PD_{fat_{all}} - PD_{fat_{subset}})$$

where PD_{subset} for milk, fat, and protein is based on daughter records with protein information, the b's are the coefficients in Table B1, and the PD_{all} for milk and fat is based on all daughter records.



Appendix C: Calculation of Predicted Difference Dollars Cheese

To calculate Predicted Difference dollars cheese (PD$ cheese) for 1986 USDA-DHIA genetic evaluations, payment by cheese plants for milk was assumed to be at the same milk price as the 1985 average price received by dairy producers. What a plant had to pay for milk to produce 1 pound of cheddar cheese (cheese price) was derived with[17]

$$\begin{aligned}\text{milk price} = {} & (\text{cheese price} \times \text{f/dry matter} \\ & \times \text{casein percentage} \times PD_{protein}) \\ & + [(\text{cheese price} \times (\text{f} \times \text{g/dry matter}) \times PD_{fat})] \\ & + [(-.01 \times \text{cheese price} \times (\text{f} \times \text{h/dry matter}) \times PD_{milk})]\end{aligned}$$

where f, g, and h are coefficients, the dry matter is the dry matter content of the cheese, and the casein percentage is the proportion of the protein that is casein. Then

$$\begin{aligned}\text{dry matter} \times \text{milk price} = {} & (\text{cheese price} \times \text{f} \times \text{casein percentage} \times 3.2) \\ & + (\text{cheese price} \times \text{f} \times \text{g} \times 3.5) \\ & + (-.01 \times \text{cheese price} \times \text{f} \times \text{h} \times 100)\end{aligned}$$

and

$$\begin{aligned}\text{cheese price} = {} & \text{dry matter} \times \text{milk price} / \\ & [\text{f} \times (\text{casein percentage} \times 3.2 + \text{g} \times 3.5 - \text{h})]\end{aligned}$$

For 37 percent moisture cheddar cheese, a milk price of $11.70 per hundredweight, protein that is 78 percent casein, and coefficients of f = 1.09, g = 0.9, and h = 0.1,

$$\begin{aligned}\text{cheese price} = {} & .63 \times 11.70 / [1.09 \times (.78 \times 3.2 + .9 \times 3.5 - .1)] = 1.2193.\end{aligned}$$

Thus, the value of milk for making 1 pound of cheddar cheese was $1.2193.

To calculate PD$ cheese, two pricing formulas were needed, depending on whether or not the milk had an excess of fat to be removed before making cheese. For breeds with milk above or equal to the critical ratio of casein to fat (Ayrshire, Holstein, Brown Swiss, Milking Shorthorn, and Red and White) and using the 1984 average milk price,

$$\begin{aligned}\text{PD\$ cheese} = {} & -.01 \times \text{cheese price} \times 1.09 \times (.1/.63) \times PD_{milk} \\ & + \text{cheese price} \times 1.09 \times (.9/.63) \times PD_{fat} \\ & + \text{cheese price} \times (1.09/.63) \times .78 \times PD_{protein} \\ = {} & -\$.00211 \times PD_{milk} + \$1.899 \times PD_{fat} + \$1.646 \times PD_{protein}\end{aligned}$$

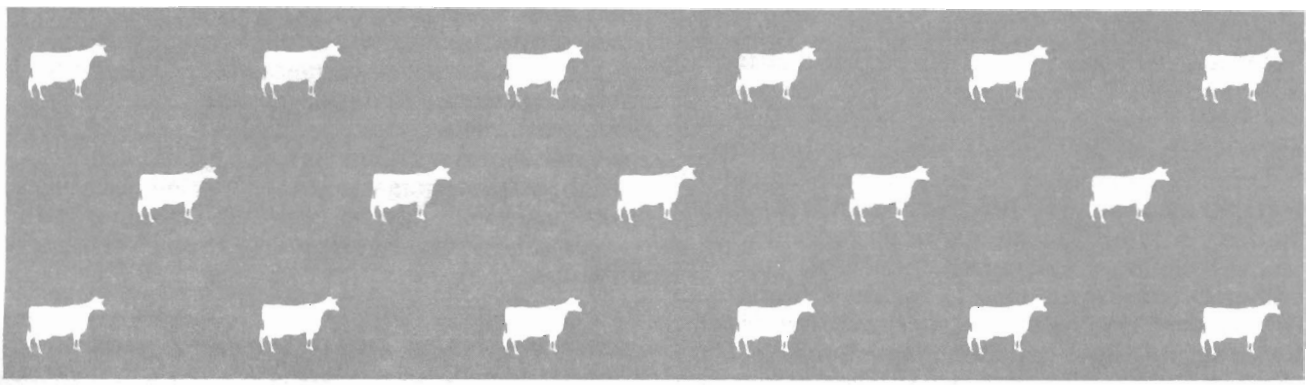
For breeds with milk below the critical ratio of casein to fat (Guernsey and Jersey),

$$\begin{aligned}\text{PD\$ cheese} = {} & -.01 \times \text{cheese price} \times (\text{f} \times \text{h/dry matter}) \times PD_{milk} \\ & + \text{value of excess fat} \times \text{PDF} \\ & + [\text{cheese price} \times \text{f} \times \text{g} / (\text{casein:fat critical ratio} \\ & \times \text{dry matter}) \\ & + \text{cheese price} \times \text{f/dry matter} \\ & - \text{excess value of fat/casein:fat critical ratio})] \\ & \times \text{casein percentage} \times PD_{protein}.\end{aligned}$$

The critical ratio of casein to fat is .64, and the value of excess fat is $1.64; therefore,

$$\begin{aligned}\text{PD\$ cheese} = {} & -.01 \times \text{cheese price} \times 1.09 \times (.1/.63) \times PD_{milk} \\ & + 1.64 \times PD_{fat} \\ & + [\text{cheese price} \times 1.09 \times .9/(.64 \times .63) \\ & + \text{cheese price} \times 1.09/.63 - 1.64/.64] \times .78 \times PD_{protein} \\ = {} & -\$.00211 \times PD_{milk} + \$1.64 \times PD_{fat} + \$1.961 \times PD_{protein}\end{aligned}$$

For both formulas, total weight of milk is deducted.



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