Paul VR [illegible]

THE USDA-DHIA MODIFIED CONTEMPORARY COMPARISON

SIRE SUMMARY AND COW INDEX PROCEDURES

Agricultural Research Service
United States Department of Agriculture
Production Research Report No. 165

PREFACE

Implementation of the Modified Contemporary Comparison is the culmination of approximately 4 years of research and development work by USDA-ARS scientists, data processing personnel, and various cooperating university researchers.

Results of such research are made available in the publication in the form of five articles that are:

1. An Introduction to the USDA-DHIA Modified Contemporary Comparison. Describes reasons a new genetic evaluation procedure for dairy cattle was needed in the United States. It also describes in general terms the improvements in the new procedure over the formerly used USDA-DHIA Herdmate Comparison.

2. Theoretical Background for the USDA-DHIA Modified Contemporary Comparison Sire Summary Procedure. Describes the underlying mathematical models and their derivation.

3. Procedures Used to Calculate the USDA-DHIA Modified Contemporary Comparison. Describes step-by-step procedures, dataflow, and formulas used in the USDA-DHIA Modified Contemporary Comparison computing system.

4. The USDA-DHIA Modified Contemporary Comparison Cow Index. Describes the changes that were made in the Cow Indexing procedure concurrently with the adoption of the Modified Contemporary Comparison for sire evaluation.

5. Procedures for Approximating Components of Predicted Difference. Presents concepts and formulas, including tables, for approximating components of Predicted Difference in the field including procedures for estimating Repeatability, the Modified Contemporary Deviation, and the Genetic Group Average.

These materials should be of interest to educators, researchers, students, industry personnel, breed societies, and dairymen who are involved in the genetic improvement of dairy cattle.

CONTENTS

Washington, D.C.

Issued March 1976

THE USDA-DHIA MODIFIED CONTEMPORARY COMPARISON SIRE SUMMARY AND COW INDEX PROCEDURES

AN INTRODUCTION TO THE USDA-DHIA MODIFIED CONTEMPORARY COMPARISON

F. N. Dickinson, R. L. Powell, and H. D. Norman,
respectively, chief, research geneticist (animal), and research
scientist (genetics), Animal Improvement Programs Laboratory,
Animal Physiology and Genetics Institute, Northeastern Region,
Agricultural Research Service

The USDA-DHIA Modified Contemporary Comparison (MCC) was implemented in the fall of 1974 to replace the USDA-DHIA Herdmate Comparison that had been used for national genetic evaluations of dairy cows and bulls since 1962. The Herdmate Comparison had been modified twice: (1) In 1965 to subtract the breed average from Predicted Average (PA) to obtain what was called Predicted Difference (PD), and (2) In 1967 to add Repeatability (R) to the Predicted Difference formula. Implementation of the Modified Contemporary Comparison was the culmination of approximately 4 years of research and development work by USDA scientists and data processing personnel and various cooperating university researchers.

The adoption of the Modified Contemporary Comparison was necessitated by the rapid genetic progress that had occurred under the Herdmate Comparison due to its immediate marked improvement in accuracy over the Daughter-Dam Comparison. The acceleration of genetic progress starting in 1962 caused some of the important assumptions underlying the Herdmate Comparison to become untenable. The most important of these assumptions were:

(1) All the sires, dams, and herdmates that are involved in a bull's summary are random samples of one single genetic population in each breed.

(2) There is no genetic trend in each population; i.e., breed.

The genetic progress in U.S. dairy cattle (negating assumption 2) has occurred to varying degrees in different herds and different regions of the country and thereby negated assumption 1. This differential rate of progress has been due to a number of factors. Primary among these is the more extensive use of higher PD bulls in some herds and areas than in others. Two other important assumptions were:

(3) There is no differential culling among the daughters of a bull compared with their herdmates.

(4) Each bull's daughters receive no preferential treatment over their herdmates.

Assumption 3 (no differential culling) became untrue in large part because of the superior genetic information available to herds enrolled in the National Cooperative Dairy Herd Improvement Program (NCDHIP). Herds proving bulls may have different selection criteria for a bull's daughters than criteria for their herdmates. Such selection has been more effective in the past few years with the help of NCDHIP information. Potential bias from herdmate culling is less of a problem in the Modified Contemporary Comparison because daughters' first records are compared primarily with first records made by contemporaries. Any biases due to the failure of assumption 4 (no preferential treatment) to be true were not handled as effectively as possible because of the heavy weighting given to the daughters of a bull in a single herd.

The Modified Contemporary Comparison reduces the need to make any of these assumptions. This is done by improved statistical techniques and improved procedures for weighting the data available for each bull's evaluation.

Some understanding of these improved procedures can be gleaned from a comparison of the two basic formulas. In the Herdmate Comparison equation, four basic parts can be identified.

$$\underset{[1]}{PD} = \underset{[2]}{R}\ [\underbrace{D-HM}_{[3]} + \underbrace{0.1\ (HM-BA)}_{[4]}]$$

Part [1] was the Predicted Difference (PD) or estimate of genetic transmitting ability expressed to an unknown moving genetic base in each breed. The base was changed each year. Part [2], Repeatability (R), was both the accuracy of the evaluation and also a regression factor used in calculating PD. Part [3] was the average deviation of daughter production (D) from the herdmate production (HM). Part [4] was an approximation to adjust for genetic differences among herds to account for the level of competition provided by the herdmates. This correction was based on the assumption that on the average 20 percent of the differences between a herdmate average (HM) and the breed average (BA) were genetic differences. One-half of this difference, or 0.1, was credited to the sire being evaluated. The other half of the genetic difference, that from dams, was assumed not to affect sire summaries.

The performance of the daughters was regressed toward zero. In other words, all bulls were considered to have an expected PD of zero with no progeny information. This can be shown by the addition of a fifth term to the Herdmate Comparison equation. Thus,

$$\underset{[1]}{PD} = \underset{[2]}{R}\,[\underbrace{D-HM}_{[3]} + \underbrace{0.1\,(HM-BA)}_{[4]}] + \underbrace{(1-R)}_{[5]}\;0$$

Part [5] does not change the value of any PD because the term "1-R" is always multiplied by zero. However, this addition to the equation reminds us that whereas the daughter deviation received a weight of R, say 0.30 (for a 30% R bull), the other 0.70 (or 70%) came from zero. As R increased, more weight was given to the deviation and less to the assumed initial value, zero.

Much has been learned about dairy cattle genetics since the midsixties. Although the Herdmate Comparison formula was a major advancement in accuracy when it was adopted, we now have developed more accurate procedures for the genetic evaluation of dairy bulls and cows.

The Modified Contemporary Comparison contains a number of improvements that correct weaknesses in the Herdmate Comparison. The Modified Contemporary Comparison equation can be shown diagrammatically as follows:

$$\underset{[1]}{PD74} = \underset{[2]}{R}\,(\underbrace{D - MCA}_{[3]} + \underset{[4]}{SMC}) + \underbrace{(1 - R)GA}_{[5]}$$

<u>Part [1]</u>.--One improvement in the Modified Contemporary Comparison is designated by the term "PD74". This signifies the adoption of a new genetic base concept called a Stepwise Genetic Base. This new genetic base eliminates the problems of comparing bulls over time that resulted from the moving genetic base formerly used. Under the Stepwise Genetic Base procedure all bulls are summarized to the same base within breed so all summaries are directly comparable, within breed. Initially, the genetic base is related to the average calving date of the records used in the fall 1974 summaries. The Modified Contemporary Comparison PD's can be readily distinguished from PD's calculated by the herdmate method by including the genetic base designator along with the PD that is, PD 1974. When genetic change warrants, the base will be changed. The standardization of all estimates of genetic merit to the same genetic base should increase the accuracy of pedigree evaluations and increase the genetic gain from selecting bulls and cows on the basis of pedigree information.

Part [2].--The new R is calculated by using an improved formula that accounts more accurately for the within and between herd variation that exists in the present dairy cattle population. For a bull with daughters in many herds, the new R may tend to be a bit smaller due to the new weightings. This is because each record receives a weighting that considers days in milk, number of Modified Contemporaries, and the number and average R of sires of the Modified Contemporaries (explained in Part [3] below). This results in a slightly smaller and more accurate weighting for a given situation than in the past, when all records were treated as though they were 305 days in length and had an infinite amount of information on herdmates. The R may be a few percentage points higher than in the past if there is a highly disproportionate distribution of daughters across herds. This slight increase in R results from a more accurate weighting and greater emphasis on new daughters in new herds (in the summary) in proportion to large numbers of daughters and records in any one herd. Therefore, another characteristic of the new R is that the influence on the sire summary is considerably limited for any one herd having a high proportion of the bull's daughters.

Part [3].--The term "D - MCA" introduces a new concept into sire summaries, called Modified Contemporary Average (MCA). The term "Modified Contemporaries" means that the average with which a daughter record is compared is calculated by the use of contemporary groups (herdmates that are of a similar age). Two contemporary groups used in the Modified Contemporary Comparison are:

Contemporary Group 1 includes just first lactations.

Contemporary group 2 includes all second and later lactations.

The MCA is calculated primarily from the contemporary information. That is, from Contemporary Group 1 records if we are dealing with a daughter's first lactation or from Contemporary Group 2 records if we are dealing with a daughter's second or later lactation. In addition to this, the noncontemporary average (Contemporary Group 2 records for a daughter's first lactation and vice versa) is included, but counted the equivalent of only one additional contemporary. Deviating the daughter lactation record from Modified Contemporaries rather than herdmates removes some problems from herdmates being selected for yield and also reduces errors from age factors not fitting any one herd perfectly. On the other hand, noncontemporary herdmates still contribute, and daughter records can be utilized even though they have no contemporaries. The difference of each daughter's record from MCA is weighted according to how much information is available. The old difference from herdmates (D - HM) was an average difference, but the difference from Modified Contemporaries (D - MCA) is a weighted difference. In the Herdmate Comparison each daughter with a given number of records has the same degree of influence on D - HM. In the MCC a daughter in a new herd has much more influence than an additional daughter in a herd that already has daughters.

The calculation of MCA also includes an adjustment for the selection bias that occurs due to culling for yield after first lactation. This adjustment increases the benefits derived from the use of the MCA over the former herdmate average.

Part [4].--The sires of the Modified Contemporaries (SMC) are used to estimate the average genetic merit of the cows (Modified Contemporaries) to which a bull's daughters are compared. This adjustment is a major improvement over the previously used crude approximation of 0.1 (HM - BA).

In the Herdmate Comparison, a herdmate level above breed average was assumed to mean that the herdmates were genetically better than breed average and vice versa. Certainly this is not always true. A genetically inferior herd could have a high average production due to an especially high input of feeding and management. Therefore, Part [4] of PD74 considers the genetic merit of each individual herdmate sire to obtain SMC.

The beneficial impact of parts [3] and [4] of PD74 are greatly increased by a technique called iteration. In this technique, repeated estimates of genetic merit on each sire are used to make the adjustment for the sires of the Modified Contemporaries more accurate in each succeeding round of iteration. This iterated adjustment for the genetic merit of the sires of the Modified Contemporaries has two primary benefits:

(1) It accounts more accurately for the genetic level of competition a bull's daughters are up against at a given point in time, and

(2) With repeated iterations and sire summary runs it accounts for differences among bulls due to genetic trend, thereby eliminating one of the most troublesome sources of bias in the Herdmate Comparison.

Part [5].--The inclusion of pedigree information is one of the most valuable improvements in the Modified Contemporary Comparison and at the same time one of its most controversial aspects. Traditionally estimates of genetic merit of bulls have ignored ancestor information that could be valuable in predicting breeding worth. The MCC was designed to utilize information on the genetic transmitting ability (GTA) of a bull's sire and maternal grandsire in addition to the yield of his daughters. Other ancestors are presently excluded for the following reasons.

(1) The sire and maternal grandsire are the two closest ancestors whose GTA is usually known with a high degree of accuracy.

(2) Research has shown that if sire summaries with at least a medium range of R are available for the sire and maternal grandsire, the remainder of pedigree information adds little to the accuracy of pedigree evaluation.

(3) The cost of using information only on bulls is very much less than that on cows because of the differences in the size of the data files on bulls vs. cows. The major cost increase that would be incurred to utilize cow information in the pedigree evaluation cannot be justified because there is not a commensurate increase in accuracy. However, the use of cow information would undeniably have considerable public relations value.

The relative value of pedigree information varies according to the amount of progeny information available. With little or no progeny information, a bull's pedigree is of considerable importance for estimating his expected GTA. Pedigree information is very useful for selecting bulls for progeny testing. It is a valuable addition to the sire summaries with lower R, especially single-herd summaries. It is clear that valuable pedigree information has been overlooked in the past probably due at least partly to the complexity of including it with daughter information. Obviously, a bull should not be widely used in Artificial Insemination (AI) on the basis of nothing but pedigree information. We would not have suitable confidence in his genetic superiority. On the other hand, the suggestion that pedigree information is worthless, or is worthless as soon as any progeny data are available, is equally unjustified. That is tantamount to denying that yield is inherited. The proper way to utilize pedigree information is to weight it along with progeny information according to the genetic worth of each source. This is exactly what the MCC does. The genetic grouping procedure makes use of pedigree information in a manner that is very close to Selection Index Theory but in a slightly conservative manner, giving pedigree information slightly less emphasis than is justified by genetic theory.

Here is how the MCC makes use of pedigree information. First, a Pedigree Index for genetic transmitting ability is computed for each bull from sire and maternal grandsire information. Second, bulls are divided into classes within each breed depending on the presence or absence of sire and maternal grandsire information and ranked within classes. Third, each ranking is divided into genetic groups, each group usually encompassing about a 50-pound range in milk yield. Fourth, a group average is calculated for each genetic group. The genetic group average is factor GA in part [5] of the PD74 formula. The range in values of the genetic group averages will usually be less than the range of the Pedigree Indexes. We do not anticipate that any GA for any breed will go beyond the range of ±1,200 pounds of milk under the 1974 base. In fact, over half of the bulls in each breed have group averages within the range of -200 to +200. Hopefully, this distribution will be shifting upward because of genetic progress.

Two other major improvements were adopted at the time of implementation of the MCC. Records-in-Progress (RIP's) were included where available in all sire summaries. This is an outgrowth of the USDA's previous procedure where a separate Preliminary Sire Summary run was conducted that included RIP's. A study 1/ showed that the Preliminary Sire Summaries were accurate predictors of the later Official Summaries and that it would be beneficial to include RIP's in the Official USDA-DHIA Sire Summaries and Cow Indexes. These RIP's have been made available to USDA through the cooperation of the Dairy Records Processing Centers and the financial support of the National Association of Animal Breeders.

New USDA-DHIA Age and Month-of-Calving Factors 2/ were also implemented. These factors were calculated by improved procedures that account both for age of the cow at calving and the month of the year in which she calved. These factors enable more accurate standardization of lactation records used in NCDHIP, in genetic evaluation and other research.

Most of the improvements in the MCC that result in more accurate Sire Summaries also increase the accuracy of the Cow Indexes. This occurs for two reasons:

(1) The direct increase in accuracy of evaluating each cow's individual yield data as shown in parts of [3] and [4] of the PD74 formula.

(2) The increased accuracy of genetic information of each cow's sire that results from the MCC and is used in the Cow Indexing procedure.

Details of the new USDA-DHIA Cow Indexing procedure are described in the fourth article of this publication.

1/ Powell, R. L., H. D. Norman, and F. N. Dickinson. 1975. Analysis of the USDA-DHIA preliminary sire summary. J. Dairy Sci. 58:551-557.

2/ Norman, H. D., P. D. Miller, B. T. McDaniel, and others. 1974. USDA-DHIA factors for standardizing 305-day lactation records for age and month of calving. U.S. Agr. Res. Serv. ARS-NE-40, 91 pp.

THEORETICAL BACKGROUND FOR THE USDA-DHIA MODIFIED CONTEMPORARY COMPARISON SIRE SUMMARY PROCEDURE

H. D. Norman,
research scientist (genetics), Animal Improvement Programs Laboratory, Animal Physiology and Genetics Institute, Northeastern Region, Agricultural Research Service

In 1962 the Herdmate Comparison replaced the Daughter-Dam Comparison as the Official USDA-DHIA sire evaluation procedure. The change created the opportunity for dairymen using this information to increase manyfold their within-herd genetic improvement. Over a period of years such improvement created problems in the accuracy of the Herdmate Comparison because bulls were not used randomly and daughters of individual bulls were compared with herdmates of substantially different merit.

In 1970 Cornell University implemented a linear model procedure for sire evaluation with the Northeast AI Sire Comparison.[1] The procedure compares daughters of artificial insemination (AI) sires on their first lactation records. This summary eliminated the need to assume that the bulls were mated at random with respect to other bulls and also considered that the bulls selected were not of a single population. USDA's commitment to evaluate all bulls made it unfeasible to utilize this model. The required techniques for obtaining solutions for the number of bulls needed was not available in 1971 when an alternative to the Herdmate Comparison was initiated at USDA. Whether these techniques can be developed to the point where mixed model methods can be utilized in the near future for the number of bulls required needs to be determined.

In evaluating all bulls, a procedure seemed necessary to adjust for the location or distribution of daughters across herds in addition to the number of daughters. Considerable controversy still exists over whether sire summaries need to include more than first lactation records. The exclusion of second and later records simplifies procedures by not having to consider individual cow variation or the extent of selection in herdmates, and allows the use of a smaller data file. Sampling variance of sire estimates can be reduced by including more than first records, principally because of the additional daughters with comparisons, and also because of some additional records on each daughter and additional herdmates in each comparison. The unanswered question seems to be whether bulls' rankings on the performance of their daughters at various locations change enough to be worth considering.

---

[1] Cornell University, Department of Animal Science. 1970. Northeast AI Sire Comparison. Ithaca, N.Y.

Selection Index Theory has been widely used in the field of animal breeding. Because of the complexity, however, there has been a reluctance to expand its use in sire evaluation to consider information on other relatives when daughters are available. Pedigree information is more reliable than a single herd summary. 2/ Such information can be as valuable as having nine daughters in nine herds. Therefore, a substantial increase in accuracy can be achieved by including the additional information in (1) the first summaries of most bulls and (2) all summaries of low Repeatability (R) bulls. The success of using pedigree information in predicting the future performance of bulls' daughters has been shown in many studies. 2/ Such success would seem to be underrated because most pedigree estimates were based on the Herdmate Comparison procedure. This additional information on relatives should be included in the sire estimates.

In 1971 the following procedure was developed as an alternative procedure to eliminate the major weaknesses in the Herdmate Comparison method. In the process of changing the procedure a number of additional revisions to the dairy record system were made. Among these were the implementation of new age-month of calving adjustment factors 3/ and the inclusion of in-progress records of more than 40 days. 4/ The first summaries calculated using these new procedures were available to the dairy industry in the fall of 1974.

Improvements in Weighting for Accuracy of Information

The USDA-DHIA Herdmate Comparison 5/ was one of the few sire evaluation procedures used that made any adjustment for environmental correlations. In that method, the R of the sire summary was influenced by the distribution of daughters across herds. The estimates of the sire's transmitting ability (Predicted Difference) was thus affected because the sire's R was used to regress the daughter-herdmate deviation to the population mean.

2/ Norman, H. D. Factors that should be considered in a national sire summary model. 1974. J. Dairy Sci. 57:955-962.

3/ Norman, H. D., P. D. Miller, B. T. McDaniel, and others. 1974. USDA-DHIA factors for standardizing 305-day lactation records for age and month of calving. U.S. Agr. Res. Serv. ARS-NE-40.

4/ Powell, R. L., H. D. Norman, and F. N. Dickinson. 1975. Analysis of the USDA preliminary sire summary. J. Dairy Sci. 58:551-557.

5/ Plowman, R. D., and B. T. McDaniel. 1968. Changes in USDA sire summary procedures. J. Dairy Sci. 51:306.

In the USDA-DHIA Herdmate Comparison procedure, if a large number of daughters were added in a single herd when there were single daughters in several herds, the R of the sire summary could actually decrease. The summary was less reliable because a larger proportion of the progeny information was from one herd and equal weight was given to the yield of each daughter having the same number of records. If information were combined in a more effective manner (that is weighting by the expected accuracy of information considering the environmental correlation), the adding of daughters in any herd would result in at least a slight increase in the Repeatability of the summary. Sire summary procedures that ignore environmental correlation, if it exists, overestimate R, therefore giving less than optimum estimates of transmitting ability if some herds have more than one daughter.

The USDA-DHIA Herdmate Comparison [6] considered herd effects as random and in calculation added a single regional breed-year-season average into the herdmate average, resulting in the adjusted herdmate average. Each adjusted herdmate average was then given equal weight for comparison to the daughter yield in combining information across daughters. Daughters with larger numbers of herdmates by greater numbers of sires provided more information about a bull's true genetic merit than did those with only one or a few herdmates but did not receive proper credit for the additional information provided.

The daughter and herdmate milk yield are defined in the new procedure with a model which more completely considers known genetic and environmental sources of variation. The sire summary model uses the distribution of daughters across herds to give more effective evaluations assuming environmental correlation is present. Daughter milk yield is explained by the following model:

$$Y_{hgijk} = HT_{hg} + S_i + (HS)_{hi} + C_{hij} + e_{hgijk}$$

where,

Y_{hgijk} is the yield of the kth record of the jth daughter of the ith sire in the hth herd and gth year-season;

HT_{hg} is an effect common to all observations in the gth year-season in the hth herd;

S_i is an effect common to daughters of the ith sire;

$(HS)_{hi}$ is an effect common to daughters of the ith sire in the hth herd;

---

[6] See footnote 5, page 9.

C_{hij} is a cow effect of the jth daughter of the ith sire in the hth herd; and,

e_{hgijk} is unexplained variation associated with the kth record of the jth daughter of the ith sire in the hth herd and gth year-season.

Each effect in the model except HT_{hg} is assumed to be an uncorrelated random variable distributed with mean zero, and variances, $I\sigma^2{}_s, I\sigma^2{}_{hs}, I\sigma^2{}_c$ or $I\sigma^2{}_e$, respectively.

Thus, for example, the variance of randomly selected records in a specific herd is:

$$Var(Y_{h'gijk}) = E\{[HT_{h'g} + S_i + (HS)_{h'i} + C_{h'ij} + e_{h'gijk}]$$

$$-E[HT_{h'g} + S_i + (HS)_{h'i} + C_{h'ij} + e_{h'gijk}]\}^2$$

$$= E\{[S_i + (HS)_{h'i} + C_{h'ij} + e_{h'gijk}]\}^2$$

$$= E\{S^2{}_i + (HS)^2{}_{h'i} + C^2{}_{h'ij} + e^2{}_{h'gijk} + \text{Cross Products}\}$$

$$= \sigma^2{}_s + \sigma^2{}_{hs} + \sigma^2{}_c + \sigma^2{}_e.$$

Likewise,

the variance of randomly selected daughter records of a specific sire in a randomly selected herd is:

$$Var(Y_{hgi'jk}) = \sigma^2{}_{hs} + \sigma^2{}_c + \sigma^2{}_e,$$

the variance of randomly selected daughter records of a specific sire in a specific herd is:

$$Var(Y_{h'gi'jk}) = \sigma^2{}_c + \sigma^2{}_e,$$

and the variance of randomly selected records of a specific cow in a specific herd is:

$$Var(Y_{h'gi'j'k}) = \sigma^2{}_e.$$

Since each herdmate's yield is described with the same model as each daughter's, the variance of total or average herdmates' yield for a sire can be calculated in the same manner. For the herdmate yield, the cow and error effects are confounded since each herdmate has but one record in the herd and season of interest. Thus,

$$a_{hgij} = C_{hij} + e_{hgijk}.$$

The model is therefore:

$$Y_{hgij} = HT_{hg} + S_i + (HS)_{hi} + a_{hgij},$$

where,

S_i = the herdmate's sire effect, distributed with mean zero and variance $I\sigma^2{}_s$, i = 1, ..., B,

a_{hgij} = cow + error effect of the herdmate, distributed with mean zero and variance $I(\sigma^2{}_c + \sigma^2{}_e)$, j = 1, n_{hgi}.

The i*th* sire of herdmates has n_{hgi} progeny in the g*th* season in the h*th* herd. For simplicity in definition bull i', whose daughters are being evaluated, was excluded from summation thus giving herdmate yield instead of herd yield. The herdmate average ($\overline{Y}_{h'g'..}$) for daughters of the i'*th* sire in the g'*th* season in the h'*th* herd is:

$$\overline{Y}_{h'g'..} = \sum_{i=1}^{B} \sum_{j=1}^{n_{h'g'i}} Y_{h'g'ij}/n_{h'g'.} = [n_{h'g'.}HT_{h'g'} + \sum_{i=1}^{B} n_{h'g'i}S_i$$

$$+ \sum_{i=1}^{B} n_{h'g'i}(HS)_{h'i} + \sum_{i=1}^{B} \sum_{j=1}^{n_{h'g'i}} a_{h'g'ij}]/n_{h'g'.}$$

The variance is, therefore:

$$\mathrm{Var}(\overline{Y}_{h'g'..}) = E\{\overline{Y}_{h'g'..} - E(\overline{Y}_{h'g'..})\}^2$$

$$= E\{n_{h'g'.}HT_{h'g'} + \sum_{i=1}^{B} n_{h'g'i}S_i + \sum_{i=1}^{B} n_{h'g'i}(HS)_{h'i} + \sum_{i=1}^{B} \sum_{j=1}^{n_{h'g'i}} a_{h'g'ij}$$

$$-E(n_{h'g'.}HT_{h'g'}) - E(\sum_{i=1}^{B} n_{h'g'i}S_i) - E[\sum_{i=1}^{B} n_{h'g'i}(HS)_{h'i}]$$

$$-E(\sum_{i=1}^{B} \sum_{j=1}^{n_{h'g'i}} a_{h'g'ij})\}^2 / n_{h'g'.}{}^2$$

$$= (\sum_{i=1}^{B} n_{h'g'i}{}^2/n_{h'g'.}{}^2)\ (\sigma^2{}_s + \sigma^2{}_{hs}) + \sigma^2{}_a/n_{h'g'.}$$

$$= \left(\sum_{i=1}^{B} n_{h'g'i}{}^{2}/n_{h'g'.}{}^{2}\right)(\sigma^2{}_{s} + \sigma^2{}_{hs}) + (\sigma^2{}_{c} + \sigma^2{}_{e})/n_{h'g'.}$$

The variance of daughter-herdmate deviations of individual records are calculated in the same manner as the variances of daughter yield and herdmate average yield. Each cow's records are then combined weighting by the inverse of their variances, thus utilizing the accuracy with which each appeared. Following this, daughter averages are also combined within and between herds by the inverse of their respective variances. Examples of the weighted daughter averages and their variances used in combining daughter information are given below:

<u>Weighting records within daughters</u>.--The variance of daughter herdmate deviations $[D_{h'gi'j'k} = Y_{h'gi'j'k} - \bar{Y}_{h'g..}]$ of randomly selected records of a specific cow (j') are:

$$\mathrm{Var}(D_{h'gi'j'k}) = \sigma^2{}_{e} + \sum_{i=1}^{B} n_{h'gi}{}^{2}/n_{h'g.}{}^{2}\,(\sigma^2{}_{s} + \sigma^2{}_{hs}) + (\sigma^2{}_{c} + \sigma^2{}_{e})/n_{h'g.} \qquad [1]$$

This variance is used in combining information across records within daughters. The resulting weighted deviation from herdmate average $(\tilde{D}_{h'.i'j'.})$ for $r_{h'i'j'}$ records of the j'th daughter is:

with weights = 1/Var($D_{h'gi'j'k}$).

$$\tilde{D}_{h'.i'j'.} = \left\{\sum_{k=1}^{r_{h'i'j'}} D_{h'gi'j'k}/\mathrm{Var}(D_{h'gi'j'k})\right\}/\left\{\sum_{k=1}^{r_{h'i'j'}} 1/\mathrm{Var}(D_{h'gi'j'k})\right\}. \qquad [2]$$

The variance of weighted average herdmate deviation yields of $r_{h'i'j'}$ randomly selected records of a specific daughter is:

$$\mathrm{Var}(\tilde{D}_{h'.i'j'.}) = 1/\left\{\sum_{k=1}^{r_{h'i'j'}} 1/\mathrm{Var}(D_{h'gi'j'k})\right\}. \qquad [3]$$

If all the daughter's records have an equal number of herdmates and herdmate sires with the same distribution of herdmate sires, then,

$$\mathrm{Var}(\tilde{D}_{h'.i'j'.}) = \mathrm{Var}(D_{h'gi'j'k})/r_{h'i'j'}.$$

Weighting daughter information within herds.--The variance of weighted average herdmate deviation yields ($\tilde{D}_{h'.i'j.}$) of randomly selected daughters (j) with $r_{h'i'j}$ records in a specific herd (h') sired by a specific bull (i') is:

$$\mathrm{Var}(\tilde{D}_{h'.i'j.}) = \sigma^2_c + \mathrm{Var}(\tilde{D}_{h'.i'j'.}). \qquad [4]$$

This cow variance is used in combining information across daughters within a specific herd. The resulting weighted daughter deviation from herdmate average ($\tilde{D}_{h'.i'..}$) for $d_{h'i'}$ daughters of the i'th bull for the h'th herd is:

$$\tilde{D}_{h'.i'..} = \{\sum_{j=1}^{d_{h'i'}} \tilde{D}_{h'.i'j.}/\mathrm{Var}(\tilde{D}_{h'.i'j.})\}/\{\sum_{j=1}^{d_{h'i'}} 1/\mathrm{Var}(\tilde{D}_{h'.i'j.})\}. \qquad [5]$$

The variance of weighted average herdmate deviation yields ($\tilde{D}_{h'.i'..}$) of $d_{h'i'}$ randomly selected daughters with unequal numbers of ($r_{h'i'j}$) records in a specific herd (h') sired by a specific bull (i') is:

$$\mathrm{Var}(\tilde{D}_{h'.i'..}) = 1/\{\sum_{j=1}^{d_{h'i'}} 1/\mathrm{Var}(\tilde{D}_{h'.i'j.})\}. \qquad [6]$$

If all cows have the same number of records and herdmate information, then the expected cow variance is the same for each cow, and

$$\mathrm{Var}(\tilde{D}_{h'.i'..}) = \mathrm{Var}(\tilde{D}_{h'.i'j.})/d_{h'i'}.$$

Weighting information across herds.--The variance of daughter information from each herd is used in weighting across randomly selected herds. This variance of weighted herdmate deviation yields ($\tilde{D}_{h.i'..}$) of $d_{hi'}$ randomly selected daughters with unequal numbers of ($r_{hi'j}$) records in any randomly selected herd (h) sired by a specific sire (i') is:

$$\mathrm{Var}(\tilde{D}_{h.i'..}) = \sigma^2_{hs} + \mathrm{Var}(\tilde{D}_{h'.i'..}). \qquad [7]$$

The weighted daughter deviation from herdmate average ($\tilde{D}_{..i'..}$) across p different herds for bull i' is thus:

$$\tilde{D}_{..i'..} = \{\sum_{h=1}^{p} (\tilde{D}_{h.i'..})/\mathrm{Var}(\tilde{D}_{h.i'..})\}/\{\sum_{h=1}^{p} 1/\mathrm{Var}(\tilde{D}_{h.i'..})\}. \qquad [8]$$

The variance of weighted average herdmate deviation yields ($\tilde{D}_{..i'..}$) of $d_{.i'}$ randomly selected daughters with unequal numbers of ($r_{hi'j}$) records from p randomly selected herds sired by a specific bull (i') is:

$$\mathrm{Var}(\tilde{D}_{..i'..}) = 1/\{\sum_{h=1}^{p} 1/\mathrm{Var}(\tilde{D}_{h.i'..})\}. \qquad [9]$$

As indicated in equation 7, as the numbers of daughters and records increase in any randomly selected herd, the expected variance of average yield aproaches the herd-by-sire variance. The variance of weighted yield in a single herd cannot decrease below this, thus placing an upper limit on the value of information coming from one herd. If, in contrast, the daughters are located in more than one herd (equation 9), the expected variance of weighted herdmate deviation yield can approach zero as the number of herds in the sample increases. If the herd-by-sire variances in the procedure were assumed to be zero, the weighting across herds would be the same as in the Herdmate Comparison.[7]

Considering the Genetic Level of the Herdmates' Sires

The changes in weighting thus far described give an improved Herdmate Comparison sire evaluation. Without additional improvements, however, the procedure would be most effective when all bulls are from a single population and selected for use at random within each herd. The more genetic differences among subpopulations, the greater the bias in ranking bulls in a Herdmate Comparison procedure.

Therefore, a second and very important modification is made to the Herdmate Comparison. Each daughter-herdmate deviation is adjusted for the average genetic value of the herdmates' sires. This change results in a measure of the differences among all bulls instead of the difference between each specific bull and the average of whatever other bulls are represented in the daughters' herdmates.

The herdmate deviation is replaced by a modified deviation. This means in simplified terms that the equation for the herdmate deviation:

---

[7] See footnote 5, page 9.

(Daughter Average - Adjusted Herdmate Average) +
0.1 (Adjusted Herdmate Average - Breed Average)

is replaced by:

Daughter Average - Herdmate Average + Average Genetic Merit of Herdmate Sires.

The improvement in the modified deviation formula over the old herdmate deviation is that each daughter-herdmate deviation is adjusted for the genetic merit of individual herdmates' sires. Thus, the "average" correction for the genetic level of the herd is replaced by a correction for each individual herdmate's sire.

Correcting for genetic differences in herdmates' sires requires a change in the expected variance from equation 1. The variation attributed to the herdmates' sire (σ^2_s) is reduced to zero if these bulls have accurate information and intermediate for sires of herdmates with lower Repeatabilities.

The variance of a daughter's records deviated from herdmate average adjusted for the average genetic value is considered in this procedure to be:

$$\mathrm{Var}(D_{h'gi'j'k}) = \sigma^2_e + \sigma^2_s\{\sum_{i=1}^{B} n_{h'gi}{}^2(1-R_i)\}/n_{h'g.}{}^2 + \sigma^2_{hs}\{\sum_{i=1}^{B} n_{h'gi}{}^2\}/n_{h'g.}{}^2 + (\sigma^2_c + \sigma^2_e)/n_{h'g.} \qquad [10]$$

The adjustment for herdmates sires is used to calculate repeated and improved modified deviations by a procedure known as iteration. That is, the correction to the daughter-herdmate difference for each individual herdmate sire is repeated. The new modified deviation on each sire is again used as improved corrections in calculating the average genetic value on herdmates' sires. This iterated adjustment for genetic merit of the herdmates within herd and season eliminates the bias that exist when bulls are not selected at random. Iterating on a within herd-year basis eliminates genetic differences in herdmates' sires among bulls sampled at the same time and genetic differences for those sampled at different times (genetic trend).

Adjustment for genetic differences in herdmates' sires to produce the modified deviations results in meaningful phenotypic differences among daughter yield for most bulls in the data (the few bulls not compared in the same herd-year-season with other bulls receiving wide distribution cannot be evaluated by this procedure). Iterated bull differences in daughter yield are unregressed with respect to the number of daughters and thus do not reflect that portion of the differences due to heredity versus environmental variation. The modified deviations are, therefore, multiplied by the Repeatability, and in this manner are regressed to the genetic group means.

The R of each sire summary is calculated by:

$$R = \frac{\sigma^2_s}{\sigma^2_s + \mathrm{Var}(\tilde{D}..i'..)} .$$

Combining Pedigree Information with Daughter Yield

In the Herdmate Comparison, daughter yield was regressed toward zero. Thus, no advantage was taken of the fact that additional information was available about the population from which the bull was selected. This pedigree information can be considered if bulls having similar pedigree indexes are grouped together and individual bull deviations are regressed to the average performance of the bulls' daughters in that group. Assuming there are a sufficient number of bulls in each, the group average represents the genetic merit for transmitting ability of the population from which the bull was selected while the individual bull deviations represent a combination of both phenotypic and genetic variation. A sire estimate of transmitting ability is calculated by regressing the bull deviation to the genetic group average using the Repeatability:

Sire's Estimated Transmitting Ability = Genetic Group Average +
R (Modified Deviation - Genetic Group Average)

If pedigree grouping is an ineffective method of characterizing bulls from different populations, then all group means will be nearly equal and information on relatives will not improve estimates of sires' transmitting ability. If pedigree grouping proves to be as effective as theory suggests, substantial accuracy will be added in predicting milk and fat yield of the future daughters of most bulls.

PROCEDURES USED TO CALCULATE THE USDA-DHIA MODIFIED CONTEMPORARY COMPARISON

F. N. Dickinson, H. D. Norman, R. L. Powell, L. G. Waite, and B. T. McDaniel, respectively, chief, research scientist (genetics), research geneticist (animal), supervisory computer specialist, Animal Improvement Programs Laboratory, Animal Physiology and Genetics Institute, Agricultural Research Service, professor, Animal Science Department, North Carolina State University

The description of the Modified Contemporary Comparison that follows is complete and detailed. A step-by-step summary of the flow of data (fig. 1) and operations actually executed in the system during the first run in the fall of 1974 are presented. Before final specifications were developed, a brief description was written. The following supersedes the briefer one.

The procedures used to calculate the USDA-DHIA Modified Contemporary Comparison were developed over a period of several years. Implementation of these procedures required the reprogramming of the scientific part of the USDA computing system. The early part of the computing system was left essentially the same as in the USDA-DHIA Herdmate Comparison, that is, the editing and file updating referred to in the upper left (unnumbered) block of figure 1.

The first additional operation required by the Modified Contemporary Comparison (MCC) is to look up the identification of the maternal grandsire in the female pedigree system for each new registered bull entering the system (step 1). For each bull the maternal grandsire identification is required in addition to the sire identification for placing bulls in appropriate genetic groups during the summary. Each bull's sire identification is already available in the master sire identification file from the early part of the system.

The next step (2) is to decide which bulls are to be summarized in this run. The critera for summarization have been changed slightly from the herdmate comparison for several reasons:

- The USDA files have over 1 million bulls with at least one daughter.

- A partial history run was made in fall 1974 so that most of the older bulls that still have any daughters milking or are prevalent in pedigrees were summarized by using the Modified Contemporary Comparison.

- The cost of resummary is high and little new information is gained from resummarizing bulls born over 20 years ago.

The criteria for summary may have to be changed slightly over the next several sire summary runs until they can be stabilized. The criteria for summary are somewhat arbitrary because not all the information that would be desirable for making the decision is available at the point in the system where the decision must be made.

Once the bulls to be summarized have been designated, their daughters' lactation records must be collected for analysis (step 3). The records come from the master sire file and current records. Master sire file records are those that have been submitted for previous Sire Summary runs. Current records are those that have been submitted for the current run. Two types of current records are completed records and Records-in-Progress. Completed records are those of 305 days or less with a USDA-DHIA Lactation Termination Code [1] indicating that the cow went dry or stopped milking for some other reason. Records-in-Progress contain the latest available yield for cows that were still milking when the Dairy Records Processing Centers pulled records from their files to send to USDA for the Sire Summary run. Only Official DHI and DHIR records are used.

Records that fall into two categories are pulled from the master sire file. These are (1) records made by cows whose sires are being summarized this run and (2) previous records made by cows that have a current record (step 4). All registered cows from these two categories are cow indexed.

The Modified Contemporary Comparison takes into account the genetic merit of each individual contemporary's sire. That is, the sire's weighted average unregressed Modified Contemporary Deviation milk and fat and Repeatability (R) are added to each current record (step 5). The same sire information must be added to master file records for daughters of bulls that were summarized in the previous Sire Summary run. This will be done in step 7. But first the current records must be sorted to breed-herd-sire-cow sequence to update the herd master file. This is shown as the sort between steps 5 and 6 (fig. 1).

Then several steps are performed by one of the more complex programs in the system. The herd master file is updated with current records (step 6). The records already in the herd master file are updated with the lastest sire's deviation milk and fat and Repeatability from sires that were summarized in the last Sire Summary run (step 7). The value zero is used for the sire

---

[1] King, G. J., and B. T. McDaniel. 1970. USDA termination codes--What are they? Why are they used? How are they used? U.S. Agr. Res. Serv. ARS 44-221: 2-7.

information for daughters of bulls that have never been summarized. At the same time all records to be used in the Sire Summaries and Cow Indexes are standardized to a 2X-305 day-ME basis 2/ and the length of lactation weighting factor is looked up for each record (step 8). Each lactation is weighted according to its length, based on the phenotypic correlation between 305-day records and shorter records. These correlations are shown in table 1.

Table 1.--Phenotypic correlations between records of 305 days in length and shorter durations

	Months in milk									
Cow	1	2	3	4	5	6	7	8	9	10
2-year-olds	0.72	0.83	0.88	0.92	0.94	0.96	0.97	0.98	0.99	1.00
3-year-olds and over	.60	.74	.82	.86	.91	.93	.96	.98	.99	1.00

This weighting for lactation length is done both for Records-in-Progress and for completed records of less than 305 days. Then, the dynamic monthly herd totals are calculated separately for Contemporary Groups 1 and 2 (see below) for later use in computing the rolling 5-month Modified Contemporary Average for each daughter lactation record (step 9). At the same time that the dynamic monthly herd totals are being calculated, all records to be used in the Sire Summaries and Cow Indexes are being accumulated on a separate file (step 10).

Point Ⓐ in figure 1 signifies the start of the Sire Summary and Cow Index calculations. Part of the system between Ⓐ and Ⓑ is also referred to as the iteration part of the system. The first series of operations in the iteration portion of the system is represented by step 11. This step comprises the calculation of

---

2/ Anonymous. 1972. Factors for reducing 305-day, age corrected records to a twice-a-day milking basis. *In* Dairy Herd Improvement Letter. U.S. Agr. Res. Serv. ARS-44-239, p. 8.

Norman, H. D., P. D. Miller, B. T. McDaniel, and others. 1974. USDA-DHIA factors for standardizing 305-day lactation records for age and month of calving. U.S. Agr. Res. Serv. ARS-NE-40, 91-pp.

McDaniel, B. T., R. H. Miller, and E. L. Corley. 1965. DHIA factors for projecting incomplete records to 305 days. *In* Dairy Herd Improvement Letter, U.S. Agr. Res. Serv. ARS-44-164.

the following four items of information needed for each daughter record of each bull to be summarized.

(1) The Modified Contemporary Average for each daughter record.

(2) The number of different sires associated with the Modified Contemporary information for each daughter record.

(3) The weighted average Modified Contemporary Deviation of the sires of the Modified Contemporaries associated with each daughter record.

(4) The weighted average Repeatability of the sires of the Modified Contemporaries.

Calculation of the Modified Contemporary Average for each daughter's record.--The first step is to divide all lactation records into two Contemporary Groups as follows:

(1) Contemporary Group 1 contains first lactations.

(2) Contemporary Group 2 contains second and later lactations.

Then, Contemporary Group information is calculated for each daughter's record (using the updated herd master file) based on a moving 5-month average centered on the month of daughter's calving. Paternal half-sib data are eliminated from each daughter's Contemporary Group information. This is done by generating a series of 5-month herd-sire totals of daughter-production information separately for Contemporary Groups 1 and 2, each centered on a month where a cow calved that is either the daughter of a bull to be summarized or is a cow that will be cow indexed. These 5-month herd-sire totals are subtracted from the 5-month dynamic herd totals to obtain the 5-month totals that comprise the sums of weightings and the weighted sums in the equations given below. Then, the Modified Contemporary Average for each daughter's lactation record is calculated. For a daughter's first (Contemporary Group 1) record this is done by using the equation.

$$\frac{\sum_i W_i C_i + W_\ell \left[\frac{(\sum_j W_j C_j)}{\sum_j W_j} - B \right]}{\sum_i W_i + W_\ell} \qquad [1]$$

where,

Σ = summation,

W_i = length of lactation weighting for i^{th} Contemporary Group 1 record,

C_i = standardized (2X-305 day-ME) yield of milk or fat for i^{th} Contemporary Group 1 record,

W_ℓ = weighting factor for Contemporary Group 2 records in Modified Contemporary Average for a daughter's first record,

W_j = length of lactation weighting for j^{th} Contemporary Group 2 record,

C_j = standardized (2X-305 day-ME) yield of milk or fat for j^{th} Contemporary Group 2 record, and,

B = adjustment for cow selection bias in Contemporary Group 2 records.

The factor W_ℓ in this formula has been set equal to 1.0. The use of the factor W_ℓ is one of the primary reasons for adopting the nomenclature "Modified" Contemporary Comparison for this genetic evaluation procedure. The effect of W_ℓ is to place the emphasis on the contemporary information while also permitting the use of noncontemporary data. Weighting in this manner enables emphasis or greatest weight to be placed on the within herd-year-season comparisons that are most accurate as they are least affected by the failure of the age and month of calving factors to fit each herd precisely. At the same time this method of weighting permits the use of a daughter's record even though there may be no contemporary records for a comparison. The factor B is used to adjust the Contemporary Group 2 records, because they are made by cows that survive culling after first lactation when most culling for yield takes place. On the average Contemporary Group 2 cows are genetically superior because they have been selected to remain in the herd. The value 0.013 X breed average is assigned to factor B based on research by J. F. Keown.[3]

---

[3] Keown, J. F. Unpublished material on file at the Animal Physiology and Genetics Institute, Northeastern Region, U.S. Agricultural Research Service.

An equation based on the same principles is used to calculate the Modified Contemporary Average for a daughter's second or later record:

$$\frac{\sum_j W_j C_j + W_f \left[\frac{\sum_i W_i C_i}{\sum_i W_i} + B \right]}{\sum_j W_j + W_f} \qquad [2]$$

where,

W_f = weighting factor for Contemporary Group 1 records in Modified Contemporary Average for a daughter's second or later record, and, the other terms are the same as defined previously.

In equation 2, W_f is set equal to 1.0 same as was W_ℓ in equation 1. The factor B is added to the Contemporary Group 1 data in this equation to put that data on the same basis as the Contemporary Group 2 records.

<u>Calculation of the number of different sires associated with the Modified Contemporary information for each daughter's record.</u>--For a daughter's first record the weighting equation for number of Modified Contemporary sires is:

$$\frac{\left(\sum_i W_i + W_\ell\right)^2}{\frac{\left(\sum_i W_i\right)^2}{N_f} + \frac{\left(W_\ell\right)^2}{W'_\ell}} \qquad [3]$$

where,

N_f = number of different sires of Contemporary Group 1 cows,

W'_ℓ = W_ℓ = 1.0 if $W_\ell <$ sum of lactation length weighting factors for Contemporary Group 2 records, or

W'_ℓ = lactation length weighting factor in the special case where there is only one Contemporary Group 2 record, and, the other terms are the same as defined previously.

For a daughter's second or later record the weighting for number of Modified Contemporary sires is:

$$\frac{\left(\sum_j W_j + W_f\right)^2}{\frac{\left(\sum_j W_j\right)^2}{N_\ell} + \frac{(W_f)^2}{W'_f}} \qquad [4]$$

where,

N_ℓ = number of different sires of Contemporary Group 2 cows,

W'_f = W_f = 1.0 if W_f < sum of lactation length weighting factors for Contemporary Group 1 records, or

W'_f = lactation length weighting factor in the special case where there is only one Contemporary Group 1 record, and, the other terms are the same as defined previously.

Calculation of the weighted average Modified Contemporary Deviation of the sires of the Modified Contemporaries associated with each daughter's record.--For a daughter's first record this is calculated as shown in equation 5:

$$\frac{\sum_i W_i D_i + W_\ell \left[\frac{\sum_j W_j D_j}{\sum_j W_j}\right]}{\sum_i W_i + W_\ell} \qquad [5]$$

where,

D_i = Modified Contemporary Deviation for the sire of i^{th} cow in Contemporary Group 1,

D_j = same for j^{th} cow in Contemporary Group 2, and, the other terms are the same as defined previously.

The equation for the weighted average Modified Contemporary Deviation for the sires of Modified Contemporaries associated with a daughter's second or later record is:

$$\frac{\sum_j W_j D_j + W_f \left[\frac{\sum_i W_i D_i}{\sum_i W_i} \right]}{\sum_j W_j + W_f} \qquad [6]$$

where,

all terms have been defined previously.

The calculation of the terms "D_i" and "D_j", in equations 5 and 6 will be explained below since they are the primary product of the iteration procedure. They are actually calculated in step 12. However, during each round of iteration, including the first one, values must be available for D_i and D_j. Therefore, in the first round of iteration in fall 1974 Sire Summary run, the unregressed herdmate deviations from the May 1974 run were used in lieu of weighted average Modified Contemporary Deviations.

Calculation of the weighted average Repeatability of the sires of the Modified Contemporaries associated with each daughter's record.--For a daughter's record this is calculated as shown in equation 7:

$$\frac{\sum_i W_i R_i + W_\ell \left[\frac{\sum_j W_j R_j}{\sum_j W_j} \right]}{\sum_i W_i + W_\ell} \qquad [7]$$

where,

R_i = Repeatability of Predicted Difference (PD) for sire of the i^{th} cow in Contemporary Group 1,

R_j = Repeatability of PD for sire of j^{th} cow in Contemporary Group 2, and, the other terms are the same as defined previously.

For a daughter's second or later record, the equation for weighted average Repeatability of the sires of the Modified Contemporaries is:

$$\frac{\sum_j W_j R_j + W_f \left[\frac{\sum_i W_i R_i}{\sum_i W_i} \right]}{\sum_j W_j + W_f} \qquad [8]$$

where,

all terms have been defined previously.

In the first iteration round of the fall 1974 run, the R's from the May 1974 run were used.

The information needed to calculate the Modified Contemporary Deviation for each daughter's record has now been computed and incorporated into each daughter's record. The daughters' records are next sorted to sire sequence (the sort between steps 11 and 12). They are then passed to the program that assembles the daughters' information and calculates the weighted average Modified Contemporary Deviation for each bull with the following series of operations.

(1) For each daughter's lactation calculate the Modified Contemporary Deviation milk and fat which is adjusted for the genetic merit of the sires of the Modified Contemporaries.

(2) Summarize the Modified Contemporary Deviations over all lactations for each daughter.

(3) For each bull summarize the daughters' Modified Contemporary Deviations over all daughters within each herd.

(4) For each bull summarize the daughters' within herd Modified Contemporary Deviations over all herds.

Calculate the Modified Contemporary Deviation milk and fat which is adjusted for the genetic merit of the sires of the Modified Contemporaries.--This is done by using the equation:

Adjusted Modified Contemporary Deviation milk and fat = standardized lactation yield - Modified Contemporary Average + average Modified Contemporary Deviation for the sires of the Modified Contemporaries.

Summarize the Modified Contemporary Deviations over all lactations for each daughter.--To do this a weighting factor is calculated for each daughter's lactation by the equation:

$$\frac{1}{\dfrac{\text{error variance}}{\text{daughter's lactation length weight}} + \dfrac{\text{sire variance (1-R of MC sires) + herd x sire variance}}{\text{weighting for number of sires of MC}} +}$$

(Denominator continued on following page).

$$\frac{\text{cow variance} + \text{error variance}}{\sum_i W_i + W_\ell \quad \text{or} \quad \sum_j W_j + W_f} \qquad [9]$$

where,

Sire variance = 0.05,

Herd x sire variance = .14,

Cow variance = .31,

Error variance = .50, and

the weighting for lactation length of the Modified Contemporaries is $\sum_i W_i + W_\ell$ for a daughter's first record and $\sum_j W_j + W_f$ for a daughter's second or later record, and R of MC sires = Average R of the PD of the sires of the Modified Contemporaries.

Then the Modified Contemporary Deviation for each daughter is calculated from the equation:

$$\frac{\Sigma(\text{weighting factor for each lactation x Modified Contemporary Deviation for each lactation})}{\Sigma \text{ weighting factors for each lactation}} \qquad [10]$$

For each bull summarize the daughters' Modified Contemporary Deviations over all daughters within each herd.--A weighting factor is calculated for each daughter's information using the equation:

$$\frac{1}{\text{cow variance} + \dfrac{1}{\Sigma \text{ weighting factors for each lactation}}} \qquad [11]$$

then,

the weighted average Modified Contemporary Deviation milk and fat for each bull's daughters in each herd is calculated by the equation:

$$\frac{\Sigma(\text{weighting factor for daughter} \times \text{each daughter's Modified Contemporary Deviation})}{\Sigma\ \text{weighting factors for each daughter}} \qquad [12]$$

For each bull summarize the daughters' within herd Modified Contemporary Deviations over all herds.--Weighting factors must be calculated for each bull's daughters' information in each herd according to the equation:

$$\frac{1}{\text{herd} \times \text{sire variance} + \dfrac{1}{\Sigma\ \text{weighting factors for each daughter}}} \qquad [13]$$

Then each bull's weighted average Modified Contemporary Deviation is calculated from the equation:

$$\frac{\Sigma(\text{weighting factor for each herd} \times \text{daughters' Modified Contemporary Deviation in that herd}}{\Sigma\ \text{weighting factors for each herd}} \qquad [14]$$

That completes the calculation of each bull's Modified Contemporary Deviation.

The Repeatability for each bull's summary is also calculated in step 12, according to the equation:

$$\frac{\text{sire variance}}{\text{sire variance} + \dfrac{1}{\Sigma\ \text{weighting factors for each herd}}} \qquad [15]$$

The Repeatability is calculated in each iteration round because each bull's R is dependent to a small degree on the R's of the sires of his daughters' contemporaries as shown in equation 9. That completes the work done in step 12.

At the same time the calculations just described were being done, the information needed for cows to be cow indexed was pulled off on a separate file (Point Ⓒ). Sire and maternal grandsire search records are then generated for all bulls to be summarized (step 13). These records are used to search the master sire file for the bulls that will provide the pedigree information for the genetic grouping procedure. At this point the pedigree information is updated where necessary (step 14). That is, missing identification is furnished where available and identification errors are corrected.

At step 15 each bull's Modified Contemporary Deviation is adjusted to a uniform genetic base so that summaries can be compared directly from one iteration round to the next and from one run to the next. This adjustment is made by using a group of high Repeatability bulls in each breed, the average of whose summaries should have very little random fluctuation from one run to another. In each breed the amount by which the Modified Contemporary Deviation of these high R bulls deviates from their average in the fall 1974 run is used to adjust all summaries to maintain a constant genetic base by subtracting this difference from all bulls being summarized.

We have now progressed to step 16, where the decision is made whether or not to conduct another round of iteration. This decision is made on a subjective basis dependent on the magnitude of changes in the Modified Contemporary Deviations of a selected group of bulls in each breed. This procedure was developed from an empirical study by H. D. Norman and R. L. Powell. If another round of iteration is to be done, the system proceeds to step 17. The latest Modified Contemporary Deviation and Repeatability for each cow's sire are inserted in each cow's lactation records. Then the dynamic monthly herd totals are updated with the new sire information (step 18), in order to adjust the Modified Contemporary Deviation for each daughter's record with the latest genetic information on the contemporaries' sires. The system returns to point A and commences the next round of iteration.

If no more rounds of iteration are needed the system proceeds to point B. First, each bull's sire and maternal grandsire search records from step 13 are sorted into sequence by sire and maternal grandsire registration numbers. Then the PD's of the sires and maternal grandsires are looked up in the sire master file for use in grouping the bulls to be summarized (step 19). The sire and maternal grandsire search records with the PD's are then sorted back to the sequence of the bulls being summarized. The pedigree grouping procedure is handled in step 20. This consists of several different operations.

First, a pedigree estimate of genetic transmitting ability is calculated for each bull being summarized by using the sire and maternal grandsire PD's looked up in step 19, according to the equation:

1/2 (Sire's PD) + 1/4 (Maternal grandsire's PD). [16]

Then, each bull is placed in its appropriate grouping category. The five basic grouping categories are:

(1) Bulls with both sire and maternal grandsire PD's.

(2) Bulls with only sire PD's.

(3) Bulls with only maternal grandsire PD's.

(4) Bulls that are registered but have neither sire nor maternal grandsire PD's.

(5) Grade bulls (for which there is no pedigree information).

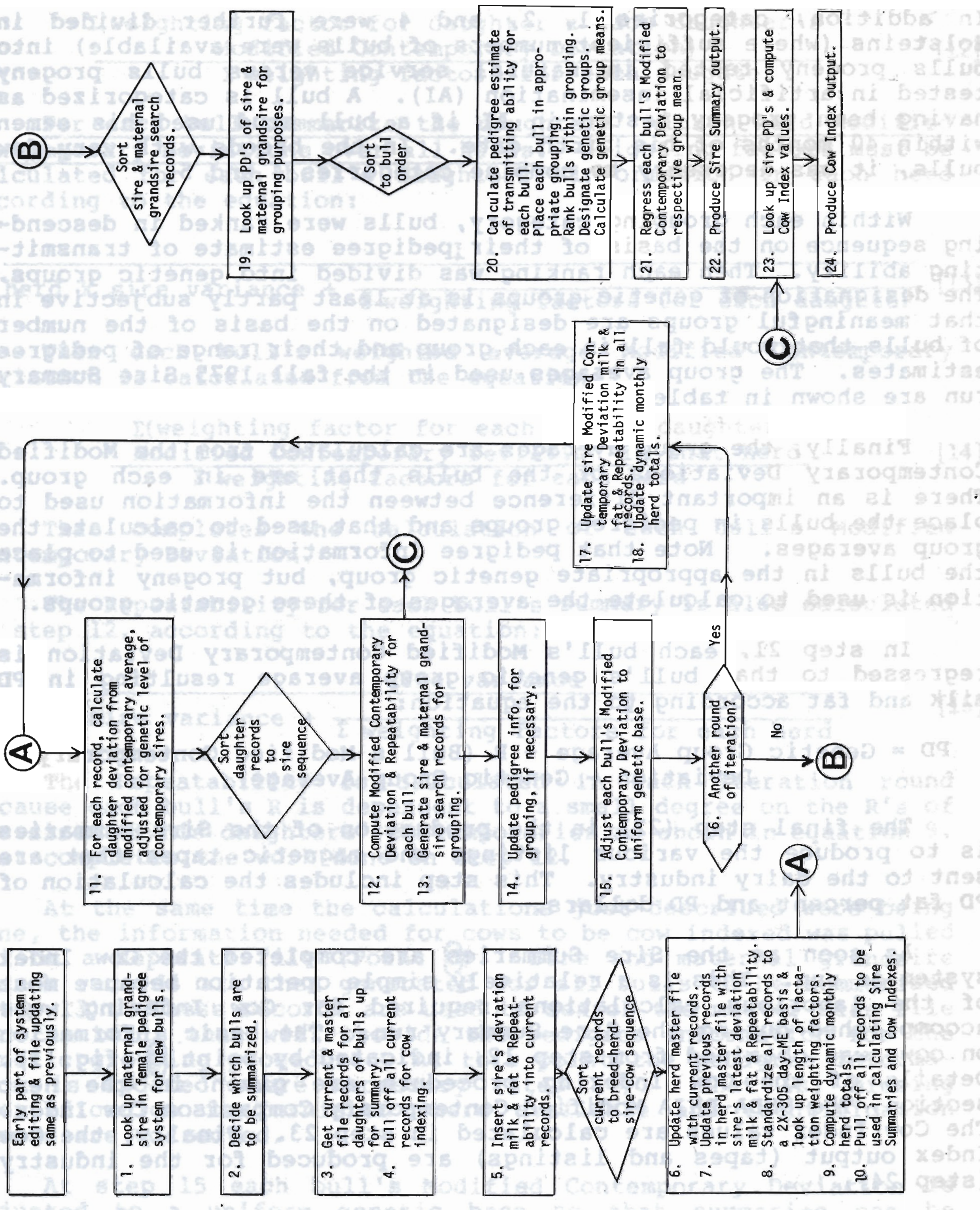

Figure 1. Flowchart showing major operations in the USDA-DHIA Modified Contemporary Comparison system

In addition, categories 1, 2, and 4 were further divided in Holsteins (where sufficient numbers of bulls were available) into bulls progeny tested in natural service versus bulls progeny tested in artificial insemination (AI). A bull is categorized as having been progeny tested in AI if a bull stud used his semen within 40 months of his birth date. In the breeds with very few bulls, it was necessary to combine categories 4 and 5.

Within each grouping category, bulls were ranked in descending sequence on the basis of their pedigree estimate of transmitting ability. Then each ranking was divided into genetic groups. The designation of genetic groups is at least partly subjective in that meaningful groups are designated on the basis of the number of bulls that would fall in each group and their range of pedigree estimates. The group averages used in the fall 1975 Sire Summary run are shown in table 2.

Finally, the group averages are calculated from the Modified Contemporary Deviations of the bulls that are in each group. There is an important difference between the information used to place the bulls in pedigree groups and that used to calculate the group averages. Note that pedigree information is used to place the bulls in the appropriate genetic group, but progeny information is used to calculate the averages of these genetic groups.

In step 21, each bull's Modified Contemporary Deviation is regressed to that bull's genetic group average resulting in PD milk and fat according to the equation:

PD = Genetic Group Average + R (Bull's Modified Contemporary
Deviation - Genetic Group Average)

The final step (22) in the production of the Sire Summaries is to produce the various listings and magnetic tapes that are sent to the dairy industry. This step includes the calculation of PD fat percent and PD dollars.

As soon as the Sire Summaries are completed the Cow Index system is run. This is a relatively simple operation because most of the laborious calculations required for Cow Indexing were accomplished during the Sire Summary run. The basic information on cows was obtained from step 12, indicated by point Ⓒ (fig. 1). Details of the Cow Indexing procedure are given in the next section, The USDA-DHIA Modified Contemporary Comparison Cow Index. The Cow Index values are calculated in step 23. Finally, the Cow Index output (tapes and listings) are produced for the industry (step 24).

Table 2.--Genetic group averages for given pedigree index (PI) ranges of bulls with both father and maternal grandfather PD's

Milk PI range	Number of bulls	Genetic group average Milk	Genetic group average Fat
	AYRSHIRE		
601+	96	+483	+16
501 to 600	44	+306	+14
301 to 500	71	+348	+10
201 to 300	87	+113	+3
101 to 200	140	-111	-4
51 to 100	115	-137	-2
1 to 50	124	-183	-7
-49 to 0	142	-94	-7
-99 to -50	135	-284	-9
-199 to -100	265	-406	-15
-299 to -200	199	-451	-16
≤ to -300	205	-551	-18
	GUERNSEY		
501+	98	+394	+17
451 to 500	98	+200	+7
401 to 450	83	+393	+16
351 to 400	125	+242	+6
301 to 350	207	+158	+3
251 to 300	359	+95	0
201 to 250	476	+111	+3
151 to 200	645	+87	+1
101 to 150	863	-1	-1
51 to 100	939	-67	-2
1 to 50	905	-112	-5
-49 to 0	852	-119	-4
-99 to -50	791	-200	-6
-149 to -100	740	-273	-10
-199 to -150	553	-263	-9
-249 to -200	381	-361	-13
-299 to -250	286	-399	-13
-349 to -300	203	-413	-13
-399 to -350	150	-382	-14
≤ to -400	156	-511	-16
	HOLSTEIN		
701+	329	+489	+10
651 to 700	185	+358	+9
601 to 650	289	+466	+12
551 to 600	342	+330	+6

Table 2.--Genetic group averages for given pedigree index (PI) ranges of bulls with both father and maternal grandfather PD's

Milk PI range	Number of bulls	Genetic group average Milk	Fat
		HOLSTEIN - Continued	
501 to 550	439	+319	+6
451 to 500	517	+193	+3
401 to 450	673	+359	+8
351 to 400	947	+185	+2
301 to 350	1034	+170	+2
251 to 300	1273	+81	0
201 to 250	1595	+47	-2
151 to 200	1884	-23	-3
101 to 150	2147	-73	-6
51 to 100	2160	-85	-5
1 to 50	2405	-144	-7
-49 to 0	2551	-190	-8
-99 to -50	2516	-203	-8
-149 to -100	2583	-285	-11
-199 to -150	2487	-310	-12
-249 to -200	2531	-398	-14
-299 to -250	2228	-449	-15
-349 to -300	1855	-474	-16
-399 to -350	1580	-546	-17
-449 to -400	1259	-563	-19
-499 to -450	914	-579	-20
-549 to -500	757	-704	-22
-599 to -550	530	-715	-23
-649 to -600	413	-770	-25
-699 to -650	301	-837	-25
≤ to -700	764	-932	-26
	JERSEY		
501+	166	+685	+24
451 to 500	92	+657	+23
401 to 450	138	+433	+19
351 to 400	205	+316	+11
301 to 350	225	+167	+7
251 to 300	203	+182	+7
201 to 250	307	+137	+6
151 to 200	302	+149	+5
101 to 150	353	+12	0
51 to 100	368	+3	0
1 to 50	421	-71	-4
-49 to 0	489	-198	-8
-99 to -50	485	-263	-10
-149 to -100	484	-304	-13

Table 2.--Genetic group averages for given pedigree index (PI) ranges of bulls with both father and maternal grandfather PD's

Milk PI range	Number of bulls	Genetic group average	
		Milk	Fat
	JERSEY - Continued		
-199 to -150	466	-359	-15
-249 to -200	376	-401	-17
-299 to -250	331	-402	-16
-349 to -300	243	-541	-25
-399 to -350	187	-621	-25
≤ to -400	366	-756	-33
	BROWN SWISS		
401+	110	+459	+15
301 to 400	75	+446	+15
251 to 300	38	+292	+6
201 to 250	89	+197	+4
151 to 200	120	+109	0
101 to 150	109	+46	+1
51 to 100	153	+148	+3
1 to 50	181	-61	-2
-49 to 0	168	-137	-1
-99 to -50	184	-253	-6
-149 to -100	195	-190	-5
-199 to -150	178	-186	-8
-249 to -200	114	-352	-13
-299 to -250	79	-558	-19
-349 to -300	59	-472	-13
-449 to -350	95	-289	-9
≤ to -450	66	-472	-15
	MILKING SHORTHORN		
51+	108	+151	+3
-99 to 50	96	+59	+1
≤ to -100	97	-242	-7

THE USDA-DHIA MODIFIED CONTEMPORARY COMPARISON COW INDEX

R. L. Powell, H. D. Normán, and F. N. Dickinson, respectively, research geneticist (animal), research scientist (genetics), and chief, Animal Improvement Programs Laboratory, Animal Physiology and Genetics Institute, Northeastern Region, Agricultural Research Service

The Modified Contemporary Comparison is now used to produce Cow Indexes. As with Predicted Difference (PD) for sires, the new procedures result in more accurate estimates of genetic merit, but the interpretation remains the same. The major changes from the Herdmate Comparison Cow Indexing procedure are for the cow's deviated production and the weighting for the amount of information in that deviation. Previously, merit of sires of herdmates was considered only in an approximate manner. Now the merit of each sire of a herdmate is considered in the cow's Modified Contemporary Deviation.

The Cow Index results from combining the individual cow's production with the information on her sire by Selection Index weights. First, let us consider a theoretical approach to determine weights for the Selection Index on the cow that will be used to combine the mean deviated production of the n_1 records of the cow ($\overline{X}_1$) and n_2 paternal half sisters ($\overline{X}_2$). These weights maximize the correlation between the cow's additive genotype, G, and the index, I, where $I = b_1\overline{X}_1 + b_2\overline{X}_2$. The two equations that must be solved simultaneously are:

$$b_1 \ V(\overline{X}_1) + b_2 \ Cov(\overline{X}_1,\overline{X}_2) = Cov(\overline{X}_1,G), \text{ and}$$

$$b_1 \ Cov(\overline{X}_1,\overline{X}_2) + b_2 \ V(\overline{X}_2) = Cov(\overline{X}_2,G).$$

Values for the variances (V) and covariances (Cov) are as follows:

$$V(\overline{X}_1) = V(X) \ \frac{1 + (n_1-1)r}{n_1}; \ V(\overline{X}_2) = V(X) \ \frac{4 + (n_2-1) \ h^2}{4n_2};$$

$$Cov(\overline{X}_1,\overline{X}_2) = 1/4 \ V(G); \ Cov(\overline{X}_1,G) = V(G); \text{ and } Cov(\overline{X}_2,G) = 1/4 \ V(G),$$

where,

h^2 = heritability (0.20), or V(G)/V(X),

r = within-sire repeatability of records (0.50),

V(X) = phenotypic variance of individual records, and

V(G) = additive genetic variance.

The means, variances, and covariances are based on a number of assumptions. All means are assumed to be deviations from a common base. All records are complete, and each paternal half sister is in a different herd and has only one record. Further, each record is assumed to be deviated from a mean containing an infinite number of herdmates. These assumptions are not met in practice, but the effects of discrepancies are minimized if n_1, n_2, $\overline{X}_1$, and $\overline{X}_2$ are defined as follows:

n_1 = sum of lactation weights/2, or ΣLACWT/2,

n_2 = 19R/(1-R), where R = Repeatability of sire's PD,

$\overline{X}_1$ = Cow's $\overline{\text{MCD}}$', and

$\overline{X}_2$ = PD/R.

The prime (') on the abbreviation for the cow's Modified Contemporary Deviation (cow's $\overline{\text{MCD}}$') is to indicate a difference from the cow's Modified Contemporary Deviation used in calculating the Sire Summary. The latter includes merit of sires of Modified Contemporaries as the average $\overline{\text{MCD}}$ of those sires. For Cow Index purposes, cow's $\overline{\text{MCD}}$' considers the $\overline{\text{MCD}}$ of those sires times their average R.

After substituting the above variances and covariances into the selection index equations and dividing each equation by V(G), we have

$$b_1 \frac{1 + (n_1 - 1)r}{n_1 h^2} + \frac{b_2}{4} = 1, \text{ and}$$

$$\frac{b_1}{4} + b_2 \frac{4 + (n_2 - 1)h^2}{4 n_2 h^2} = 1/4 .$$

This is equivalent to the simpler form:

$$\frac{b_1}{A} + \frac{b_2}{4} = 1$$

$$\frac{b_1}{4} + \frac{b_2}{4R} = 1/4$$

where,

$$A = \frac{h^2}{0.5 + 1/\Sigma \text{LACWT}} .$$

Then,

$$b_1 = \frac{4A-AR}{4-AR} \text{ and } b_2 = \frac{4R(1-A)}{4-AR} \quad .$$

The solutions for b_1 and b_2 provide the Selection Index weights for $\overline{X}_1$ and $\overline{X}_2$. However, since $\overline{X}_2$ is calculated from PD, it is easier to use PD directly in the index. Hence, $I = w_1\overline{X}_1 + w_2$ PD, where $w_1 = b_1$ and $w_2 = b_2/R$. It can be shown that $w_2 = 1-w_1$ so $I = w\overline{X}_1 + (1-w)$ PD, where w_1 is replaced by w. The breeding value of the cow is estimated by I, so the estimated transmitting ability is I/2, and the CI equation is:

$$CI = 1/2\ [w(\text{Cow's } \overline{MCD}') + (1-w) \text{ Sire's PD}].$$

Values for w in various situations are given in table 1. To simplify use of the table, the amount of information available on the cow is given as the approximate number of records as well as the sum of her lactation weights.

The reliability of the Cow Index is a function of the amount of information available on a cow and her paternal half sisters. The reliability is expressed in terms of percent Repeatability (R'), the same terminology that is used for the reliability of PD values on bulls. Note that R' refers to the cow's CI and R refers to the sire's PD. Example R' values are given in table 2. The values were obtained from the equation $w + R(1-w)/4$ which is equivalent to $b_1 + b_2/4$.

The Repeatability of the Cow Index reflects the information on both the cow and her sire. This is in contrast to the procedure for the Sire Summary, where the R is calculated only from the amount of information on daughters with no consideration of the added information from the Genetic Group Average. Therefore, while R is the correct value for use in the PD formula, it is an underestimate of the reliability of the PD. The exact reliability is unknown. Because the R used in calculating w is less than it should be, slightly too much weight is given to the cow's $\overline{MCD}'$ at the expense of the PD on her sire. Also, this causes a very slight depression in the R'. Repeatabilities for Cow Indexes are much lower than can be obtained for a sire's PD. Therefore, less confidence should be placed in an individual CI, especially with low R', than for most PD's.

The general form of the Cow Index formula is parallel to that for PD. In both cases, an average Modified Contemporary Deviation is combined with an estimate of merit from the pedigree. The "pedigree" estimate for a bull is the Genetic Group Average while for a cow it is one-half the PD of her sire. This similarity resulted from the inclusion of information from a second source for calculating PD as has been done in the Cow Index since its beginning.

A definite improvement in the new Cow Index procedure is its timeliness. Records-in-progress of 40 days or more are included in calculations of CI's for registered cows provided to the breed associations. Of these, the highest indexing cows that are likely to be alive are included in the Cow Index List. For single-lactation cows, only those with at least 150 days in milk are eligible for consideration. Most of these Cow Indexes will be available for use in planning matings one lactation earlier than had previously been possible.

An important contribution can be made to the genetic improvement of yield and income in a herd if effective selection of cows is continually made. Cow Indexes should always be considered if they are available, because they provide a more accurate estimate of the genetic transmitting ability of a cow than her own production or even her herdmate deviation.

TABLE 1.--WEIGHTS (W) FOR THE PERFORMANCE OF THE COW AS A FUNCTION OF THE SUM OF HER LACTATION WEIGHTS AND THE REPEATABILITY OF THE SUMMARY ON HER SIRE

APPROX. NO. OF RECORDS	SUM OF LACTATION WEIGHTS	PERCENT REPEATABILITY OF SIRE SUMMARY							
		20	30	40	50	60	70	80	90
	1.0	0.13	0.12	0.12	0.12	0.12	0.11	0.11	0.11
	1.1	.14	.13	.13	.13	.12	.12	.12	.11
	1.2	.14	.14	.14	.13	.13	.13	.12	.12
	1.3	.15	.15	.14	.14	.14	.13	.13	.13
	1.4	.16	.15	.15	.15	.14	.14	.14	.13
	1.5	.16	.16	.16	.15	.15	.15	.14	.14
	1.6	.17	.17	.16	.16	.16	.15	.15	.14
1	1.7	.18	.17	.17	.16	.16	.16	.15	.15
	1.8	.18	.18	.17	.17	.17	.16	.16	.15
	1.9	.19	.18	.18	.17	.17	.17	.16	.16
	2.0	.19	.19	.18	.18	.18	.17	.17	.16
	2.1	.20	.19	.19	.18	.18	.18	.17	.17
	2.2	.20	.20	.19	.19	.18	.18	.17	.17
	2.3	.21	.20	.20	.19	.19	.18	.18	.17
	2.4	.21	.21	.20	.20	.19	.19	.18	.18
	2.5	.21	.21	.20	.20	.20	.19	.19	.18
	2.6	.22	.21	.21	.20	.20	.19	.19	.18
	2.7	.22	.22	.21	.21	.20	.20	.19	.19
	2.8	.22	.22	.22	.21	.21	.20	.20	.19
	2.9	.23	.22	.22	.21	.21	.20	.20	.19
	3.0	.23	.23	.22	.22	.21	.21	.20	.20
2	3.5	.24	.24	.24	.23	.22	.22	.21	.21
	4.0	.26	.25	.25	.24	.24	.23	.23	.22
	4.5	.27	.26	.26	.25	.25	.24	.23	.23
3	5.0	.28	.27	.26	.26	.25	.25	.24	.24
	5.5	.28	.28	.27	.27	.26	.26	.25	.24
	6.0	.29	.28	.28	.27	.27	.26	.26	.25
	6.5	.30	.29	.28	.28	.27	.27	.26	.25
4	7.0	.30	.29	.29	.28	.28	.27	.27	.26
	7.5	.30	.30	.29	.29	.28	.28	.27	.26
	8.0	.31	.30	.30	.29	.29	.28	.27	.27
5	8.5	.31	.31	.30	.30	.29	.28	.28	.27
	9.0	.32	.31	.30	.30	.29	.29	.28	.27
	9.5	.32	.31	.31	.30	.30	.29	.28	.28
6	10.0	.32	.32	.31	.30	.30	.29	.29	.28
	10.5	.32	.32	.31	.31	.30	.29	.29	.28
	11.0	.33	.32	.32	.31	.30	.30	.29	.28
	11.5	.33	.32	.32	.31	.31	.30	.29	.29
7	12.0	.33	.33	.32	.31	.31	.30	.29	.29

TABLE 2.--PERCENT REPEATABILITY OF THE COW INDEX ACCORDING TO THE SUM OF HER LACTATION WEIGHTS AND THE REPEATABILITY OF THE SUMMARY ON HER SIRE

APPROX. NO. OF RECORDS	SUM OF LACTATION WEIGHTS	PERCENT REPEATABILITY OF SIRE SUMMARY							
		20	30	40	50	60	70	80	90
	1.0	17	19	21	23	25	27	29	31
	1.1	18	20	22	24	25	27	29	31
	1.2	19	20	22	24	26	28	30	32
	1.3	19	21	23	25	27	29	30	32
	1.4	20	22	24	25	27	29	31	33
	1.5	21	22	24	26	28	30	31	33
	1.6	21	23	25	26	28	30	32	34
1	1.7	22	23	25	27	29	30	32	34
	1.8	22	24	26	27	29	31	33	34
	1.9	23	24	26	28	30	31	33	35
	2.0	23	25	27	28	30	32	33	35
	2.1	24	25	27	29	30	32	34	35
	2.2	24	26	27	29	31	32	34	36
	2.3	25	26	28	29	31	33	34	36
	2.4	25	26	28	30	31	33	35	36
	2.5	25	27	28	30	32	33	35	37
	2.6	26	27	29	30	32	34	35	37
	2.7	26	28	29	31	32	34	35	37
	2.8	26	28	29	31	32	34	36	37
	2.9	27	28	30	31	33	34	36	38
	3.0	27	28	30	31	33	35	36	38
2	3.5	28	30	31	33	34	36	37	39
	4.0	29	31	32	34	35	37	38	40
	4.5	30	32	33	34	36	37	39	40
3	5.0	31	32	34	35	37	38	39	41
	5.5	32	33	34	36	37	39	40	41
	6.0	32	34	35	36	38	39	40	42
	6.5	33	34	36	37	38	39	41	42
4	7.0	34	35	36	37	39	40	41	43
	7.5	34	35	36	38	39	40	42	43
	8.0	34	36	37	38	39	41	42	43
5	8.5	35	36	37	38	40	41	42	43
	9.0	35	36	37	39	40	41	42	44
	9.5	35	36	38	39	40	41	43	44
6	10.0	36	37	38	39	40	42	43	44
	10.5	36	37	38	39	41	42	43	44
	11.0	36	37	38	40	41	42	43	45
	11.5	36	37	39	40	41	42	43	45
7	12.0	36	38	39	40	41	42	44	45

PROCEDURES FOR APPROXIMATING COMPONENTS OF PREDICTED DIFFERENCE

R. L. Powell, and H. D. Norman, research geneticist (animal) and research scientist (genetics), Animal Improvement Programs Laboratory, Animal Physiology and Genetics Institute, Northeastern Region, Agricultural Research Service

The increase in accuracy of sire evaluation by the Modified Contemporary Comparison was accompanied by an increase in the complexity of calculation. Therefore, the approximation of Predicted Difference (PD) is of great importance to many segments of the dairy industry. Some approximation procedures will be presented for components of the PD equation,

$$PD = R(\overline{MCD}) + (1-R)GA,$$

where PD is Predicted Difference, R is Repeatability, $\overline{MCD}$ is the bull's Modified Contemporary Deviation, and GA is the Genetic Group Average.

Estimation of Predicted Difference

The formulas and tables allow accurate approximation of Repeatability. The estimation of the GA is not as accurate but is sufficient for the purpose. The remaining element, the average MCD is the major impediment to accurate estimation of PD. That estimation necessitates age and length adjustments for daughter and contemporary records, estimation of merit of sires of contemporaries, and may involve pooling information across herds. Those operations are not only laborious but also may result in less than desirable accuracy. Considerable caution should be exercised in the use of approximated PD's. R's, however, can be estimated accurately. A section is presented on the relative importance of pedigree data. Although that information is not needed for estimating PD, the explanation enhances the understanding of PD by relating the emphasis on GA to that for $\overline{MCD}$.

Repeatability

A common question concerning the Modified Contemporary Comparison is how one can approximate Repeatability. While it is not feasible to provide R's for all situations, the following equations are presented for two representative cases.

If all daughters are in one herd:

$$R \simeq \frac{N}{3.8N + 18}$$

where R is Repeatability and N is the number of daughters.

If each daughter is in a different herd:

$$R \simeq \frac{N}{N + 20.8}.$$

Thus, 20 daughters in one herd would be expected to result in an R of about 21 percent. If each was in a different herd, the expected R would be about 49 percent.

These approximation formulas result from the following assumptions:

(1) Each daughter has one 305-day record.

(2) Each daughter has 15 Modified Contemporaries with 305-day records.

(3) Five sires of the Modified Contemporaries have an average Repeatability of 70 percent.

These approximations are close to correct even for substantial deviations from the assumptions. For example, in the one herd case, assume only seven Modified Contemporaries are by three sires and each daughter and contemporary has 7 months of production. The correct R is still 21 percent. If daughters are distributed one per herd, the correct R is 47 percent. Therefore, while the exact formulas are needed to properly weight each production deviation, one can easily estimate the R in these two situations of most interest.

For some other situations, a more general formula may be used. It is assumed that each of N daughters has the same sum of lactation weights (ΣLACWT) and that there are H herds each having N/H daughters. For each record the lactation weight is:

$$\text{LACWT} = \frac{1}{\dfrac{0.50}{\text{Length wt.}} + \dfrac{0.05(1\text{-MCSR})+0.14}{\text{No. Mod.Cont.Sires}} + \dfrac{0.81}{\Sigma\text{Length wts of Mod.Cont}}}$$

where $\overline{\text{MCSR}}$ is the average R for sires of the Modified Contemporaries. The length weights are the phenotypic correlations between part and whole lactations. They are in the introductory material to the Sire Summary List and in the third paper of this series.

Then,

$$R \simeq \frac{N}{N + \dfrac{2.8N}{H} + 6.2 + \dfrac{20}{\Sigma\text{LACWT}}}.$$

If our initial example is modified so that each of five herds has four daughters, R = 41 percent. (The ΣLACWT is 1.709).

The calculations needed for approximating R can be reduced or eliminated through the use of tables 1 to 17. Lactation weights for selected average contemporary sire R's are presented in tables 1 to 7. All lactations are assumed to be complete (305 days) and, therefore, all length weights are 1.0. The arguments for entering the tables are the number of Modified Contemporaries and the number of their sires. For example, assume a first lactation cow has 11 first lactation contemporaries by 4 sires having an average Repeatability of 80 percent and at least one second or later lactation herdmate whose sire's average Repeatability is 80 percent. There are 12 Modified Contemporaries by five sires so the lactation weight is 1.674. Table 6 is used because the average R for Modified Contemporary sires is 80 percent. If the herdmates each have a length weight of 0.94, the number of Modified Contemporaries would be used as 11, 12 x 0.94.

Tables 8 to 17 provide R for various sums of lacation weights per daughter and number of herds across which the daughters are equally distributed. If each of 50 daughters has a sum of lactation weights of 1.664, we enter table 12 with 1.7. The daughters are in 25 herds (2 per herd) so the R is 68 percent. If each daughter has a second lactation with a lactation weight of 1.854, the sum of lactation weights is 3.518 and 3.5 is used to enter table 12. The R is 74 percent.

These tables will be most useful for approximating R for use in planning sire sampling programs. For actual situations where the distribution of daughters is not approximately equal across herds, a more complex procedure for approximating R is presented as a sidelight of the next section.

Modified Contemporary Deviation

The logical situation for approximating a PD is for young bulls so let us assume each daughter has only a first record. The bull's Modified Contemporary Deviation ($\overline{MCD}$) is a weighted average of daughter MCD's or D - MCA + SMC. The daughter record (D) has been adjusted to a 2X-305 day - ME basis, as have the records of herdmates used in the Modified Contemporary Average (MCA). The MCA is approximately the contemporary average so it can be taken as the average of first lactation herdmates. A herdmate is a cow calving in the same 5 month rolling season as the daughter and sired by another bull. The estimate of genetic merit of sires of Modified Contemporaries (SMC) is the average Modified Contemporary Deviation for those sires. This can be approximated by the average PD of the sires of contemporaries.

The individual daughter MCD's can be averaged for the herd, forming a herd deviation value. To estimate the bull's MCD, one must combine these herd values across herds if daughters are in more than one herd. The herd deviations are weighted by herd weights (HRDWT). A herd weight can be approximated by

$$\text{HRDWT} \simeq \frac{N}{0.14\,N + 0.9}$$

where N is the number of daughters in that herd. For example, herd A has 17 daughters with an average MCD of +1,000. Herd B has 3 daughters with an average MCD of +400. Without considering the distribution across herds, the average deviation is +910. However, the approximate herd weights are 5.2 and 2.3 so the bull's MCD is actually

$$\frac{(5.2 \times 1000) + (2.3 \times 400)}{5.2 + 2.3} = +816,$$

almost 100 pounds below the unweighted average. The sum of the herd weights, in this case 7.5, can also be used to approximate R because

$$R = \frac{0.05}{0.05 + 1/\Sigma\text{HRDWT}}$$

In this case the approximate R is 27 percent. This is a more appropriate method to estimate R than that given in the previous section when daughters are not evenly distributed across herds.

Genetic Group Average

The Genetic Group Average (GA) is the average performance (Modified Contemporary Deviation) of bulls having a similar production pedigree. Bulls are grouped based on pedigree index (PI) for milk where,

PI = 1/2 father's PD + 1/4 maternal grandfather's PD.

The GA can be estimated reasonably well by PI minus 150 pounds for milk and 0.8 x PI minus 7 pounds for fat. In general terms,

$$\widehat{GA} = \alpha + b\ PI$$

where $\widehat{GA}$ is the approximate Genetic Group Average, $\underline{\alpha}$ is the y-intercept, and $\underline{b}$ is the regression of GA on PI. Some actual values are given in table 18.

Weights for Pedigree Information

The predictive quality of any equation improves as more variables are included. The degree of improvement and the weight going to an added variable depend on the relationships of that variable with the other variables and with that which is being predicted. These statements apply to any set of data. We will consider them as they relate to predicting genetic merit of a bull.

The accuracy of predicting individual merit can be improved by using information on ancestors. This information is used in part by the Modified Contemporary Comparison. This section deals with the weight or emphasis going to the pedigree versus that going to daughter performance.

Consider the formula for the new PD,

$$PD = R(\overline{MCD}) + (1-R)GA$$

where R is Repeatability, $\overline{MCD}$ is the average Modified Contemporary Deviation for a bull's daughters, and GA is the Genetic Group Average. When R is very low, say 20 percent, or 0.2, the weight for the GA is large, 0.8. It is tempting to say that the pedigree is getting four times the weight of the daughter performance. But that is an unwarranted comparison of variables not on the same scale. We must consider that GA is a function of $\overline{MCD}$'s that have been halved, quartered, and regressed. To compare the emphasis or weight going to daughters and that for daughters of various male ancestors, let's use $\overline{MCD}$ as the standard unit of measurement. Then weights for any animal will be the weight going to that animal's $\overline{MCD}$. To simplify the explanation, letters are used in figure 1 to identify the males in the pedigree of the bull being evaluated, A. Animals further removed are assumed to have no influence.

Let us assume that we can replace the GA with the PI. It is emphasized that this is not the way GA is calculated but the relationship between GA and PI is very high. Then an approximate equation for PD for bull A in figure 1 is

$$PD \simeq R_A\ (\overline{MCD_A}) + (1-R_A)(1/2\ PD_B + 1/4\ PD_D).$$

Then, further replace the ancestral PD's with their components, $\overline{MCD}$, PI, and R. Continue until the PD approximation is a function of only $\overline{MCD}$'s and R's as in figure 2. The weights going to information from various ancestors are in table 19 with examples.

The weight (Wt) for the $\overline{MCD}$ of any bull, say bull X, can be represented as

$$Wt_X = R_X\ (1/2)^n\ \Pi_i(1-R_i)$$

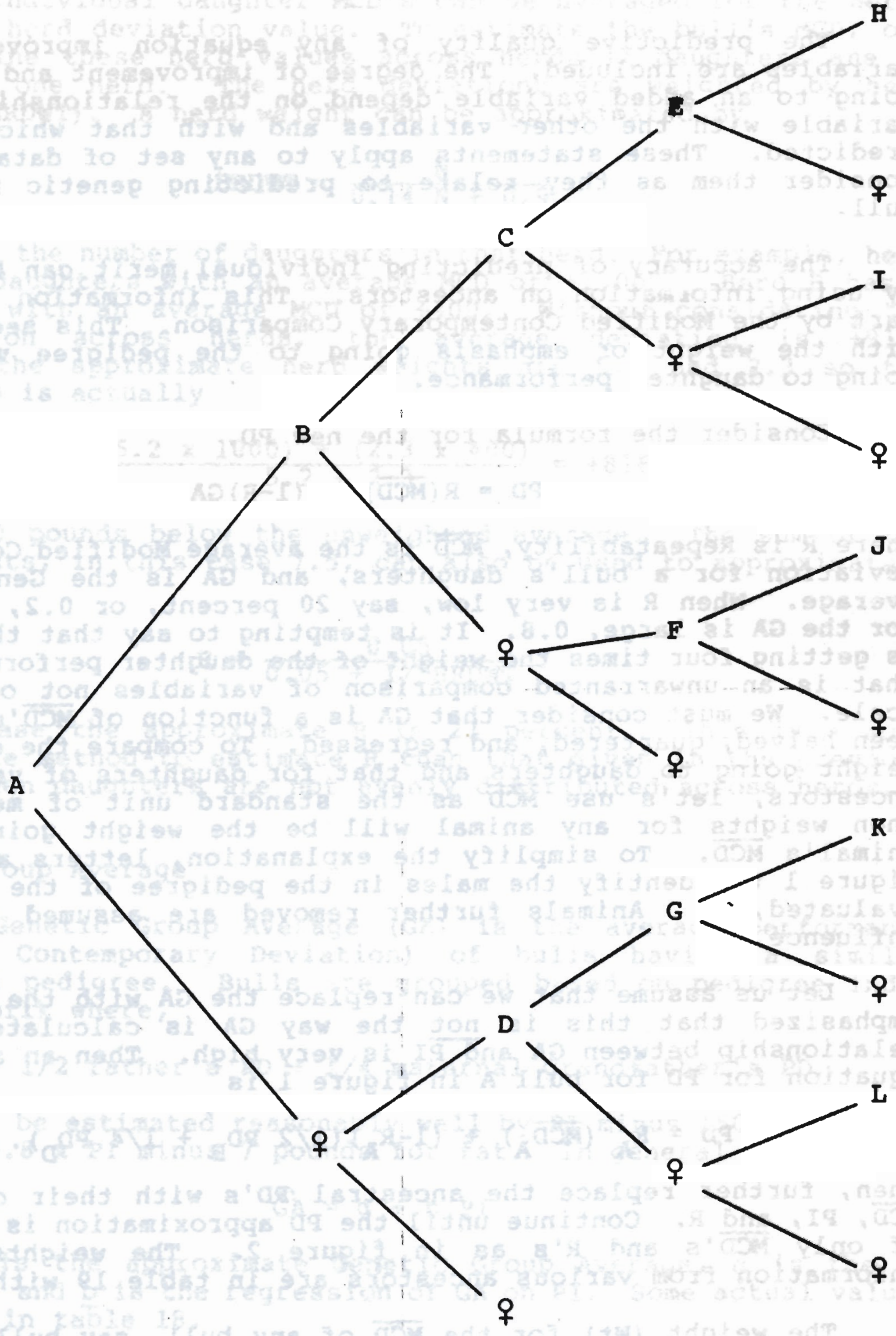

Figure 1.--Pedigree diagram with letters denoting males. (Consecutive females terminate path.)

$$
\begin{aligned}
PD \simeq R_A(\overline{MCD}_A) &+ (1-R_A)(1/2)(R_B)(\overline{MCD}_B) \\
&+ (1-R_A)(1/4)(1-R_B)(R_C)(\overline{MCD}_C) \\
&+ (1-R_A)(1/8)(1-R_B)(1-R_C)(R_E)(\overline{MCD}_E) \\
&+ (1-R_A)(1/16)(1-R_B)(1-R_C)(1-R_E)(R_H)(\overline{MCD}_H) \\
&+ (1-R_A)(1/16)(1-R_B)(1-R_C)(R_I)(\overline{MCD}_I) \\
&+ (1-R_A)(1/8)(1-R_B)(R_F)(\overline{MCD}_F) \\
&+ (1-R_A)(1/16)(1-R_B)(1-R_F)(R_J)(\overline{MCD}_J) \\
&+ (1-R_A)(1/4)(R_D)(\overline{MCD}_D) \\
&+ (1-R_A)(1/8)(1-R_D)(R_G)(\overline{MCD}_G) \\
&+ (1-R_A)(1/16)(1-R_D)(1-R_G)(R_K)(\overline{MCD}_K) \\
&+ (1-R_A)(1/16)(1-R_D)(R_L)(\overline{MCD}_L)
\end{aligned}
$$

Figure 2.--PD formula modified to show approximate weights for the $\overline{MCD}$ by daughters of the subject and the males in a four generation pedigree.

where, n is the number of generations (or genetic segregations) between X and A, and i is the identifying letter for each male in the path from X through A. For example, the Wt_F is $R_F(1/2)^3(1-R_A)(1-R_B)$. For bull H, the weight is $R_H(1/2)^4(1-R_A)(1-R_B)(1-R_C)(1-R_E)$. When R_A is above 0.33, $\overline{MCD}_A$ receives more weight than the $\overline{MCD}$ for any other animal in the pedigree, even if the father's R is 99 percent. When R_A is above 0.43, $\overline{MCD}_A$ receives more weight than for the combined $\overline{MCD}$'s for the father and maternal grandfather even if both ancestors have R's of 99 percent.

The weights in table 19 are approximations of weights that may be applied to individual bull $\overline{MCD}$'s to approximate a PD. However, they do not consider differences in the variability of the various $\overline{MCD}$'s. The approximate relative weight of progeny information to that for progeny of ancestors in determination of PD is in table 20. The weights from formulas in table 19 have been standardized to relative weights by multiplying by the expected standard deviation of the corresponding $\overline{MCD}$. That standard deviation is $\sqrt{1/4R}$. From table 19 we find weights of 0.20, 0.28, and 0.14 for R's of 0.2 on the bull and 0.7 on both father and maternal grandfather. The standardized weights are 0.2236, 0.1673, and 0.0837. Then the approximate ratio of weight for progeny of the bull to progeny of the two ancestors is 47:53 as seen in table 20. This table places the concern over weights going to the pedigree in proper perspective. Certainly the ancestor's weights are far from overwhelming.

If all of the pedigree influence were from the father and maternal grandfather, it would be easy to calculate the accuracy of prediction squared for varying amounts of information on those two ancestors. By using that squared correlation as R, the approximate number of daughters for that R can be calculated. Table 21 contains the results of such estimation of the comparable number of daughters, each with one complete record and in a separate herd. The value of sire information alone is in the column under zero and the value of the maternal grandfather alone is in the top row.

Three points need to be made concerning these weights for ancestors relative to information on the bull's own daughters.

(1) The pedigree information can be very important for low R_A, depending on the R's for relatives, but its importance decreases rapidly as R_A increases.

(2) If the R for any animal is increased, the weights for animals further removed along that branch are decreased. So if R_A is high, little will be gained from ancestral data. If R_D is high, G, K, and L can be ignored with

little loss. In practice, if any ancestor is not summarized then the weights for him and his ancestors are zero.

(3) The weights are different for each situation. Cases differ by which ancestors have summaries and their individual R's as well as that of the subject. While exact relative weights are different for each situation, tables 19 through 21 provide approximate values that place the emphasis going to ancestors in proper perspective.

The procedures presented for approximating components of PD or emphasis on ancestors are applicable for most cases. Their proper use can be very beneficial. Certainly, there will be situations where these estimates are misleading. Users should recognize the existence of such exceptions and exercise considerable caution in decisions based on approximations.

TABLE 1.--LACTATION WEIGHTS FOR RECORDS HAVING VARYING NUMBERS OF MODIFIED CONTEMPORARIES (MOD CONT) BY VARYING NUMBERS OF SIRES WITH AN AVERAGE REPEATABILITY OF 30%

NO. OF MOD CONT	AVERAGE NUMBER OF SIRES OF MODIFIED CONTEMPORARIES							
	1	2	3	5	10	15	20	30
1	0.673							
2	0.926	1.008						
3	1.058	1.166	1.207					
4	1.140	1.266	1.314					
5	1.195	1.334	1.388	1.435				
6	1.235	1.384	1.442	1.493				
7	1.265	1.422	1.484	1.537				
8	1.288	1.452	1.516	1.572				
9	1.307	1.476	1.542	1.600				
10	1.323	1.496	1.564	1.623	1.671			
11	1.336	1.513	1.582	1.643	1.692			
12	1.347	1.527	1.598	1.660	1.709			
13	1.356	1.539	1.611	1.674	1.725			
14	1.365	1.550	1.623	1.687	1.738			
15	1.372	1.559	1.633	1.698	1.750	1.768		
16	1.378	1.567	1.642	1.708	1.760	1.778		
17	1.384	1.574	1.650	1.716	1.769	1.788		
18	1.389	1.581	1.657	1.724	1.778	1.796		
19	1.393	1.587	1.664	1.731	1.785	1.804		
20	1.398	1.592	1.670	1.738	1.792	1.811	1.821	
21	1.401	1.597	1.675	1.743	1.798	1.817	1.827	
22	1.405	1.602	1.680	1.749	1.804	1.823	1.833	
23	1.408	1.606	1.685	1.754	1.809	1.829	1.838	
24	1.411	1.610	1.689	1.758	1.814	1.833	1.843	
25	1.414	1.613	1.693	1.762	1.819	1.838	1.848	
26	1.416	1.616	1.696	1.766	1.823	1.842	1.852	
27	1.418	1.619	1.700	1.770	1.826	1.846	1.856	
28	1.421	1.622	1.703	1.773	1.830	1.850	1.860	
29	1.423	1.625	1.706	1.776	1.833	1.853	1.863	
30	1.425	1.627	1.708	1.779	1.837	1.856	1.867	1.877
35	1.432	1.638	1.720	1.792	1.850	1.870	1.880	1.890
40	1.438	1.645	1.728	1.801	1.860	1.880	1.890	1.901
50	1.447	1.656	1.741	1.814	1.874	1.894	1.905	1.916
80	1.460	1.673	1.759	1.834	1.895	1.916	1.927	1.938
100	1.464	1.679	1.765	1.841	1.903	1.924	1.935	1.946
200	1.473	1.690	1.778	1.855	1.917	1.939	1.950	1.961

TABLE 2.--LACTATION WEIGHTS FOR RECORDS HAVING VARYING NUMBERS OF MODIFIED CONTEMPORARIES (MOD CONT) BY VARYING NUMBERS OF SIRES WITH AN AVERAGE REPEATABILITY OF 40%

NO. OF MOD CONT	AVERAGE NUMBER OF SIRES OF MODIFIED CONTEMPORARIES							
	1	2	3	5	10	15	20	30
1	0.676							
2	0.930	1.010						
3	1.064	1.170	1.210					
4	1.146	1.270	1.317					
5	1.202	1.339	1.391	1.437				
6	1.242	1.389	1.446	1.495				
7	1.273	1.427	1.487	1.539				
8	1.297	1.457	1.520	1.574				
9	1.316	1.481	1.546	1.603				
10	1.332	1.502	1.568	1.626	1.672			
11	1.345	1.518	1.587	1.646	1.693			
12	1.356	1.533	1.602	1.663	1.711			
13	1.366	1.545	1.616	1.677	1.726			
14	1.374	1.556	1.627	1.690	1.740			
15	1.381	1.565	1.638	1.701	1.751	1.769		
16	1.388	1.573	1.647	1.710	1.762	1.779		
17	1.393	1.581	1.655	1.719	1.771	1.789		
18	1.399	1.587	1.662	1.727	1.779	1.797		
19	1.403	1.593	1.669	1.734	1.787	1.805		
20	1.407	1.599	1.675	1.741	1.794	1.812	1.821	
21	1.411	1.604	1.680	1.747	1.800	1.818	1.828	
22	1.415	1.608	1.685	1.752	1.806	1.824	1.834	
23	1.418	1.612	1.690	1.757	1.811	1.830	1.839	
24	1.421	1.616	1.694	1.761	1.816	1.835	1.844	
25	1.424	1.620	1.698	1.766	1.820	1.839	1.849	
26	1.426	1.623	1.701	1.769	1.824	1.843	1.853	
27	1.429	1.626	1.705	1.773	1.828	1.847	1.857	
28	1.431	1.629	1.708	1.776	1.832	1.851	1.861	
29	1.433	1.632	1.711	1.780	1.835	1.854	1.864	
30	1.435	1.634	1.713	1.783	1.838	1.858	1.867	1.877
35	1.443	1.644	1.725	1.795	1.851	1.871	1.881	1.891
40	1.449	1.652	1.733	1.804	1.861	1.881	1.891	1.901
50	1.457	1.663	1.746	1.818	1.875	1.896	1.906	1.916
80	1.470	1.680	1.764	1.838	1.897	1.918	1.928	1.939
100	1.475	1.686	1.771	1.845	1.904	1.925	1.936	1.946
200	1.484	1.698	1.783	1.859	1.919	1.940	1.951	1.962

TABLE 3.--LACTATION WEIGHTS FOR RECORDS HAVING VARYING NUMBERS OF MODIFIED CONTEMPORARIES (MOD CONT) BY VARYING NUMBERS OF SIRES WITH AN AVERAGE REPEATABILITY OF 50%

NO. OF MOD CONT	AVERAGE NUMBER OF SIRES OF MODIFIED CONTEMPORARIES							
	1	2	3	5	10	15	20	30
1	0.678							
2	0.935	1.013						
3	1.070	1.173	1.212					
4	1.153	1.274	1.320					
5	1.209	1.343	1.395	1.439				
6	1.250	1.394	1.449	1.497				
7	1.281	1.432	1.491	1.542				
8	1.305	1.463	1.524	1.577				
9	1.325	1.487	1.550	1.605				
10	1.340	1.507	1.572	1.629	1.674			
11	1.354	1.524	1.591	1.648	1.695			
12	1.365	1.538	1.606	1.665	1.712			
13	1.375	1.551	1.620	1.680	1.728			
14	1.383	1.562	1.632	1.692	1.741			
15	1.391	1.571	1.642	1.704	1.753	1.770		
16	1.397	1.579	1.651	1.713	1.763	1.781		
17	1.403	1.587	1.659	1.722	1.773	1.790		
18	1.408	1.594	1.667	1.730	1.781	1.799		
19	1.413	1.600	1.673	1.737	1.788	1.806		
20	1.417	1.605	1.679	1.744	1.795	1.813	1.822	
21	1.421	1.610	1.685	1.750	1.802	1.820	1.829	
22	1.425	1.615	1.690	1.755	1.807	1.825	1.835	
23	1.428	1.619	1.694	1.760	1.813	1.831	1.840	
24	1.431	1.623	1.699	1.764	1.817	1.836	1.845	
25	1.434	1.626	1.702	1.769	1.822	1.840	1.850	
26	1.436	1.630	1.706	1.773	1.826	1.844	1.854	
27	1.439	1.633	1.709	1.776	1.830	1.848	1.858	
28	1.441	1.636	1.713	1.780	1.833	1.852	1.862	
29	1.443	1.638	1.715	1.783	1.837	1.856	1.865	
30	1.445	1.641	1.718	1.786	1.840	1.859	1.868	1.878
35	1.453	1.651	1.730	1.798	1.853	1.872	1.882	1.892
40	1.459	1.659	1.738	1.808	1.863	1.882	1.892	1.902
50	1.468	1.670	1.751	1.821	1.877	1.897	1.907	1.917
80	1.481	1.687	1.770	1.841	1.899	1.919	1.929	1.939
100	1.486	1.693	1.776	1.848	1.906	1.926	1.937	1.947
200	1.495	1.705	1.789	1.862	1.921	1.942	1.952	1.963

TABLE 4.--LACTATION WEIGHTS FOR RECORDS HAVING VARYING NUMBERS OF MODIFIED CONTEMPORARIES (MOD CONT) BY VARYING NUMBERS OF SIRES WITH AN AVERAGE REPEATABILITY OF 60%

NO. OF MOD CONT	AVERAGE NUMBER OF SIRES OF MODIFIED CONTEMPORARIES							
	1	2	3	5	10	15	20	30
1	0.680							
2	0.939	1.015						
3	1.075	1.176	1.215					
4	1.159	1.278	1.323					
5	1.217	1.348	1.398	1.441				
6	1.258	1.399	1.453	1.499				
7	1.289	1.437	1.495	1.544				
8	1.314	1.468	1.528	1.579				
9	1.333	1.493	1.554	1.608				
10	1.350	1.513	1.576	1.631	1.675			
11	1.363	1.530	1.595	1.651	1.696			
12	1.375	1.544	1.611	1.668	1.714			
13	1.384	1.557	1.624	1.683	1.729			
14	1.393	1.568	1.636	1.695	1.743			
15	1.401	1.577	1.647	1.706	1.754	1.771		
16	1.407	1.586	1.656	1.716	1.765	1.782		
17	1.413	1.593	1.664	1.725	1.774	1.791		
18	1.418	1.600	1.671	1.733	1.783	1.800		
19	1.423	1.606	1.678	1.740	1.790	1.807		
20	1.428	1.612	1.684	1.747	1.797	1.814	1.823	
21	1.431	1.617	1.689	1.753	1.803	1.821	1.830	
22	1.435	1.621	1.694	1.758	1.809	1.827	1.835	
23	1.438	1.625	1.699	1.763	1.814	1.832	1.841	
24	1.441	1.629	1.703	1.768	1.819	1.837	1.846	
25	1.444	1.633	1.707	1.772	1.823	1.841	1.850	
26	1.447	1.636	1.711	1.776	1.828	1.846	1.855	
27	1.449	1.639	1.714	1.779	1.832	1.850	1.859	
28	1.452	1.642	1.717	1.783	1.835	1.853	1.862	
29	1.454	1.645	1.720	1.786	1.838	1.857	1.866	
30	1.456	1.647	1.723	1.789	1.842	1.860	1.869	1.879
35	1.464	1.658	1.735	1.801	1.855	1.873	1.883	1.892
40	1.470	1.666	1.743	1.811	1.865	1.884	1.893	1.903
50	1.479	1.677	1.756	1.824	1.879	1.898	1.908	1.917
80	1.492	1.695	1.775	1.845	1.901	1.920	1.930	1.940
100	1.497	1.700	1.781	1.852	1.908	1.928	1.938	1.948
200	1.506	1.712	1.794	1.865	1.923	1.943	1.953	1.963

TABLE 5.--LACTATION WEIGHTS FOR RECORDS HAVING VARYING NUMBERS OF MODIFIED CONTEMPORARIES (MOD CONT) BY VARYING NUMBERS OF SIRES WITH AN AVERAGE REPEATABILITY OF 70%

NO. OF MOD CONT	AVERAGE NUMBER OF SIRES OF MODIFIED CONTEMPORARIES							
	1	2	3	5	10	15	20	30
1	0.683							
2	0.943	1.018						
3	1.081	1.180	1.217					
4	1.166	1.282	1.326					
5	1.224	1.352	1.401	1.443				
6	1.266	1.404	1.456	1.502				
7	1.297	1.443	1.498	1.546				
8	1.322	1.473	1.532	1.582				
9	1.342	1.498	1.558	1.610				
10	1.359	1.519	1.581	1.634	1.676			
11	1.372	1.536	1.599	1.654	1.697			
12	1.384	1.550	1.615	1.671	1.715			
13	1.394	1.563	1.629	1.685	1.731			
14	1.403	1.574	1.641	1.698	1.744			
15	1.410	1.584	1.651	1.709	1.756	1.772		
16	1.417	1.592	1.660	1.719	1.766	1.783		
17	1.423	1.600	1.669	1.728	1.776	1.792		
18	1.429	1.606	1.676	1.736	1.784	1.801		
19	1.433	1.613	1.683	1.743	1.792	1.808		
20	1.438	1.618	1.689	1.750	1.799	1.815	1.824	
21	1.442	1.623	1.694	1.756	1.805	1.822	1.830	
22	1.445	1.628	1.699	1.761	1.811	1.828	1.836	
23	1.449	1.632	1.704	1.766	1.816	1.833	1.842	
24	1.452	1.636	1.708	1.771	1.821	1.838	1.847	
25	1.455	1.640	1.712	1.775	1.825	1.843	1.851	
26	1.457	1.643	1.716	1.779	1.829	1.847	1.856	
27	1.460	1.646	1.719	1.783	1.833	1.851	1.860	
28	1.462	1.649	1.722	1.786	1.837	1.854	1.863	
29	1.464	1.652	1.725	1.789	1.840	1.858	1.867	
30	1.466	1.654	1.728	1.792	1.843	1.861	1.870	1.879
35	1.475	1.665	1.740	1.805	1.857	1.874	1.884	1.893
40	1.481	1.673	1.749	1.814	1.867	1.885	1.894	1.903
50	1.490	1.684	1.761	1.827	1.881	1.899	1.909	1.918
80	1.503	1.702	1.780	1.848	1.902	1.921	1.931	1.941
100	1.508	1.708	1.786	1.855	1.910	1.929	1.939	1.948
200	1.517	1.720	1.799	1.869	1.925	1.944	1.954	1.964

TABLE 6.--LACTATION WEIGHTS FOR RECORDS HAVING VARYING NUMBERS OF MODIFIED CONTEMPORARIES (MOD CONT) BY VARYING NUMBERS OF SIRES WITH AN AVERAGE REPEATABILITY OF 80%

NO. OF MOD CONT	AVERAGE NUMBER OF SIRES OF MODIFIED CONTEMPORARIES							
	1	2	3	5	10	15	20	30
1	0.685							
2	0.948	1.020						
3	1.087	1.183	1.220					
4	1.173	1.286	1.329					
5	1.232	1.357	1.404	1.445				
6	1.274	1.408	1.460	1.504				
7	1.306	1.448	1.502	1.549				
8	1.331	1.479	1.536	1.584				
9	1.351	1.504	1.563	1.613				
10	1.368	1.524	1.585	1.637	1.678			
11	1.382	1.542	1.603	1.657	1.699			
12	1.394	1.556	1.619	1.674	1.717			
13	1.404	1.569	1.633	1.688	1.732			
14	1.413	1.580	1.645	1.701	1.746			
15	1.420	1.590	1.656	1.712	1.757	1.773		
16	1.427	1.598	1.665	1.722	1.768	1.784		
17	1.433	1.606	1.673	1.731	1.777	1.793		
18	1.439	1.613	1.681	1.739	1.786	1.802		
19	1.444	1.619	1.687	1.746	1.793	1.810		
20	1.448	1.625	1.693	1.753	1.800	1.817	1.825	
21	1.452	1.630	1.699	1.759	1.806	1.823	1.831	
22	1.456	1.634	1.704	1.764	1.812	1.829	1.837	
23	1.459	1.639	1.709	1.769	1.817	1.834	1.843	
24	1.463	1.643	1.713	1.774	1.822	1.839	1.848	
25	1.465	1.646	1.717	1.778	1.827	1.844	1.852	
26	1.468	1.650	1.721	1.782	1.831	1.848	1.856	
27	1.471	1.653	1.724	1.786	1.835	1.852	1.860	
28	1.473	1.656	1.727	1.789	1.838	1.856	1.864	
29	1.475	1.659	1.730	1.792	1.842	1.859	1.868	
30	1.477	1.661	1.733	1.795	1.845	1.862	1.871	1.880
35	1.486	1.672	1.745	1.808	1.858	1.876	1.885	1.893
40	1.492	1.680	1.754	1.817	1.868	1.886	1.895	1.904
50	1.501	1.691	1.766	1.831	1.883	1.900	1.909	1.919
80	1.515	1.709	1.785	1.851	1.904	1.923	1.932	1.941
100	1.520	1.715	1.792	1.858	1.912	1.930	1.939	1.949
200	1.529	1.727	1.805	1.872	1.927	1.945	1.955	1.964

TABLE 7.--LACTATION WEIGHTS FOR RECORDS HAVING VARYING NUMBERS OF MODIFIED CONTEMPORARIES (MOD CONT) BY VARYING NUMBERS OF SIRES WITH AN AVERAGE REPEATABILITY OF 90%

NO. OF MOD CONT	AVERAGE NUMBER OF SIRES OF MODIFIED CONTEMPORARIES							
	1	2	3	5	10	15	20	30
1	0.687							
2	0.952	1.023						
3	1.093	1.187	1.222					
4	1.180	1.290	1.332					
5	1.239	1.361	1.408	1.447				
6	1.282	1.413	1.463	1.506				
7	1.315	1.453	1.506	1.551				
8	1.340	1.484	1.539	1.587				
9	1.361	1.509	1.567	1.616				
10	1.377	1.530	1.589	1.639	1.679			
11	1.392	1.548	1.608	1.659	1.700			
12	1.404	1.563	1.624	1.676	1.718			
13	1.414	1.575	1.638	1.691	1.734			
14	1.423	1.586	1.650	1.704	1.747			
15	1.431	1.596	1.660	1.715	1.759	1.774		
16	1.438	1.605	1.670	1.725	1.770	1.785		
17	1.444	1.613	1.678	1.734	1.779	1.794		
18	1.449	1.619	1.685	1.742	1.787	1.803		
19	1.454	1.626	1.692	1.749	1.795	1.811		
20	1.459	1.631	1.698	1.756	1.802	1.818	1.826	
21	1.463	1.636	1.704	1.762	1.808	1.824	1.832	
22	1.467	1.641	1.709	1.767	1.814	1.830	1.838	
23	1.470	1.646	1.714	1.772	1.819	1.835	1.843	
24	1.473	1.649	1.718	1.777	1.824	1.840	1.848	
25	1.476	1.653	1.722	1.781	1.828	1.845	1.853	
26	1.479	1.657	1.726	1.785	1.833	1.849	1.857	
27	1.481	1.660	1.729	1.789	1.837	1.853	1.861	
28	1.484	1.663	1.732	1.792	1.840	1.857	1.865	
29	1.486	1.665	1.735	1.796	1.844	1.860	1.869	
30	1.488	1.668	1.738	1.799	1.847	1.863	1.872	1.880
35	1.497	1.679	1.750	1.811	1.860	1.877	1.885	1.894
40	1.503	1.687	1.759	1.821	1.870	1.887	1.896	1.904
50	1.512	1.699	1.771	1.834	1.884	1.902	1.910	1.919
80	1.526	1.716	1.791	1.855	1.906	1.924	1.933	1.942
100	1.531	1.722	1.797	1.862	1.914	1.931	1.940	1.950
200	1.541	1.734	1.810	1.876	1.928	1.947	1.956	1.965

TABLE 8.--PERCENT REPEATABILITY FROM 10 DAUGHTERS EQUALLY DISTRIBUTED IN VARYING NUMBERS OF HERDS AND WITH VARYING SUMS OF LACTATION WEIGHTS (LACWT)

APPROX. NO. OF RECORDS	AVERAGE SUM OF LACWT	NUMBER OF HERDS			
		1	2	5	10
	0.7	14	17	20	21
	0.8	14	18	21	23
	0.9	15	19	23	24
	1.0	16	20	24	26
	1.1	16	21	25	27
	1.2	16	21	26	28
	1.3	17	22	27	29
	1.4	17	22	28	30
	1.5	17	23	28	31
	1.6	18	23	29	32
1	1.7	18	24	30	33
	1.8	18	24	30	33
	1.9	18	25	31	34
	2.0	18	25	31	34
	2.1	19	25	32	35
	2.2	19	25	32	36
	2.3	19	26	33	36
	2.4	19	26	33	37
	2.5	19	26	34	37
	2.6	19	26	34	37
	2.7	19	27	34	38
	2.8	19	27	35	38
	2.9	20	27	35	39
	3.0	20	27	35	39
	3.1	20	27	35	39
	3.2	20	27	36	40
	3.3	20	28	36	40
	3.4	20	28	36	40
2	3.5	20	28	36	40
	3.6	20	28	37	41
	3.7	20	28	37	41
	3.8	20	28	37	41
	3.9	20	28	37	41
	4.0	20	28	37	42

TABLE 9.--PERCENT REPEATABILITY FROM 20 DAUGHTERS EQUALLY DISTRIBUTED IN VARYING NUMBERS OF HERDS AND WITH VARYING SUMS OF LACTATION WEIGHTS (LACWT)

APPROX. NO. OF RECORDS	AVERAGE SUM OF LACWT	NUMBER OF HERDS					
		1	2	4	5	10	20
	0.7	18	24	29	30	33	35
	0.8	19	25	31	32	35	37
	0.9	19	26	32	34	37	39
	1.0	20	27	33	35	39	41
	1.1	20	28	34	36	40	42
	1.2	20	28	35	37	41	44
	1.3	20	29	36	38	42	45
	1.4	21	29	37	39	43	46
	1.5	21	30	37	39	44	47
	1.6	21	30	38	40	45	48
1	1.7	21	30	38	41	46	49
	1.8	21	31	39	41	47	50
	1.9	22	31	39	42	47	51
	2.0	22	31	40	42	48	51
	2.1	22	31	40	43	48	52
	2.2	22	32	41	43	49	53
	2.3	22	32	41	43	49	53
	2.4	22	32	41	44	50	54
	2.5	22	32	41	44	50	54
	2.6	22	32	42	44	51	55
	2.7	22	32	42	45	51	55
	2.8	22	33	42	45	51	55
	2.9	22	33	42	45	52	56
	3.0	23	33	43	45	52	56
	3.1	23	33	43	46	52	56
	3.2	23	33	43	46	53	57
	3.3	23	33	43	46	53	57
	3.4	23	33	43	46	53	57
2	3.5	23	33	44	46	53	58
	3.6	23	33	44	47	54	58
	3.7	23	34	44	47	54	58
	3.8	23	34	44	47	54	58
	3.9	23	34	44	47	54	59
	4.0	23	34	44	47	54	59

TABLE 10.--PERCENT REPEATABILITY FROM 30 DAUGHTERS EQUALLY DISTRIBUTED IN VARYING NUMBERS OF HERDS AND WITH VARYING SUMS OF LACTATION WEIGHTS (LACWT)

APPROX. NO. OF RECORDS	AVERAGE SUM OF LACWT	NUMBER OF HERDS					
		1	2	5	10	15	30
	0.7	20	28	37	41	43	44
	0.8	21	29	38	43	45	47
	0.9	21	30	40	45	47	49
	1.0	21	31	41	46	49	51
	1.1	22	31	42	48	50	52
	1.2	22	32	43	49	51	54
	1.3	22	32	44	50	52	55
	1.4	22	32	45	51	53	56
	1.5	22	33	45	52	54	57
	1.6	23	33	46	53	55	58
1	1.7	23	33	46	53	56	59
	1.8	23	34	47	54	57	60
	1.9	23	34	47	54	57	61
	2.0	23	34	48	55	58	61
	2.1	23	34	48	55	58	62
	2.2	23	34	48	56	59	62
	2.3	23	35	49	56	59	63
	2.4	23	35	49	57	60	63
	2.5	23	35	49	57	60	64
	2.6	23	35	49	57	61	64
	2.7	24	35	50	58	61	65
	2.8	24	35	50	58	61	65
	2.9	24	35	50	58	62	65
	3.0	24	35	50	59	62	66
	3.1	24	35	50	59	62	66
	3.2	24	36	51	59	62	66
	3.3	24	36	51	59	63	67
	3.4	24	36	51	59	63	67
2	3.5	24	36	51	60	63	67
	3.6	24	36	51	60	63	67
	3.7	24	36	51	60	64	68
	3.8	24	36	51	60	64	68
	3.9	24	36	52	60	64	68
	4.0	24	36	52	60	64	68

TABLE 11.--PERCENT REPEATABILITY FROM 40 DAUGHTERS EQUALLY DISTRIBUTED IN VARYING NUMBERS OF HERDS AND WITH VARYING SUMS OF LACTATION WEIGHTS (LACWT)

APPROX. NO. OF RECORDS	AVERAGE SUM OF LACWT	NUMBER OF HERDS					
		1	2	5	10	20	40
	0.7	21	31	41	47	50	52
	0.8	22	31	43	49	52	54
	0.9	22	32	44	50	54	56
	1.0	22	33	45	52	56	58
	1.1	23	33	46	53	57	60
	1.2	23	34	47	54	58	61
	1.3	23	34	48	55	60	62
	1.4	23	34	48	56	61	63
	1.5	23	35	49	57	61	64
	1.6	23	35	49	57	62	65
1	1.7	24	35	50	58	63	66
	1.8	24	35	50	58	64	67
	1.9	24	35	51	59	64	67
	2.0	24	36	51	59	65	68
	2.1	24	36	51	60	65	68
	2.2	24	36	51	60	66	69
	2.3	24	36	52	61	66	69
	2.4	24	36	52	61	67	70
	2.5	24	36	52	61	67	70
	2.6	24	36	52	61	67	71
	2.7	24	36	53	62	68	71
	2.8	24	37	53	62	68	71
	2.9	24	37	53	62	68	72
	3.0	24	37	53	62	68	72
	3.1	24	37	53	63	69	72
	3.2	24	37	53	63	69	72
	3.3	24	37	54	63	69	73
	3.4	24	37	54	63	69	73
2	3.5	24	37	54	63	70	73
	3.6	24	37	54	64	70	73
	3.7	24	37	54	64	70	74
	3.8	24	37	54	64	70	74
	3.9	24	37	54	64	70	74
	4.0	25	37	54	64	70	74

TABLE 12.--PERCENT REPEATABILITY FROM 50 DAUGHTERS EQUALLY DISTRIBUTED IN VARYING NUMBERS OF HERDS AND WITH VARYING SUMS OF LACTATION WEIGHTS (LACWT)

APPROX. NO. OF RECORDS	AVERAGE SUM OF LACWT	NUMBER OF HERDS					
		1	2	5	10	25	50
	0.7	22	32	44	51	55	57
	0.8	23	33	46	53	58	60
	0.9	23	34	47	54	60	62
	1.0	23	34	48	55	61	63
	1.1	23	35	49	57	63	65
	1.2	23	35	50	58	64	66
	1.3	24	35	50	58	65	67
	1.4	24	36	51	59	66	68
	1.5	24	36	51	60	67	69
	1.6	24	36	52	60	67	70
1	1.7	24	36	52	61	68	71
	1.8	24	36	52	61	69	71
	1.9	24	37	53	62	69	72
	2.0	24	37	53	62	70	72
	2.1	24	37	53	63	70	73
	2.2	24	37	54	63	71	73
	2.3	24	37	54	63	71	74
	2.4	24	37	54	64	71	74
	2.5	24	37	54	64	72	75
	2.6	25	37	54	64	72	75
	2.7	25	37	55	64	72	75
	2.8	25	37	55	65	73	76
	2.9	25	38	55	65	73	76
	3.0	25	38	55	65	73	76
	3.1	25	38	55	65	73	76
	3.2	25	38	55	65	73	77
	3.3	25	38	55	66	74	77
	3.4	25	38	56	66	74	77
2	3.5	25	38	56	66	74	77
	3.6	25	38	56	66	74	77
	3.7	25	38	56	66	74	78
	3.8	25	38	56	66	75	78
	3.9	25	38	56	66	75	78
	4.0	25	38	56	66	75	78

TABLE 13.--PERCENT REPEATABILITY FROM 60 DAUGHTERS EQUALLY DISTRIBUTED IN VARYING NUMBERS OF HERDS AND WITH VARYING SUMS OF LACTATION WEIGHTS (LACWT)

APPROX. NO. OF RECORDS	AVERAGE SUM OF LACWT	NUMBER OF HERDS 1	2	5	10	30	60
	0.7	23	34	47	54	60	61
	0.8	23	34	48	56	62	64
	0.9	23	35	49	57	64	66
	1.0	24	35	50	58	65	67
	1.1	24	36	51	59	67	69
	1.2	24	36	52	60	68	70
	1.3	24	36	52	61	69	71
	1.4	24	36	53	62	70	72
	1.5	24	37	53	62	70	73
	1.6	24	37	53	63	71	74
1	1.7	24	37	54	63	72	74
	1.8	24	37	54	64	72	75
	1.9	25	37	54	64	73	75
	2.0	25	37	55	65	73	76
	2.1	25	38	55	65	74	76
	2.2	25	38	55	65	74	77
	2.3	25	38	55	65	75	77
	2.4	25	38	55	66	75	78
	2.5	25	38	56	66	75	78
	2.6	25	38	56	66	75	78
	2.7	25	38	56	66	76	79
	2.8	25	38	56	67	76	79
	2.9	25	38	56	67	76	79
	3.0	25	38	56	67	76	79
	3.1	25	38	56	67	77	80
	3.2	25	38	57	67	77	80
	3.3	25	38	57	67	77	80
	3.4	25	38	57	68	77	80
2	3.5	25	38	57	68	77	80
	3.6	25	39	57	68	78	80
	3.7	25	39	57	68	78	81
	3.8	25	39	57	68	78	81
	3.9	25	39	57	68	78	81
	4.0	25	39	57	68	78	81

TABLE 14.--PERCENT REPEATABILITY FROM 70 DAUGHTERS EQUALLY DISTRIBUTED IN VARYING NUMBERS OF HERDS AND WITH VARYING SUMS OF LACTATION WEIGHTS (LACWT)

APPROX. NO. OF RECORDS	AVERAGE SUM OF LACWT	NUMBER OF HERDS					
		1	2	5	10	35	70
	0.7	23	35	49	56	63	65
	0.8	24	35	50	58	66	67
	0.9	24	36	51	59	67	69
	1.0	24	36	52	60	69	71
	1.1	24	36	52	61	70	72
	1.2	24	37	53	62	71	73
	1.3	24	37	54	63	72	74
	1.4	24	37	54	64	73	75
	1.5	25	37	54	64	74	76
	1.6	25	37	55	65	74	77
1	1.7	25	38	55	65	75	77
	1.8	25	38	55	65	75	78
	1.9	25	38	56	66	76	78
	2.0	25	38	56	66	76	79
	2.1	25	38	56	66	77	79
	2.2	25	38	56	67	77	79
	2.3	25	38	56	67	77	80
	2.4	25	38	57	67	78	80
	2.5	25	38	57	67	78	80
	2.6	25	38	57	68	78	81
	2.7	25	39	57	68	78	81
	2.8	25	39	57	68	79	81
	2.9	25	39	57	68	79	81
	3.0	25	39	57	68	79	82
	3.1	25	39	57	68	79	82
	3.2	25	39	58	69	80	82
	3.3	25	39	58	69	80	82
	3.4	25	39	58	69	80	82
2	3.5	25	39	58	69	80	83
	3.6	25	39	58	69	80	83
	3.7	25	39	58	69	80	83
	3.8	25	39	58	69	80	83
	3.9	25	39	58	69	81	83
	4.0	25	39	58	69	81	83

TABLE 15.--PERCENT REPEATABILITY FROM 80 DAUGHTERS EQUALLY DISTRIBUTED IN VARYING NUMBERS OF HERDS AND WITH VARYING SUMS OF LACTATION WEIGHTS (LACWT)

APPROX. NO. OF RECORDS	AVERAGE SUM OF LACWT	NUMBER OF HERDS					
		1	2	5	10	40	80
	0.7	24	35	50	58	66	68
	0.8	24	36	51	60	68	70
	0.9	24	36	52	61	70	72
	1.0	24	37	53	62	72	73
	1.1	24	37	54	63	73	75
	1.2	24	37	54	64	74	76
	1.3	25	37	55	65	75	77
	1.4	25	38	55	65	75	77
	1.5	25	38	55	66	76	78
	1.6	25	38	56	66	77	79
1	1.7	25	38	56	66	77	79
	1.8	25	38	56	67	78	80
	1.9	25	38	57	67	78	80
	2.0	25	38	57	67	79	81
	2.1	25	39	57	68	79	81
	2.2	25	39	57	68	79	82
	2.3	25	39	57	68	80	82
	2.4	25	39	57	68	80	82
	2.5	25	39	58	69	80	82
	2.6	25	39	58	69	80	83
	2.7	25	39	58	69	81	83
	2.8	25	39	58	69	81	83
	2.9	25	39	58	69	81	83
	3.0	25	39	58	69	81	84
	3.1	25	39	58	70	81	84
	3.2	25	39	58	70	82	84
	3.3	25	39	58	70	82	84
	3.4	25	39	58	70	82	84
2	3.5	25	39	59	70	82	84
	3.6	25	39	59	70	82	85
	3.7	25	39	59	70	82	85
	3.8	25	39	59	70	82	85
	3.9	25	39	59	70	83	85
	4.0	25	39	59	70	83	85

TABLE 16.--PERCENT REPEATABILITY FROM 90 DAUGHTERS EQUALLY DISTRIBUTED IN VARYING NUMBERS OF HERDS AND WITH VARYING SUMS OF LACTATION WEIGHTS (LACWT)

APPROX. NO. OF RECORDS	AVERAGE SUM OF LACWT	NUMBER OF HERDS 1	2	5	10	45	90
	0.7	24	36	51	60	69	71
	0.8	24	36	52	61	71	73
	0.9	24	37	53	63	73	74
	1.0	24	37	54	64	74	76
	1.1	25	37	55	64	75	77
	1.2	25	38	55	65	76	78
	1.3	25	38	56	66	77	79
	1.4	25	38	56	66	78	79
	1.5	25	38	56	67	78	80
	1.6	25	38	57	67	79	81
1	1.7	25	38	57	68	79	81
	1.8	25	39	57	68	80	82
	1.9	25	39	57	68	80	82
	2.0	25	39	57	68	81	83
	2.1	25	39	58	69	81	83
	2.2	25	39	58	69	81	83
	2.3	25	39	58	69	81	84
	2.4	25	39	58	69	82	84
	2.5	25	39	58	70	82	84
	2.6	25	39	58	70	82	84
	2.7	25	39	58	70	82	85
	2.8	25	39	59	70	83	85
	2.9	25	39	59	70	83	85
	3.0	25	39	59	70	83	85
	3.1	25	39	59	70	83	85
	3.2	25	39	59	71	83	86
	3.3	25	39	59	71	83	86
	3.4	25	39	59	71	84	86
2	3.5	25	39	59	71	84	86
	3.6	25	40	59	71	84	86
	3.7	25	40	59	71	84	86
	3.8	25	40	59	71	84	86
	3.9	25	40	59	71	84	86
	4.0	25	40	59	71	84	87

TABLE 17.--PERCENT REPEATABILITY FROM 100 DAUGHTERS EQUALLY DISTRIBUTED IN VARYING NUMBERS OF HERDS AND WITH VARYING SUMS OF LACTATION WEIGHTS (LACWT)

APPROX. NO. OF RECORDS	AVERAGE SUM OF LACWT	NUMBER OF HERDS					
		1	2	5	10	50	100
	0.7	24	36	52	61	71	73
	0.8	24	37	53	63	73	75
	0.9	24	37	54	64	75	76
	1.0	25	38	55	65	76	78
	1.1	25	38	55	66	77	79
	1.2	25	38	56	66	78	80
	1.3	25	38	56	67	79	80
	1.4	25	38	57	67	79	81
	1.5	25	39	57	68	80	82
	1.6	25	39	57	68	80	82
1	1.7	25	39	57	69	81	83
	1.8	25	39	58	69	81	83
	1.9	25	39	58	69	82	84
	2.0	25	39	58	69	82	84
	2.1	25	39	58	70	82	84
	2.2	25	39	58	70	83	85
	2.3	25	39	59	70	83	85
	2.4	25	39	59	70	83	85
	2.5	25	39	59	70	83	85
	2.6	25	39	59	70	84	86
	2.7	25	39	59	71	84	86
	2.8	25	39	59	71	84	86
	2.9	25	40	59	71	84	86
	3.0	25	40	59	71	84	86
	3.1	25	40	59	71	85	87
	3.2	25	40	59	71	85	87
	3.3	25	40	59	71	85	87
	3.4	26	40	59	71	85	87
2	3.5	26	40	60	71	85	87
	3.6	26	40	60	72	85	87
	3.7	26	40	60	72	85	87
	3.8	26	40	60	72	85	88
	3.9	26	40	60	72	86	88
	4.0	26	40	60	72	86	88

Table 18.--Regression and y-intercept values for predicting the genetic group average from pedigree index 1/

	Milk		Fat	
Breed	Intercept	Regression	Intercept	Regression
Ayrshire	-188	0.965	-7.1	0.892
	-103	0.964	-4.5	0.871
Guernsey	-120	0.973	-4.8	0.730
	-96	0.942	-3.8	0.750
Holstein	-162	0.989	-7.7	0.762
	-114	0.981	-5.8	0.775
Jersey	-135	0.984	-7.0	0.884
	-114	0.969	-5.5	0.832
B. Swiss	-53	0.919	-3.2	0.775
	-46	0.873	-2.2	0.721
M. Shorthorn	+1	0.827	-0.2	0.669
	-57	0.820	-3.4	0.767

1/ For each breed, the top line is for bulls indexed on father and grandfather and bottom line is for father only. From fall 1974 Sire Summary data.

Table 19.--Formulas for weighting Modified Contemporary Deviations and sample weights

Bull	Weights			
		Example bulls 1/		
	General	Young	Average	Established
A	R_A	0.2000	0.7000	0.9000
B	$R_B(1/2)(1-R_A)$	0.2800	0.1050	0.0350
C	$R_C(1/4)(1-R_A)(1-R_B)$	0.0420	0.0158	0.0052
D	$R_D(1/4)(1-R_A)$	0.1400	0.0525	0.0175
E	$R_E(1/8)(1-R_A)(1-R_B)(1-R_C)$	0.0063	0.0024	0.0008
F	$R_F(1/8)(1-R_A)(1-R_B)$	0.0210	0.0079	0.0026
G	$R_G(1/8)(1-R_A)(1-R_D)$	0.0210	0.0079	0.0026
H	$R_H(1/16)(1-R_A)(1-R_B)(1-R_C)(1-R_E)$	0.0009	0.0004	0.0001
I	$R_I(1/16)(1-R_A)(1-R_B)(1-R_C)$	0.0032	0.0012	0.0004
J	$R_J(1/16)(1-R_A)(1-R_B)(1-R_F)$	0.0032	0.0012	0.0004
K	$R_K(1/16)(1-R_A)(1-R_D)(1-R_G)$	0.0032	0.0012	0.0004
L	$R_L(1/16)(1-R_A)(1-R_D)$	0.0105	0.0039	0.0013

1/ Repeatabilities (R's) for all ancestors are 0.7.

TABLE 20.--APPROXIMATE RATIO OF WEIGHT FROM DAUGHTERS OF THE BULL TO THAT FROM DAUGHTERS OF THE SIRE AND MATERNAL GRANDSIRE IN DETERMINATION OF PREDICTED DIFFERENCE

R ON BULL (%)	REPEATABILITY (%) FOR SIRE AND MATERNAL GRANDSIRE OF THE BULL								
	20	30	40	50	60	70	80	90	95
20	63:37	58:42	54:46	51:49	49:51	47:53	45:55	44:56	43:57
30	70:30	66:34	62:38	60:40	57:43	55:45	54:46	52:48	52:48
40	76:24	72:28	69:31	67:33	64:36	63:37	61:39	60:40	59:41
50	81:19	77:23	75:25	73:27	71:29	69:31	68:32	67:33	66:34
60	85:15	82:18	80:20	79:21	77:23	76:24	74:26	73:27	73:27
70	89:11	87:13	85:15	84:16	83:17	82:18	81:19	80:20	79:21
80	93: 7	92: 8	90:10	89:11	89:11	88:12	87:13	86:14	86:14
90	97: 3	96: 4	95: 5	95: 5	94: 6	94: 6	93: 7	93: 7	93: 7
95	98: 2	98: 2	98: 2	97: 3	97: 3	97: 3	97: 3	96: 4	96: 4
99	100: 0	100: 0	100: 0	99: 1	99: 1	99: 1	99: 1	99: 1	99: 1

TABLE 21.--PEDIGREE INFLUENCE ON PREDICTED DIFFERENCE IN TERMS OF AN APPROXIMATE NUMBER OF DAUGHTERS DISTRIBUTED ONE PER HERD

R OF FATHER (%)	REPEATABILITY (%) ON MATERNAL GRANDFATHER										
	0	20	30	40	50	60	70	80	90	95	99
0	0	0	0	0	1	1	1	1	1	1	1
20	1	1	1	2	2	2	2	2	2	2	2
30	2	2	2	2	2	2	3	3	3	3	3
40	2	2	3	3	3	3	3	3	4	4	4
50	3	3	3	3	4	4	4	4	4	4	4
60	3	4	4	4	4	4	5	5	5	5	5
70	4	4	5	5	5	5	5	6	6	6	6
80	5	5	5	6	6	6	6	6	7	7	7
90	6	6	6	6	7	7	7	7	7	8	8
95	6	6	7	7	7	7	7	8	8	8	8
99	6	7	7	7	7	8	8	8	8	8	9