EVALUATION OF OPTIMUM AND NEAR OPTIMUM PAIR SELECTION METHODS FOR INCREASING PREDICTED RELATIVE NET INCOME IN JERSEY CATTLE

by

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Thesis submitted to the Faculty of the

Virginia Polytechnic Institute and State University

in partial fulfillment of the requirements for the degree of

Master of Science

in

Dairy Science

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August 20, 1987

Blacksburg, Virginia

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(ABSTRACT)

To evaluate the importance of non-linear relationships between Relative net income per day of productive life (RNI/DPL) and individual traits, 921,915 potential offspring were simulated from all possible matings of 20,487 Jersey cows and 45 active AI sires. Predicted milk yield, fat yield, and 13 linear type traits of potential progeny were used to predict RNI/DPL of all potential progeny.

Five methods of mate selection and pairing were evaluated for their effectiveness in choosing mates and the amount of computer time required to choose those pairings. Results of a linear programming (LP) method were used as a comparison for the other four more easily applied methods. Two of the other four methods were not significantly ($P > .01$) different from the LP method. Although the random pairing method was significantly different, similarity of results for this method indicated non-linear relationships between RNI/DPL and individual trait scores are of minor importance. All four methods used considerable less computer time than the LP method.

Analysis of variance for predicted RNI/DPL (all possible offspring) indicated herd, dam within herd, sire, and inbreeding class to be significant ($P < .01$) variables in determining RNI/DPL. However the sire by dam within herd interaction did not signif-

icantly affect RNI/DPL, again indicating non-linear relationships between traits and RNI/DPL were not very important.

Regressing PD's, CI's, and their crossproducts for milk yield, fat yield, and 13 linear type traits showed the relative importance of crossproducts to be minimal in comparison to the linear effects of parental genetic evaluations.

Acknowledgements

The author wishes to express his sincere appreciation to Dr. William E. Vinson for his continuous guidance, assistance, and patience over the past several years. Gratitude is also expressed to Dr. Ronald E. Pearson and Dr. Bennet G. Cassell for their advice during thesis preparation. Appreciation is also expressed to Dr. John M. White as well as the faculty and staff of the Dairy Science Department for their encouragement and their role in the authors education.

The author is also grateful to for his encouragement and spiritual support. The author is also indebted to friends as well as his fiancee for their support and encouragement in completing all degree requirements.

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Introduction

In 1978 approximately 1.5 million dollars was spent for mating services, commonly called "corrective mating", to select a mate for approximately 9 million cows (2). Prompted by descriptive classification systems, programs of corrective mating are offered by nearly every bull stud, and the number of dairymen interested in having their cattle correctively mated is increasing. As these mating systems become more popular it has become increasingly important to document the value of corrective mating and to assist the dairy farmer in choosing programs that will maximize profitability.

Corrective mating procedures have given rise to considerable confusion. Most are defined by loosely specified goals and implemented using arbitrary and likely inconsistent rankings of trait importance. For example, a common goal of corrective mating services is to mate a cow to a bull that will "correct" her "weakest point". In general "weakest point" is an arbitrary decision based on subjective phenotypic evaluation without regard to economic importance of the weakness or consideration of other traits. In addition Thomas et al. (21) concluded that average performance of offspring can be more accurately predicted by using the dam's cow index, rather than her phenotypic score.

Corrective mating often has been defined as a form of negative assortative mating. Negative assortative mating can be described as a tool for producing a more (or less) uniform group of animals rather than to make directional changes in performance. Allaire (1) further discouraged the use of negative assortative mating based on results which are expected to be small and temporary and because increasing production or profit through directional selection are of far greater importance.

Due to problems associated with assigning goals for corrective mating programs, considerable interest has arisen in developing indexes which would include both type traits and production variables to estimate some function of profitability. The linear type system implemented in 1980 is a useful aid in making such an index. A reasonable breeding goal using selection indexes would be to maximize the average profitability or net value (NV) of offspring from a set of matings, which would treat the herd as a breeding unit.

An additional shortcoming of typical mating programs is the failure to optimize, in any sense, the allocation of semen from bulls in limited supply. When supplies of semen are limited for one or more bulls, goals of the mating program can no longer logically be expressed relative to the offspring of individual cows since the question is whether to mate one cow or another with the limited semen. Mating goals in such situations must, rather, be defined in terms of the average performance of offspring of all matings in the herd at a given time. Additionally, the number of possible ways to mate a herd (different combinations of cows(increases dramatically after semen supplies are limited for some bulls.

The objective of this study was to compare approximate methods of pair selection with exact (LP) methods of best pair selections and individual selection when representative general restrictions are imposed on semen availability.

Review of Literature

Assortative Mating

Assortative mating can be defined as mating sires and dams in a non-random manner with respect to values of one or more phenotypic traits (6, 10, 20). Assortative mating may be described as "positive" when mates are chosen to be of like phenotypes and "negative" when mates are chosen because they have unlike phenotypic traits.

Crow and Kimura (6) have contrasted assortative mating based on phenotypes with inbreeding or outcrossing which represent matings that are non-random with respect to their genetic relationships. Since individuals of similar phenotypes will tend to have similar genotypes, positive assortative mating will tend to have similar effects as mild inbreeding, while negative assortative mating will mimic mild outcrossing. In a large population, however, positive assortative mating is by no means synonymous with inbreeding as it is possible to mate individuals of like phenotypic (or genetic) value while avoiding consanguineous matings. "Pure" assortative mating, as defined by Crow and Kimura (6), can take place only when all genotypes make the same average contribution.

Pure assortative mating, positive or negative, will not change the gene frequency of a population (6) but will make the offspring more or less like the parents, respectively. In many assortative mating systems and especially negative assortative mating, (disassortative mating in Crow), there are different contributions of different genotypes to the phenotype.

The most simple cases of positive assortative mating, those that involve a single loci, will result in heterozygosity being reduced by one-half each generation. Partial positive assortative mating will not however, lead to complete homozygosity but will reach an equilibrium level of heterozygosity other than zero (10). Theoretically the rate of decrease in heterozygosity will depend upon the number of loci, and the degree of dominance involved. In practice, however, positive assortative mating has almost no effect on heterozygosity as there are usually many pairs of genes involved as well as dominance, epistasis, and masking of the genes by the environment, which lowers the accuracy of the breeding program. Positive assortative mating will tend to increase the resemblance of parent and offspring on the average as the genetic contributions from the parents that make up the offspring resemble each other. That is, the sire was chosen to have as many genes as possible which would produce the same kinds of phenotypic effects as do genes of the dam (6).

Negative assortative mating with only one or two loci will reach an equilibrium state within a few generations (6). Negative assortative mating is usually used in practice where the ideal is an intermediate (10). Most dairy breeders use negative assortative mating to some extent along with selection. Since there are some traits of interest (of varying degrees of importance) where the intermediate often is the optimum, a breeder may choose a mate for his livestock by choosing a sire that is as near as possible to the opposite extreme as the dam. Negative assortative mating, at best, will increase heterozygosity very little. It does, however, have a tendency to make the whole popu-

lation more uniform since the extremes are mated together. The offspring is therefore somewhere near the breed average (10).

The major effect of assortative mating on a population as noted by Wright (23) and Lush (10) is on population variance. In general, positive assortative mating is expected to increase population variance while negative assortative mating will tend to decrease variation around the mean. These expected changes in population variance with assortative mating have been shown experimentally in *Nicotiana* by Breese (5) and in *Drosophila* by McBride and Robertson (11).

Where optimum performance occurs at one extreme, the goal of the breeding program is to move the population toward that extreme. Positive assortative mating will tend to increase variation and therefore, should increase potential selection differentials, thereby leading to more rapid population improvement (21). If the optimum expression of a trait is an intermediate, negative assortative mating, by reducing variation around the mean, (which is directed by selection toward the intermediate optimum), should yield a preferred mean performance by yielding higher frequencies of optimum and near optimum individuals.

Economic Heterosis

The economic value of each trait needs to be considered in developing any mating program. If the economic value is not assessed or is improperly assessed, there is the danger of making recommendations to the industry that will lead to less than the most profitable solution (13). This problem is further complicated when the traits of interest have non-linear relationships to the economic worth of the animal.

Moav (14) approached this problem by the use of profit contours, developing profit diagrams with two economically important traits representing X and Y axes. The economic value of the two traits were represented by profit contours. Moav used two inversely related traits, (food conversion ratio of the sire line and number of pigs per sow in the dam line), to show that the point where profit was maximized was a value intermediate to the maxima for the two traits.

Moav and Moav (15) found that profit was non-linearly related to egg production. They found that at low production levels profit was increased more with an increase of eggs per hen than with the same increase in eggs per hen when production levels were high.

Miller and Pearson (13) discussed two methods to determine optimum solutions for mating systems; (i) use procedures such as linear or dynamic programming to uniquely identify the optimum combination, and (ii) model the selection or production process and numerically calculate net returns from all possible feasible combinations of resources or alternative structures of the production process. The system analysis approach (i above) would allow many complex factors to be considered, not limited to, but including non-linear relations between the traits and economic value.

Corrective Mating Problems

For convenience, we can define six general classes of corrective mating problems. These are from combinations of three objectives of corrective mating and two designations of sire usage. The three objectives of corrective mating are as follows:

1. Mate Pairing: sires and dams are pre-selected, using individual selection, from a larger set of potential sires and dams. The objective is to pair these individuals in some optimum way.
2. Mate Selection and Pairing (called "Mate Selection" by Allaire(2)): dams are pre-selected from all potential dams, but all available sires are examined as a potential mate for selected dams. The mating combinations which achieve the highest average NV for expected offspring are then chosen, and specific matings made.
3. Selection and pairing: no preselection is practiced. All potential sires and dams are examined for expected offspring net value. Selections and pairings are determined based on expected offspring net value.

These three objectives differ in the number of sire-dam combinations that must be considered. Theoretically, objective three will always yield an expected progeny average that is as high or higher than either objectives one and two. If non-linear relationships exists between the traits of interests and NV, then pre-selection of the individuals can only decrease the expected NV of the offspring. The superiority of objective three will depend on the degree of non-linear relationships between individual traits and NV.

The designation of sire usage can be expressed as follows:

1. Unrestricted use of sires: sires can mate none to all dams chosen for breeding.
2. Restricted use of sires: restrictions are placed on the amount that one or more sires can be used. These restrictions may be due to limited semen supplies, previous sire usage, concern for inbreeding, risk avoidance, etc.; or a requirement that a sire should mate exactly some number of cows (e.g., Maxbull (12) selections designate sire usage in this manner.)

The distinction between restricted and unrestricted use of sires determines the size of the problem. With unrestricted use of sires we would simply need to calculate the expected offspring NV from all potential matings, and then chose the best mating for each dam. In total, m x f expected offspring are examined (expected NV computed), where m and f are the numbers of potential sires and dams respectively. However when sire usage is restricted, matings can no longer be chosen on a cow by cow bases. Under restricted sire usage the herd rather than the individual must be treated as the breeding unit.

Mate Selection and Pairing

Mate selection and pairing can be defined as choosing a sire and a dam by using a multi-trait selection method depending on the trait(s) of preselected cows and all available sires (2). It often is assumed in livestock selection theory that selected males and females are mated at random. However, if the overall merit of the offspring is not additively inherited or if individual traits which determine selection decisions are related non-linearly to net merit, then mate selection may increase the average net merit of the offspring (4). The pattern of changes in net merit over the range of interest for some traits may be described by a non-linear model (2), and may follow several general patterns.

1. Intermediate optimum: an intermediate optimum trait has highest net merit at or near a mid point value. The slope of the curve describing net merit on either side of the vertex is negative and may or may not be of the same magnitude, such that a one unit move toward or away from the vertex may not have the same effect on

net merit. Examples of traits generally considered to have intermediate optima are udder and teat conformation, set of legs, and body size (4).

2. Threshold value: an increasing score yields an increase in net merit to an maximum value after which increases in score has no effect (or no significant effect) on net merit. Examples of threshold traits are calving ease, susceptibility to disease (milk fever, edema), and ability to reproduce and function (move, eat, breed, etc..) (4).

The value of mate selection will depend on how strong are the non-linear relationships between the traits contributing to the selection criterion and net merit.

The first step in selecting mating pairs is to predict the merit of the potential progeny. If the traits reflecting net merit are inherited additively and related linearly to net merit, that is, net merit is made up of a simple linear combination of trait genetic values for sires and dams, then net merit of the progeny can be expressed as follows (2):

$$\mathrm{Ip} = 1/2A_1(I_1^{\times} + I'_1) + 1/2A_2(I_2^{\times} + I'_2) + \ldots + 1/2A_k(I_k^{\times} + I'_k)$$

where:

Ip is the progeny net merit index,

$I_i^{\times}$ is an index predicting the genetic value of trait i of the dam,

I'_i is an index predicting the genetic value of trait i of the sire,

A_i is the constant economic value contributed toward net worth by each unit difference in genetic value of the ith trait.

The expected progeny net merit can then be rearranged so that the sire and the dam components are expressed independently:

$$\mathrm{Ip} = 1/2\,(\sum_{i=1}^{k} A_1 I_1^{\times}) + 1/2(\sum_{i=1}^{k} A_1 I'_1)$$

$= 1/2I^{\times} + 1/2I'$

where $I^{\times}$ and I' are net merit indexes for sire and dam.

Under these conditions, the best sire is best for any dam and vise versa.

However if one or more traits contributing to net merit are not linearly related to net merit (intermediate optimum or some other non-linear relationship between economic value and score), the importance of the combination of trait genetic values for sire and dam increases. These non-linear relationships describe the pattern of charges in economic values over the range of interest for a trait (2).

If all traits are linearly related to NV, the best bull (i.e., that producing progeny with highest expected RNI/DPL) is always the best for any cow (Allaire (2)). Selection of superior sires and dams, followed by random mating would yield maximum expected average NV of progeny. For some traits, such as rear legs, there is an intermediate optimum, and perhaps a non-linear relationship to NV. In this case the expected NV for each possible mating pair must be computed to determine matings yielding maximum expected average NV of the progeny. If we had 5 potential sires and 50 dams we would have 250 possible offspring, and the top 50 matings could be chosen. If the use of bulls is restricted (by availability of semen, by the farmer, or by pre-assignment of the extent of bull usage), the problem becomes more complex.

Jansen et al. (9) shows if f mating pairs are chosen from all possible matings between M males and F females, so that predicted merit of of the progeny is maximized, given that f females are selected and mated only once, and the ith male mated no more than K times, with m being selected, there are $\binom{M}{m}\binom{F}{f} f!/(K!)^m$ mating combinations. If we set F = M = 10, f = 8, m = 4, and K = 2, the number of mating combinations is equal to $\binom{10}{4}\binom{10}{8} 8!/(2!)^4$ or 2×10^7 possibilities.

Jansen et al. (9) suggested that linear programming (LP) would be best suited to find the optimum solution, as LP can be used to consider all possibilities implicitly, while only explicitly evaluating a small subset of them. The LP model would be to maximize:

$$\sum_{i=1}^{M}\sum_{i=1}^{F} x_{ij}X_{ij}$$

subject to:

$$\sum_{i=1}^{M} X_{ij} \leq 1 \text{ for j} = 1,\text{F};$$

$$\sum_{j=1}^{F} X_{ij} \leq K_i \text{ for i} = 1,\text{M};$$

$$\sum_{i=1}^{M}\sum_{i=1}^{F} X_{ij} = f; \text{ and}$$

$$X_{ij} \in (0,1)$$

Where: x_{ij} is the predicted merit of a progeny from the ith male mated to the jth female, and X_{ij} in the number of progeny from the ijth mating pair, restricted to 0 or 1. This procedure could be applied to all available males and females or to subsets of males and females pre-selected on some criteria. The former theoretically will yield average NV of progeny which equals or exceeds the later. However, increasing numbers of potential parents may require large amounts of computer time, possibly making the program impractical. Therefore it would be advantageous to develop a near optimum solution which would be less expensive to compute.

Predicting Performance of Offspring

The expected performance for any of offspring from a given mating can be predicted under average environmental conditions from genetic evaluations of the sire and the dam. The accuracy of such a prediction is dependent, even on average, upon the accu-

racy of predicting the true genetic values of the parents. Thomas et al. (21) concluded that it was more accurate to predict the average performance of offspring by using the dam's CI rather than her phenotypic score.

Shook et al. (20) suggest predicting performance of potential offspring in a given herd from estimates of genetic and phenotypic parameters for parents, herd, and breed as:

$$E(T) = [PD + CI - HG] + [b(HP - HG - BA) + HG + BA]$$

where:

E(T) is the expected performance for a trait of the offspring,

PD is predicted difference of sire,

CI is cow index of dam,

HP is observed herd average phenotype,

HG is estimated herd average genotype,

BA is breed average, and

b is regression of herd environmental effect on herd average phenotype, given herd average breeding value.

The first term, (PD + CI - HG), is the expected genetic difference between the expected offspring and the average cow in the herd. The second term [b(HP - HG - BA) + HG + BA] is the estimated "true" herd average consisting of the herd environmental effect, herd average breeding value, and breed average. The theoretical regression of herd average environmental effect on herd average phenotype, holding herd average breeding value constant, is estimated as:

$$b = V(H)/[V(H) + (1 - h^2)\, V(P)/N]$$

where:

V(H) is variance among herds,

V(P) is variance among cows within herd,

h^2 is heritability, and

N is number of cows in the herd.

Predicted trait scores could then be placed into a net merit index to determine net merit of the potential offspring. Jansen et al. (9) suggested that predicted net merit could be organized into a matrix with rows and columns representing sires and dams respectively. If no other restrictions exists, (i.e. limited sire usage), the potential offspring with the highest score could be found and its corresponding sire and dam chosen. This procedure would require a minimum amount of computer time since all evaluations and mate selections could be made cow by cow. Problems arise, however, if mating to a sire is limited, (reproductive capacity, semen availability or by subjective constraint by the breeder).

Prediction of Net Value

The primary objective of dairy cattle breeders is to develop a more profitable cow. Time required, however, for lifetime profitability to be expressed prohibits direct selection on this trait. Tigges et al. (22) found the Relative Net Income (RNI) function to be a useful tool to estimate lifetime profitability. RNI is a measure of NV developed by Norman et al. (17) using data from more than 10,000 Jersey cows, and is designed to reflect major differences between cows in lifetime income and expenses. The four elements of the income function represent: a) the value of the milk produced; b) the net

value of calves produced each lactation; c) net cow depreciation; and d) fixed costs during the cows productive herd life. The formula for calculating RNI is,

RNI = (Lifetime value of product × Net Percentage)
+ (Number of lactations × Net Value)
+ Salvage Value - Value at first calving
- Feed costs for growth after first calving
+ (Days of productive life) × (feed costs for
maintenance + fixed and operating costs/DPL)

where: DPL = days of productive life; lifetime value of product is the value of actual lifetime production of milk and fat for 305 day lactations; net percentage = 80% (18.2% of milk income needed for feed to support production and 1.8% of milk discarded); net value = $27 (calf value = $50, insemination costs = $15, and feed to support gestation = $8); salvage value = $300; value at first freshening = $.82 × age at first calving in days ($600 for a heifer fresh at 24 months); feed costs for growth = $.15 × days to 42 months or disposal (which ever is first); feed cost for maintenance = $.46/DPL; and fixed and operating costs = $1.24/DPL. Norman (17) defined the number of lactations by the number of freshenings.

An extension of RNI which would give an advantage to cows that achieve high RNI in the shortest amount of time is Relative Net Income per Day of Productive life (RNI/DPL). Since it is more profitable for the producer to have cows which will give the quickest return on investment, RNI/DPL would more closely express the goals of many breeders for cows with normal lactations.

Direct selection on any measure of lifetime performance is futile since the opportunity for selection is passed when performance is available. It therefore it is necessary to develop methods of predicting lifetime profitability from traits which can be measured

early in the cow's life. Although there is no easily measured, single function which can predict absolute NV of cows under different farm conditions, a function that reflects average prices and quantities should be correlated with absolute NV at least within herd. Tigges et al. (22) working with the first three lactation records from 182 Holstein dairy cows found RNI to explain 95% of the variation in total profit and 85% of the variation in profit per day. They concluded that RNI and RNI/DPL appeared to be accurate measures of relative cow profitability.

Norman et al.(17) computed simple correlations of first lactation type traits with number of lactations and lifetime RNI/DPL, as well as multiple correlations when milk yield and fat yield were included in the model (Table 1). Multiple correlations were expressed as the difference between a model containing milk, fat yield and the specific type trait in linear, quadratic, and crossproduct form and multiple correlations from a model containing milk and fat yield in linear and quadratic form. Increase in multiple correlations ranged from a high of .019 for final score to a low of .002 for feet and legs and back, rump, and tail. Those traits with the highest increase in multiple correlation after first lactation milk and fat yield will be the most useful in predicting lifetime performance. However results (Table 1) show the over-riding importance of production in determining herdlife and lifetime profitability measures.

Barton et al. (4) calculated RNI/DPL for 8969 cows in 1393 herd-years. Several models were evaluated to predict number of records and lifetime RNI/DPL from first lactation yield and linear type trait scores (Table 2). Yield traits (milk and fat) appeared to be critical for predicting RNI/DPL with multiple correlations of .24 to .36. Multiple correlations using only type traits to predict RNI/DPL were lower than those with yield included. Multiple correlations for all trait scores except final score were higher than final score alone. Linear, quadratic, and cross product terms (Table 3) were derived to predict RNI/DPL from first lactation milk yield, fat yield, and type trait scores with the model:

Table 1. Utility of individual type traits in predicting lifetime performance[1].

Type trait	Simple correlations		Increase in multiple correlations[1]	
	Number of lactations	$\hat{RNI}/DPL$	Number of lactations	$\hat{RNI}/DPL$
Final score	.21	.27	.034	.019
General appearance	.13	.15	.012	.006
Stature	.08	.10	.005	.003
Breed character	.09	.12	.005	.003
Feet and legs	.09	.08	.008	.002
Back, rump, and tail	.06	.06	.004	.002
Dairy character	.20	.34	.009	.007
Body capacity	.08	.12	.004	.005
Mammary system	.15	.17	.020	.010
Fore udder	.12	.12	.018	.008
Rear udder	.13	.16	.014	.005
Teats	.09	.12	.008	.006
Suspensory ligament	.13	.15	.016	.010

[1]Norman et al. (17)
[2]Increase represents the difference between multiple correlation from a model containing milk, fat, and the specific type traits in linear, quadratic, and crossproduct from and multiple correlation from a model containing milk and fat in linear and quadratic form.

Table 2. Summary for multiple regression analysis[1] for standardized first-lactation yield and type traits and lifetime performance traits for Jersey[2]

Trait	Multiple Correlation Coefficient (R)	
	Number of records	RNI/DPL
Milk yield, Fat yield (linear, quadratic)	.29	.59
Final Score (linear, quadratic)	.19	.24
All type traits but final score (linear, quadratic)	.22	.35
All first lactation type traits (linear, quadratic, cross-product)	.24	.36
Milk yield, Fat yield, final score (linear, quadratic, cross-product)	.31	.60
Milk yield, Fat yield, all type traits except final score (linear, quadratic, cross-product)	.32	.60
Milk yield, Fat yield, all type traits (linear, quadratic, cross-product)	.32	.60

[1]Calculated within herd-year of calving.
[2]Barton et al. (4)

Table 3. Multiple Regression Coefficients to estimate RNI/DPL from first-lactation performance (mature equivalent or age and stage adjusted)

	Linear		Quadratic		Cross products[1]	
	Mantissa	Exponent	Mantissa	Exponent	Mantissa	Exponent
Milk	.451908	-3	-.116649	-7		
Fat	.447185	-2	-.154169	-5		
Stature	.125410	-1	-.113214	-3	.329611	-5
Strength	.616432	-1	-.157944	-3	-.194299	-4
Dairy Character	.573174	-2	-.154953	-3	.134321	-4
Foot shape (angle)	.189888	-1	-.427278	-4	-.554301	-5
Rear legs (side view)	-.190005	-1	.619473	-4	.456288	-5
Pelvic angle	-.157072	-1	-.115481	-3	.171675	-4
Thurl width	-.161665	-1	.254669	-4	.573956	-5
Fore udder attachment	.104182	0	-.505411	-3	-.117602	-4
Rear udder height	-.115914	-1	.136827	-3	-.576855	-5
Rear udder width	-.880241	-1	.525198	-3	.644601	-5
Teat placement	.318467	-1	-.865637	-4	-.103189	-4
Suspensory ligament	.100176	0	-.512668	-3	-.108281	-4
Udder depth	.139251	0	-.100762	-2	.121587	-4

[1]Barton et al. (4).
[2]Crossproduct of the product value with each type trait

$$\text{RNI/DPL} = \sum_{k=1}^{15}(a_k T_k + b_k T_k^2) + \sum_{k=3}^{15} c_k T_k V$$

where:

RNI/DPL = predicted RNI/DPL

T_k = first lactation expression of trait k by a particular cow, with T_1 = milk yield and T_2 = fat yield,

a_k = linear coefficient for trait k

b_k = quadratic coefficient for trait k

c_k = coefficient for cross products between trait k and product value

V = value of the production from a particular cow

The value of production of a particular cow (V) was calculated as

$$V = gT_m + hT_f$$

where:

V is the value of product from the cow

T_m is ME milk of the cow

T_f is ME fat of the cow

g & h are coefficients reflecting the economic value of milk and fat.

Practical use of the Net Value function

Barton et al. (4) used the regression model derived from relationships between RNI/DPL and first lactation measurements to predict lifetime performance from expected trait scores of potential offspring when estimates of transmitting ability were available for the parents. Barton used a two step procedure where 1) service sires were preselected for a herd by the use of Maxbull (12) and 2) the particular service sire for

each individual cow was determined to maximize predicted RNI/DPL of expected progeny. Maxbull determines both which sires are to be used and the number of matings to each sire. By using the dam's Cow Indexes (CI) and the potential sire's Predicted differences (PD) for milk, fat, and 13 linear type traits, an estimation of the RNI/DPL of each potential offspring was computed from expected trait values of offspring and the regression coefficients in Table 3.

This expected RNI/DPL can be calculated as follows from the expected production and type traits of the potential offspring (4):

$$\text{RNI/DPL} = \sum_{k=1}^{15}(a_k T_k + b_k T_k^2) + \sum_{k=3}^{15} c_k T_k V$$

where:

RNI/DPL = predicted RNI/DPL

T_k = expected expression of trait k by progeny of a particular mating, with T_1 = milk yield and T_2 = fat yield

a_k = linear coefficient for trait k

b_k = quadratic coefficient for trait k

c_k = coefficient for cross products between trait k and product value.

V = value of the production expected from progeny of a particular mating

The value of production expected of a particular mating (V) is calculated by

$$V_{ij} = gT_{ijm} + hT_{ijf}$$

where:

V_{ij} is the value of product from the expected offspring of the ith sire and jth cow

T_{ijm} is ME milk of the expected offspring of the ith sire and jth cow

T_{ijf} is ME fat of the expected offspring of the ith sire and jth cow

g & h are coefficients reflecting the economic value of milk and fat.

Barton (4) accounted for potential decreased production due to an increase in inbreeding, by calculating inbreeding coefficients for all potential offspring using a pedigree consisting of the parents and their nearest six ancestors. Expected milk and fat yields of predicted progeny were reduced by 22.7 kg and .86 kg respectively, per percent inbreeding (Young et al.(24)), prior to calculation of V and used to determine expected RNI/DPL of predicted offspring. Potential offspring (adjusted for inbreeding) were then ranked from highest to lowest RNI/DPL, and matings designated by choosing those with the highest RNI/DPL of potential offspring for each cow until the maximum use of each sire was reached. Once a sire has reached the limit imposed by Maxbull, he was not used further. This may result in less than the maximum expected average NV of progeny for the herd since use of limited sires where highest NV progeny are produced will not necessarily yield highest NV average for all offspring.

Inbreeding

The effects of inbreeding have been discussed by several authors. Young et al. (24) reviewed data collected in the North Central regional dairy cattle breeding project (NC-2) including herds in Iowa, Michigan, Minnesota, Missouri, Ohio, South Dakota and Wisconsin. Results in these states agreed well even though herds represented Holsteins, Guernseys, and Jerseys under varying management conditions. The effects of more intense inbreeding on production was studied in South Dakota and Wisconsin. The effects of inbreeding varied in different lines in Wisconsin. Simple linear regressions within each line per .01 increase in inbreeding coefficient ranged from -.45 kg to -60.33 kg for actual milk and 0.14 kg to -2.09 kg actual fat. Production traits of inbreds and outbred controls for Wisconsin and South Dakota are listed in Table 4. The linear ef-

Table 4. Comparison of first lactation production of inbreds and outbreeds at South Dakota and Wisconsin[1]

Trait	South Dakota[2]			Wisconsin[3]		
	Outbreds	Inbreds	Diff.	Outbreds	Inbreds	Diff.
Actual milk (kg)	5479	4641	838**	4398	3809	591**
Actual fat (kg)	193	172	24**	153	137	16**
Fat test (%)	3.60	3.73	-0.13**	3.47	3.59	-0.12**
ME Milk (kg)	6838 [4]	5952	886**	5708	4909	799**
ME Fat (kg)	249 [4]	222	27**	199	176	22**

** < .01.
[1]Young et al. (24).
[2]Comparison involved 57 outbreds and 35 inbreds.
[3]Comparison involved 71 outbreds and 111 inbreds.
[4]Adjusted for sire increases over herdmates.

fects of inbreeding on production in the Wisconsin study allowed estimating regressions. For each .01 increase in inbreeding in the Wisconsin study, regressions were -23.59 kg and -.64 kg actual milk and fat respectively.

In general the NC-2 regional project on dairy cattle breeding has shown that inbreeding depresses milk yield, fat yield, growth, liveability and reproductive performance. A summary of the average effects of each of three levels of inbreeding on the traits studied in the NC-2 project are in Table 5. These results showed that the effects of inbreeding were approximately linear, at least over the levels examined. Overall the NC-2 project indicates inbreeding depresses yield approximately 22.68 kg milk and .68 kg fat for each 1% inbreeding.

Inbred calves in the NC-2 project had higher mortality than outbred controls. This relationship also was shown by Regan et al. (19) who defined mortality as all abortions, stillbirths, and deaths of calves up to four months of age. Since bull calves were disposed of at birth, data were only for heifer calves grouped into four classes (class I inbreeding coefficients ranged from 0.0 to 0.1249, class II ranged from 0.125 to 0.2449, class III from 0.245 to 0.3749, and class IV from 0.375 to a maximum of 0.47). A summary of the relationship between mortality and inbreeding is listed in Table 6. Regan et al. (19) found mortality to be significantly higher for Jersey heifers in classes II, III, and IV when compared to calves in class I (the control). Mortality in classes II and III were similar but higher in class IV. These differences were not, however significant, probably due to low sample numbers. Differences in Holstein heifers also were not significant. Low sample numbers and a change in management toward the end of the study may explain , in part, why there were no significant differences.

Young et al. (24) discouraged the use of inbreeding since in most cases inbreed offspring will perform at a inferior level compared to their outbred sisters. Inbreeding should not however be avoided at any costs. If a sire's merit is high enough his

Table 5. Average effect of three levels of inbreeding on some economically important traits in dairy cattle[1]

Trait	Level of inbreeding (%)		
	6.25	12.5	25.0
Milk yield	-136 kg	-272 kg	-544 kg
Fat yield	-4.1 kg	-8.2 kg	-16.3 kg
Fat (%)	+.02%	+.04%	+.12%
Birth weight	-0.68 kg	-1.36 kg	-2.72 kg
Yearling Weight	-4.54 kg	-11.3 kg	-27.2 kg
2-year weight	-4.54 kg	-9.07 kg	-27.2 kg
Mature weight	?	?	?
Yearling height	-0.6 cm	-1.2 cm	-2.4 cm
2-year height	-0.4 cm	-0.8 cm	-2.4 cm
Mature height	0	0	?
Yearling heart girth	-1.0 cm	-2.0 cm	-4.0 cm
2-year heart girth	-1.2 cm	-2.4 cm	-4.8 cm
Mature heart girth	-0.8 cm	-1.6 cm	-3.2 cm
Mortality (% of outbred)	112%	125%	150%

[1]Young et al. (24)

Table 6. The relationship of total mortality to the degree of inbreeding in female Jersey calves to 4 months of age.

Number of births	Coefficient of inbreeding: Class limits	Coefficient of inbreeding: Mean ± S. E.		Mortality: Mean ± S. E.	
		Jersey			
159	0.0 - 0.1249(I)	0.03	0.003	0.16	0.029
68	0.125 - 0.2449(II)	0.19	0.004	0.34	0.057
101	0.245 - 0.3749(III)	0.28	0.003	0.35	0.047
44	0.375 and over[1](IV)	0.41	0.004	0.43	0.075
		Hostein			
46	0.0 - 0.1249(I)	0.02	0.005	0.13	0.050
18	0.125 - 0.2449(II)	0.15	0.004	0.11	0.074
38	0.245 - 0.3749(III)	0.27	0.005	0.21	0.066
19	0.375 and over[2](IV)	0.39	0.005	0.10	0.069

[1]Regan et al. (19).
[2]Highest coefficient of inbreeding in the class was 0.47
[2]Highest coefficient of inbreeding in the class was 0.44

daughter's performance may be higher than daughters of alternative sires despite inbreeding, and the sire should be used.

Materials and Methods

Data for this study included 172,951 DHI lactation records of Jersey cows received from American Jersey Cattle Club (assembled at USDA Animal Improvements Programs Laboratory, USDA, Beltsville, MD). These records included mature equivalent (ME) milk, ME fat, and 13 linearly scored type traits collected from January 1980 through May, 1985.

Scores for 13 linearly scored type traits (Table 3) were adjusted for effects of age and stage of lactation using factors developed by Norman (16). Adjustments for stage of lactation were made from 8 stage categories, derived from actual days in milk and recorded stage of lactation class (unknown, milking, milking-stale, dry, dry-springing), Multiplicative adjustment factors for age were for 183 months of age at classification ranging from 18 to 200 months.

Records were restricted to those scored between 18 and 200 months of age and classified at no more than 500 days in lactation, so that all scores in the data set could be age and stage adjusted. Edits also required cows to have valid linear type scores between 50 and 99 points for all traits. To emulate conditions characteristic of on-farm

breeding decisions, cows were restricted to those who were present in the herd at the time of last classification.

A second data set also received from USDA Animal Improvements Programs Laboratory consisted of Cow Index (CI) records from the July, 1985 USDA cow evaluation run for 184,003 Jersey cows. Records were edited to those which included CI records for yields of milk and fat and for the 13 linearly scored type traits. This second data set was merged with the first data set by cow. Each cow record then consisted of a phenotypic record and a estimated genotypic record for milk, fat, and the 13 linearly scored type traits.

Herd phenotypic means for ME milk, ME fat, and 13 linearly scored type traits were computed for cows remaining in the herd after all edits by averaging phenotypic records for each trait. Estimated herd genotypic means were computed by averaging remaining records for CI milk, CI fat, and CI's for 13 linearly scored type traits in each herd and then doubling the CI averages to obtain estimated herd genotypic means. The estimates of herd phenotypic and genotypic means were added to the end of each cow's record. A final edit removed herds with less then 20 cows after all other edits.

Observations decreased to 25,203 cows after age and stage of lactation adjustments, imposing requirements of being in the herd at time of last classification, and being in both data sets. Editing for herd size further reduced observations to 20,487 cows in 440 herds.

Genetic evaluations for sires were received from USDA Animal Improvement Programs Laboratory and consisted of Predicted Differences (PD) for yield of milk and fat for 79,790 sires and PD's for linear type traits of 6,206 sires. These records were edited to contain only Jersey sires in active artificial insemination (AI) to use as a mate for the cows in simulating offspring. After edits, 45 active AI sires with genetic evaluations for production and type remained.

Sire PD's and breed averages for milk, fat, and the 13 linearly scored type traits were used to predict transmitting abilities (TA) for RNI/DPL for each sire. TA were computed by adding breed averages for each trait to the PD's of each sire. Results were then used in a modification of a prediction formula by Barton et al. (4):

$$TA = \alpha + \sum_{k=1}^{15}(a_k T_k + b_k T_k^2) + \sum_{k=3}^{15} c_k T_k V$$

where:

TA = Transmitting ability for RNI/DPL

T_k = PD of trait k + breed average for trait k

a_k = linear coefficient for trait k

b_k = quadratic coefficient for trait k

c_k = coefficient for crossproducts between trait k and product value.

V = value of the production

α = Intercept = -18.363

The value of production (V_i) was calculated for sire i as:

$$V_i = gT_{im} - hT_{if}$$

where:

T_{im} is breed average milk + PD milk of the ith sire

T_{if} is breed average fat + PD fat of the ith sire

g and h are coefficients reflecting the economic value of milk and fat.

(g = .1411/kg milk and h = 3.7787/kg fat.)

The intercept was calculated, using breed averages in the prediction equation, such that mean RNI/DPL equaled that for Jersey cows reported by Barton et al. (4). Linear,

quadratic, and crossproduct coefficients were those computed by Barton et al. (4) and are listed in Table 3.

Predicted phenotypes for milk yield, fat yield, and the 13 linearly scored type traits were computed for all possible potential offspring, (20,487 dams X 45 sires = 921,915 potential offspring estimated), using a prediction equation developed by Shook et al. (20) and found on pages 12 - 13. Breed averages used were estimated by Barton et al. (4). Variances among and within herds, and heritabilities were as estimated by Norman et al. (18). Breed averages, variances, and heritabilities are listed in Table 7. Values for b varied for the traits and for herd size, b value for milk yield in a herd of 40 was .95.

Predicted RNI/DPL was calculated for each potential offspring using expected performance levels for milk yield, fat yield and 13 linear type traits in a prediction equation given by Barton et al. (4), similar to that used to calculate TA's for RNI/DPL of the sires. This equation takes into account possible non-linear relationships between production and type traits and profitability by using linear and, quadratic effects of production and type traits, and allowing for cross products between each type trait and value of production (V). Expected RNI/DPL was calculated as follows from the expected production and type traits of the potential offspring:

$$\text{RNI/DPL} = \alpha + \sum_{k=1}^{15}(a_k T_k + b_k T_k^2) + \sum_{k=3}^{15} c_k T_k V$$

where:

RNI/DPL = predicted RNI/DPL

T_k = expected expression of trait k by progeny of a particular mating

a_k = linear coefficient for trait k

b_k = quadratic coefficient for trait k

c_k = coefficient for cross products between trait k and product value.

V = value of the production expected from progeny of a particular mating

Table 7. Components of Variance, Heritabilities (h^2), Breed Averages (BA), and Standard Deviations for Milk yield fat yield and 13 linearly scored type traits.

	Variance among herds[1]	Variance within herds[1]	h^2[1,3]	BA[2,4]	Standard deviation[2,4]
Milk yield (kg)	288,474	793,881	.25	5427	891
Fat yield (kg)	552.69	1,521	.25	260	39
Stature	8.45	37.24	.34	75.0	6.0
Chest and body	3.79	23.06	.22	81.1	5.1
Dairy Character	3.34	24.46	.15	82.0	5.3
Foot shape (angle)	4.15	21.77	.07	68.3	4.6
Rear legs (side view)	6.13	20.87	.08	80.1	4.7
Pelvic angle	3.52	21.45	.29	78.4	4.4
Rump width	9.51	34.72	.20	77.5	5.4
Fore udder attachment	4.68	33.65	.15	79.2	5.2
Rear udder height	4.34	31.83	.14	79.0	5.5
Rear udder width	8.22	34.39	.14	81.6	5.3
Udder depth	2.27	15.87	.27	68.0	4.1
Suspensory ligament	3.60	47.06	.14	79.6	5.3
Teat placement	2.01	19.84	.12	80.0	2.9

[1]Values for type from Norman et al. (18)
[2]Values for type from Barton et al. (4)
[3]within herd
[4]calculated within herd-year of calving from Jersey cows with opportunity for yield to 60 months of age.

α = Intercept = -18.363

The value of production expected from a particular mating (V) was calculated by

$$V_{ij} = gT_{ijm} - hT_{ijf}$$

where:

V_{ij} is the value of product from the expected offspring of the ith sire and jth cow

T_{ijm} is predicted ME milk of the expected offspring of the ith sire and jth cow

T_{ijf} is predicted ME fat of the expected offspring of the ith sire and jth cow

g and h are coefficients reflecting the economic value of milk and fat.

(g = .1411/kg milk and h = 3.7787/kg fat.)

Coefficients for linear, quadratic, and cross products are listed in Table 3.

Inbreeding coefficients were calculated for all potential offspring as 0%, 6.25% (sire of dam is the sire of the service sire), 12.5% (sire's maternal grandsire is the dam's sire), and 25% (sire is the dam's sire). To adjust for decreased production due to inbreeding depression, expected production of each predicted offspring was decreased by 22.7 kg milk and .86 kg fat for every 1% inbreeding (24) prior to calculating predicted RNI/DPL. In addition, Regan et al. (19) found that as inbreeding increases, calf mortality increases. A linear function relating inbreeding to calf mortality from these results indicated a 1.2% increase in calf mortality for every 1% increase in inbreeding. To account for this increase in mortality, each predicted RNI/DPL was further reduced by 1.2% for each percent increase in inbreeding.

Sire Usage

The best mating for each dam was determined by choosing the potential offspring with the highest predicted RNI/DPL. Effects of inbreeding were, as previously stated, considered in predicting RNI/DPL, and no arbitrary restrictions were imposed to avoid inbreeding.

Often bulls in highest demand or those bulls which produce a limited amount of semen will be in limited supply for the dairy farmer to use. In addition some dairy farmers may be reluctant to use much semen from high priced bulls. This problem is more pronounced in the Holstein breed than in the Jersey breed at the present time. Data regarding actual limitations on the 45 active AI Jersey sires in this study were unavailable. Therefore a nonlinear function relating semen availability to semen price was developed, to simulate limits on semen availability. Maximum usage of a bull in a herd was expressed as a function of his semen price by: $Maxuse = 99.6235 + 1.37691(Price) - .9094(Price^2) + .030988(Price^3)$ where Maxuse was as a percentage of the herd and coefficients were regression estimates to fit an arbitrary curve. For example, if a sire's semen was priced at $10, his corresponding maximum usage would be $99.6235 + 1.37691(10) - .9094(10^2) + .030988(10^3) = 55.3$. This sire could then be used as a mate for up to 55.3% of the cows in the herd. Semen prices ranged from 3 to $20 with corresponding maximum usage ranging from 96.6 to 18.7% of cows in a herd. In most cases, cost of semen will, at least to some degree, reflect demand and availability of semen from a bull.

Mate Selection and Pairing

Five different methods of assigning sires to dams were evaluated when sire usage was restricted by limits imposed in this study. Each of the five methods used the same data set composed of predicted RNI/DPL of all possible potential offspring.

The first method of assignment of sires to cows with restricted use of sires was accomplished using linear programming (LP) techniques. A transportation model (7,8) was used to chose the mating (one potential offspring) for each dam that would result in the greatest herd average expected RNI/DPL for all offspring, given the limitations on sire usage. Results of the LP method were used as a comparison to test the efficiency of the other four, more easily applied methods for assigning matings (potential offspring).

In the second method of mate selection, all possible offspring within a herd were sorted by their predicted RNI/DPL. Mates were assigned to cows from highest to lowest RNI/DPL of offspring using the restriction that each cow was mated to only one bull and each bull was used no more than indicated by his corresponding maximum usage. Once the maximum allowance for a dam or sire was reached all other possible offspring for that dam or sire were ignored. The result of this method was that restricted use sires were assigned where maximum RNI/DPL of individual offspring was achieved.

The third method of mate selection utilized deviations from the mean of all potential progeny for each dam. Means were computed for all potential offspring of each dam, (45 potential offspring in each mean), for their predicted RNI/DPL. Each offspring was then deviated from its dam's potential offspring mean. Deviations were then sorted within each herd and selections were made by choosing the highest deviations first and moving toward the lowest while maintaining limitations on dams and sires.

The result of this method was that restricted use sires were assigned where maximum increase in RNI/DPL of offspring was obtained relative to the average for each dam.

Table 8 gives an theoretical example of how methods two and three can vary. Semen from sire two is limited to one mating while semen from sire one is unrestricted. If pairings are made using method two the limited semen is used on cow one and the average predicted progeny RNI/DPL is $1.81. However, if method three is used the limited semen is used on cow four and the average predicted offspring RNI/DPL rises to $2.13.

In the fourth method matings were made by using deviations from the next highest potential offspring of the same dam. All potential offspring were sorted by their predicted RNI/DPL for each dam. Each potential offspring was then deviated from the next highest potential offspring, e.g. if the predicted RNI/DPL for the highest offspring of a dam was $1.10 and the second highest potential offsprings predicted RNI/DPL was $.90, the deviation for the highest offspring was $.20. Since the lowest offspring cannot be deviated, the new data set only contained 44 predicted offspring for each dam rather than the 45 in the previous data set. Deviations were sorted within each herd and selections were again made by choosing the highest deviations first and working toward the lowest, while maintaining limitations on dams and sires.

The fifth method employed selection of sires based on their TA for RNI/DPL and random mating to dams. All dams were assigned a random number by a random number generator. Dams, within herds, were then sorted by their random number. Sires previously had a TA for RNI/DPL calculated for them and were sorted by it. Beginning with the sire with the highest TA for RNI/DPL and the dam with the lowest random number, selections were made (one offspring per dam). The sire with the highest TA for RNI/DPL was used until its limitations were reached at which point the second highest and then third and so on were used to their limitations, respectively, until all dams were

Table 8. Example of the theoretical difference between methods two and three of assigning sires with limited semen supplies.

	Sire			
	1		2	
Cow	$\hat{RNI}/DPL$	Deviation[1]	$\hat{RNI}/DPL$	Deviation[1]
1	2.25	-.13*	2.50*	.12
2	2.00*	.12*	1.75	-.13
3	2.00*	-.13*	2.25	.12
4	0.75*	-.75	2.25	.75*

[1]Deviation of potential offspring from mean of all potential offspring from that dam.

mated. This method is essentially selection (on RNI/DPL) without attention to pairing and was used to determine if the non-linear relationships between individual traits and RNI/DPL were sufficiently important to justify the extra expense of sire and dam pairing as compared to selection and random mating.

The four methods of choosing specific mating pairs (excluding random pairing) were compared with respect to probable expense of use. Representative herd sizes were chosen, (as close to 25 cow increments as possible), and the amount of computer time necessary to make the mating selections for each method (except the random method) were recorded to make cost comparisons of each of the mating systems. The number and identity of sires used in each of the 440 herds also were recorded.

Variation in Predicted RNI/DPL

The relative importance of factors causing variation in predicted RNI/DPL of all potential offspring (921,915) were estimated from the model

$$\widehat{RNI/DPL}_{ijkl} = \mu + \alpha_i + \beta_j + \gamma(\alpha)_{ji} + \beta\gamma(\alpha)_{jki} + \delta_l + \varepsilon_{ijklm}$$

where:

$\widehat{RNI/DPL}$ is the predicted Relative Net Income per day of productive life of the potential offspring of the jth sire and the kth cow within the ith herd.

μ is the overall mean

α_i is the effect of the ith herd (i = 1,...,440),

β_j is the effect of the jth sire (j = 1,...,45),

$\gamma(\alpha)_{ki}$ is the effect of the kth dam within the ith herd,

$\beta\gamma(\alpha)_{jki}$ is the effect of the interaction between the jth sire and the kth dam

within the ith herd,

δ_l is the effect of the lth class of inbreeding (1 to 4 for F = 0, .0625, .125, and .250), and

ε_{ijklm} is error

All effects except μ and δ were assumed to be uncorrelated random variables with means 0 and variances σ^2_α, σ^2_β, $\sigma^2_{\gamma(\alpha)}$, $\sigma^2_{\beta\gamma(\alpha)}$, and σ^2_e, respectively. The analysis of variance was computed in four steps since the amount of core required for analysis in a single run was greater than was available. The first step computed sums of squares for herd and cow within herd using a nested analysis of variance with the model

$$\hat{RNI/DPL} = \mu + \alpha_i + \gamma(\alpha)_{kl} + \varepsilon_{ikl}$$

where the effect of sire, the interaction of sire with cow within herd and level of inbreeding were included in error.

The second step computed sums of squares for sires using the model:

$$\hat{RNI/DPL} = \mu + \beta_j + \varepsilon_{jl}$$

where herd , cow within herd, and the interaction of sire with cow within herd were included in error.

The third step computed sums of squares for error using the model:

$$\hat{RNI/DPL} = \mu + \rho_m + \varepsilon_{mn}$$

where ρ_m is a sire and herd subclass containing herd, sire, and sire by herd interaction (error). The error term was found by subtracting sums of squares for sire and herd.

The forth step computed sums of squares for inbreeding class using the model:

$$\hat{RNI/DPL} = \mu + \delta_l + \varepsilon_{lm}$$

where all effects except inbreeding were included in error. The sums of squares for the interaction of sire with cow within herd was found by subtracting sums of squares for herd, sire, cow within herd, inbreeding class, and the error term from the total sums of squares. Degrees of freedom (df) were found for each effect in the same manor as were the sums of squares. Mean squares (MS) were determined by dividing sums of squares for each effect by its appropriate df.

The relative importance of genetic evaluations for sires, dams, and their crossproducts in determining expected RNI/DPL of predicted progeny, was determined from the model,

$$\hat{RNI/DPL}_{ijk} = \mu + Herd_i + \sum_{j=1}^{15}[b_1PD_j + b_2CI_j + b_3(PD_j \times CI_j)] + \varepsilon_{ijk}$$

where:

$\hat{RNI/DPL}_{ijk}$ is the predicted Relative Net Income per Day Productive Life of the kth offspring in herd i, of a sire with with predicted difference PD_j and a dam with cow index CI_j for the jth trait,

$Herd_i$ is the effect of the ith herd,

PD_j is the predicted difference of the sire of the predicted offspring for the jth trait,

CI_j is the cow index of the dam of the predicted offspring for the jth trait, and

ε_{ijk} is the error of predicting RNI/DPL

Herd was accounted for in the model by absorption.

Results and Discussion

Data for this study consisted of all possible offspring (simulated) for 45 active Jersey sires, and 20,487 dams in 440 herds. Predicted RNI/DPL for all possible offspring ranged from -4.08 to 2.09 (dollars per day) with a mean of 0.288 and standard deviation of 0.75. Overall mean by herd was slightly lower ($\bar{x}$ = 0.271) with a smaller range (-3.10 to 1.83) and a standard deviation of 0.773. Means, standard deviations, and ranges for all possible offspring and for herd average RNI/DPL are listed in Table 9.

Sire data

Means, standard deviations, and ranges of transmitting abilities (TA) of sires for RNI/DPL are in Table 10. The TA for RNI/DPL was calculated using a modification of the prediction equation described previously developed by Barton et al. (4) which uses linear and quadratic terms as well as crossproducts between type traits and product value (a function of PD milk, PD fat, and the economic values of milk and fat). Also included are simple correlations between TA for RNI/DPL and TA's for milk yield, fat

Table 9. Means, standard deveations, and ranges, for all possible offspring and for herd average RNI/DPL

	N	Mean	Standard deviation	Minimum	Maximum
Overall	921,915	0.288	0.753	-4.081	2.091
Herd average	440	0.271	0.773	-3.102	1.828

Table 10. Means, standard deveations, ranges, of sire evaluations (TA) for RNI/DPL and simple correlations with TA'S for production and type traits of 45 Jersey sires in active AI.

Transmitting abilities	Mean	Standard deviation	Minimum	Maximum	Simple correlation with *RNI/DPL*
RNI/DPL	0.95	0.08	0.81	1.20	1.00
Milk yield	706.11	331.00	97.00	1503.00	.83
Fat yield	28.11	14.64	-7.00	67.00	.75
Dollar value	88.16	35.11	23.00	195.00	.98
Stature	0.10	1.46	-2.70	3.60	-.33
Strength	-0.14	1.13	-2.10	2.40	-.35
Dairy character	0.79	0.74	-0.70	3.10	.50
Foot shape (angle)	-0.00	0.73	-1.80	2.00	-.08
Rear legs (side view)	-0.02	0.90	-2.20	1.90	.14
Pelvic angle	0.36	1.02	-2.10	2.50	.01
Thurl width	-0.24	1.08	-2.80	1.90	-.02
Fore udder attachment	-0.10	1.04	-3.10	2.20	-.03
Rear udder height	0.02	0.82	-2.60	1.50	.35
Rear udder width	0.21	0.68	-1.10	1.60	.16
Teat placement	0.24	1.09	-2.30	2.40	-.29
Suspensory ligament	0.12	0.96	-2.60	1.90	-.19
Udder depth	0.02	0.68	-1.70	1.50	.12

yield, dollar value (PD$), and for each of the 13 linearly scored type traits. Simple correlations ranged from .98 for PD$ to -.35 for strength. Simple correlations for milk yield and fat yield were .83 and .75 respectively, showing the overwhelming influence of production on the RNI/DPL function. Type traits with positive simple correlations were dairy character (.50), rear legs side view (.14), pelvic angle (.01), rear udder height, (.35) rear udder width (.16),and udder depth (.12) of which dairy character and rear udder height were the most important in estimating a TA for RNI/DPL. Those traits with negative simple correlations were stature (-.33), strength (-.35), foot angle, (-.08), Thurl width (-.02), fore udder attachment (-.03), and suspensory ligament (-.18). Simple correlations of traits with intermediate optimums (foot angle, rear legs, pelvic angle, teat placement, and udder depth) are of limited value since they can not be fit by a linear equation.

Means, standard deviations, and ranges for 25,203 CI records are listed in Table 11. Included in the data are cows in herds of less than 20 cows, which were later discarded. Standard deviations for CI milk yield, fat yield, and dollar value were greater than corresponding standard deviations for the sires. Standard deviations for all 13 of the linearly scored type traits were less than those for the sire data.

Mate Selection and Pairing

Means, standard deviations, and ranges for herd average predicted RNI/DPL of expected progeny were calculated for each of the five mating systems (Table 12). The linear programming (LP) method yielded the maximum average herd mean ($\bar{x}$ = .459) . However there were no significant differences (Tukey's W, P > .05) between the LP method and methods two and three ($\bar{x}$ = .456 and .458 respectively) . Standard devi-

Table 11. Means, standard deviations, and ranges of cow indexes for milk yield, fat yield, dollar value and 13 linearly scored traits for 20,203 cows.

Cow index	Mean	Standard deviation	Minimum	Maximum
Milk yield	-482.89	367.54	-2030.00	1254.00
Fat yield	-16.97	15.83	-84.00	61.00
Dollar value	-57.89	47.60	-276.00	156.00
Stature	-0.01	1.35	-5.70	6.00
Strength	0.04	0.73	-3.70	3.20
Dairy character	0.10	0.59	-3.30	2.00
Foot shape (angle)	0.01	0.42	-2.00	1.90
Rear legs (side view)	-0.04	0.40	-2.30	1.80
Pelvic angle	-0.04	0.82	-3.70	3.30
Thurl width	0.01	0.79	-4.00	2.50
Fore udder attachment	-0.06	0.75	-3.80	2.30
Rear udder height	-0.09	0.59	-3.20	1.90
Rear udder width	-0.09	0.59	-3.20	2.20
Teat placement	-0.03	0.59	-2.70	2.60
Suspensory ligament	-0.03	0.78	-3.90	2.60
Udder depth	-0.03	0.77	-4.70	3.00

Table 12. Herd means, standard deviations, ranges,for herd average RNI/DPL and number of sires used in each of the five pair selection methods

Method	mean	Standard deviation	Minimum	Maximum	Number of sires used	Number of sires used > 1%
LP	.459	.75	-2.79	1.96	14	4
2	.456	.75	-2.79	1.95	14	4
3	.458	.75	-2.79	1.95	14	4
4	.312	.77	-2.97	1.83	41	14
Random	.453	.75	-2.84	1.95	4	4

LP: Linear Programming, Transportation model.
2: Progeny selected by highest predicted RNI/DPL for each dam.
3: Progeny selected by deviation from dams potential offspring mean.
4: Progeny selected by deviation from next highest potential offspring from the same dam.
Random: Sires are preselected and randomly mated to dams.

ations and ranges for the LP method, and methods two and three were also essentially the same. Although average herd mean RNI/DPL for the random method (selecting sires and randomly mating them to the herd) was significantly different from the LP method ($\bar{x}$ = .453) it was not significantly different from method three ($P > .05$) . The random method is essentially the procedure Maxbull (12) would employ as it maximizes the breeders goals through sire selection without specifying any pairing of mates.

The fourth method of mate pairing chose the potential offspring with the greatest deviation from the next highest potential offspring of the same dam. The largest deviations could occur for any of the potential offspring (except the lowest which could not have a deviation) but are most likely to occur near the extremes. This system could therefore chose nearly the worst pairing for a cow resulting in a lower herd average RNI/DPL than the other systems.

The number of sires used by each of the five mating systems and the number used more than 1% of the time are also recorded in Table 12. The four mating systems with the highest means all used only four sires more than 1% of the time, although 14 different sires were used in at least one mating. The random method used only the four sires with highest TA for RNI/DPL.

Effects of inbreeding were accounted for by decreasing predicted RNI/DPL of potential offspring according to level of inbreeding. As inbreeding increased, predicted RNI/DPL of the potential progeny was reduced, making unlikely a pairing which would produce a highly inbred animal. However, with random mating, such matings were not avoided. Due to limited data on the relationships of animals, inbreeding fell into four distinct categories 0%, 6.25% (mating sire to the daughter of half brother), 12.5% (mating sire to half sister), and 25% (mating sire to his own daughter). Each category was assigned a class number (1, 2, 3, and 4 respectively). The four classes and their frequencies of occurrence are listed in Table 13. Although 98% of all possible progeny

Table 13. Levels of inbreeding and their frequency of occurence over all possible matings for all possible progeny

Class	Inbreeding	Frequency	Percent	Cumulative frequency	Cumulative percent
1	0	904,841	98.1	904,841	98.1
2	6.25	2,255	0.2	907,096	98.4
3	12.50	10,532	1.1	917,628	99.5
4	25.00	4,287	0.5	921,915	100.0

were not inbred the other 2%, may at least in part, account for the lower mean for the random mating method.

The four sires which were most commonly used in the mating systems along with the number of cows to which they were mated and the number of herds represented by their mates for each of the five methods are in Table 14. These four sires had the highest TA's for RNI/DPL of the 45 possible sires. The maximum usage of these four sires (calculated as a function of their semen price) was high enough that the mating systems could mate a herd (or all herds) to only these four sires. Although data on actual semen availability was unavailable, the maximum usage function should represent to some extent availability of semen from a sire. Maximum usage for these four sires were 18.6%, 55.2%, 18.2%, and 55.2% respectively. Maximum usage, the percent of cows bred to, and percent of herds those cows were in are listed in Table 15. The second listed bull (Royal) was used the most in four of the five pair mating systems since his maximum usage was considerably higher than that of the first listed bull (Duncan).

Computational time required to make pair selections varied over the methods of pairing. Time required to make pair choices for representative herd sizes for the LP method and methods two, three and four are listed in Table 16. Time required for random mating was not recorded as in practice it would not be done by computer. The second method of mate pairing was fastest to make the matings. The LP method, as expected, required a considerably larger amount of computational time to make matings, probably making it an undesirable choice for most applications. In addition, time required by the LP method increased much more than the other systems with increasing herd size. For example as compared to the second method (the most time efficient) for a herd of 25, the LP used 5.75 times as much computer time (4.78 seconds as compared to 0.83 seconds). When herd size increased to 50 the LP used 26.96 times

Table 14. Sires most commonly used in each of the five pair selection methods

Registration number	Bull name	RNI/DPL	LP		2		3		4		Random	
			Cows	Herds	Cows	Herds	Cows	Herds	Cows	Herds	Cows	Herds
635862	Duncan	1.20	3,607	440	3,592	440	3,592	440	3,563	438	3,592	440
634142	Royal	1.12	10,919	440	10,881	440	10,930	440	163	47	11,107	440
630622	Top Brass	1.10	1,904	298	1,185	256	2,084	289	2,125	309	3,592	440
632243	Yankee	1.09	3,953	427	4,128	433	3,755	425	3,581	263	2,196	440

LP: Linear Programming, Transportation model.
2: Progeny selected by highest predicted RNI/DPL for individual offspring
3: Progeny selected by deviation from dams potential offspring mean.
4: Progeny selected by deviation from next highest potential offspring from the same dam.
Random: Sires are preselected and randomly mated to dams.

Table 15. Maximum usage and percent used of most commonly used sires in each of the five pair selection methods

Registration number	Bull name	Maximum usage	LP		2		3		4		Random	
			Cows	Herds	Cows	Herds	Cows	Herds	Cows	Herds	Cows	Herds
635862	Duncan	18.6	17.61	100	17.53	100	17.53	100	17.39	99.55	17.53	100
634142	Royal	55.2	53.30	100	53.11	100	53.35	100	0.80	10.68	54.21	100
630622	Top Brass	18.6	9.29	56.36	8.81	58.18	10.20	65.68	10.37	69.09	17.53	100
632243	Yankee	55.2	19.20	97.05	20.15	98.41	18.33	96.59	17.40	59.77	10.71	100

LP: Linear Programming, Transportation model.
2: Progeny selected by highest predicted RNI/DPI, for individual offspring
3: Progeny selected by deviation from dams potential offspring mean.
4: Progeny selected by deviation from next highest potential offspring from the same dam.
Random: Sires are preselected and randomly mated to dams.

Table 16. Computing time required for representive herd sizes for four mating systems

Herd size	Method of mate selection			
	LP	2	3	4
	(min:sec)	(sec)	(sec)	(sec)
25	4.78	.83	1.22	.96
50	33.16	1.23	1.78	1.84
75	1:08.36	1.58	2.26	2.34
100	1:39.12	1.88	2.80	2.86
123	1:08.81	2.21	3.26	3.29
151	2:43.83	2.62	3.89	3.93
205	4:25.46	3.36	5.01	4.93
238	5:41.09	3.77	5.73	5.94
252	5:56.40	4.01	6.02	5.96

LP: Linear Programming, Transportation model.
2: Progeny selected by highest predicted RNI/DPL for each dam.
3: Progeny selected by deviation from dams potential offspring mean.
4: Progeny selected by deviation from next highest potential offspring from the same dam.

as much time, for a herd of 75, 43.27 times as much, and for a herd of 252 it used 88.88 times as much computer time.

Variation in Predicted RNI/DPL

The relative importance of factors causing variation in predicted RNI/DPL for all potential offspring was estimated by analysis of variance (ANOVA) of a model including herd, dam within herd, sire, sire by dam within herd, and inbreeding level. Due to the size of the model, sums of squares were computed in four separate analyses. The first analysis calculated sums of squares (SS) and degrees of freedom (df) for herd and dam within herd. Variance for sire, sire by dam within herd interaction, and inbreeding class were contained in error (Table 17). The second analysis calculated SS and df for sire while all other variation was in error (Table 18). The third analysis utilized a sire-herd subclass which contained variance for herd, sire, and sire by herd interaction (error in the full model), (Table 19). SS and df for the sire by herd interaction was found by subtracting SS and df for herd and sire (from steps one and two respectively) from those for sire-herd subclasses. Sum of Squares and df for inbreeding class was found using a model where all variation except inbreeding class was included in error (Table 20). Lastly df and SS for the sire by dam within herd interaction was computed as the difference between total df and SS and those form all other sources. Table 21 is a composite ANOVA including F values for sources of variation in expected RNI/DPL. Analysis of variance for all possible offspring showed herd, dam, sire, and inbreeding class all to be significant in determining RNI/DPL of the offspring. ANOVA did not however find the interaction between sire and dam to be significant. These results indicate the importance of sire and dam selection, and the lack of importance of sire and

Table 17. Analysis of variance for predicted RNI/DPL used to find SS and df for herd and dam within herd from all potential offspring.

Source	df	Sum of Squares	Mean Squares
Herd	439	505,797.500	1,152.168
Dam(Herd)	20,047	9,385.256	0.468
Error	901,428	7,497.660	0.008
Total	921,914	522,680.410	

Table 18. Analysis of variance for predicted RNI/DPL used to find SS and df for sire from all potential offspring

Source	df	Sum of Squares	Mean Squares
Sire	44	6,070.90	137.975
Error	921,870	516,609.51	0.560
Total	921,914	522,680.41	

Table 19. Analysis of variance for predicted RNI/DPL used to find sire by herd interaction (error) through sire-herd subclass from all potential offspring.

Source	df	Sum of Squares	Mean Squares
Sire-Herd	19,799	512,167.75	25.868
Error	902,115	10,512.67	0.012
Total	921,914	522,680.41	

Table 20. Analysis of variance for predicted RNI/DPL used to find SS and df for inbreeding class from all potential offspring.

Source	df	Sum of Squares	Mean Squares
F Class	3	983.43	327.811
Error	921,911	521,696.98	0.566
Total	921,914	522,680.41	

Table 21. Composite analysis of variance for predicted RNI/DPL

Source	df	Sum of Squares	Mean Squares	F
Herd	439	505,797.50	1,152.168	2461.897
Dam(Herd)	20,047	9,385.26	0.468	2340.000
Sire	44	6,070.90	137.975	689,897.000
Sire X Dam(Herd)	882,065	143.97	.0002	.013
F Class	3	983.43	327.811	281,520.000
Error	19,316	299.35	0.015	
Total	921,914	522,680.41		

dam pairings, in determining expected RNI/DPL of offspring. The lack of a significant sire by dam interaction likewise is consistent with the small differences found between optimum LP pairing and other pairing methods, and further suggests that slight superiority of specific to random pairing of mates was from the avoidance of inbreeding. Apparently, non-linear relationships between RNI/DPL and the traits examined were not of sufficient magnitude to yield much benefit from optimum mate pairing.

The relative importance of genetic evaluations for individual traits of sires, dams, and their crossproducts in determining expected RNI/DPL of predicted progeny was determined using multiple regression analysis. The regression model included terms for PD's and CI's for milk yield, fat yield, and 13 linearly scored type traits and the crossproducts of PD's and CI's for each of the previously listed traits. Data for the regression consisted of 921,915 simulated offspring of 20,487 dams and 45 sires (all possible offspring).

Table 22 contains SS, F, regression estimates, and standard errors of estimates. All linear regressions except that for PD udder width were significantly different from zero. Estimates of linear regressions for PD and CI ranged from 5.80×10^{-3} for CI fore udder attachment to -2.60×10^{-3} for CI thurl width. PD's and CI's for milk yield, fat yield, stature, strength, dairy character, foot angle, fore udder udder attachment, rear udder height, rear udder width, suspensory ligament, and teat placement were positive while PD's and CI's for rear legs side view, pelvic angle, thurl width, and udder depth were negative. The magnitude of F-values for PD and CI for yields of milk and fat again indicates the importance of production in determining RNI/DPL.

Crossproducts between of PD's and CI's for milk yield, fat yield, stature, dairy character, rear legs (side view), fore udder attachment, rear udder height, udder depth, and suspensory ligament significantly ($P < .01$) affected predicted RNI/DPL. Crossproducts for strength, foot angle, pelvic angle, thurl width, rear udder width, and teat

Table 22. Degrees of freedom, sums of squares, estimated value, and standard error of estimates for PD's, CI'c and crossproducts of PD' and CI' for 15 traits effecting RNI/DPL.

Source	df	Sum of Squares	F	Estimate	STD Error of Estimate
CI Milk yield	1	585.394	$>10^5$	2.01×10^{-4}	0.38×10^{-6}
PD Milk yield	1	667.293	$>10^5$	1.75×10^{-4}	0.31×10^{-6}
CI Fat yield	1	271.897	$>10^5$	2.91×10^{-3}	8.15×10^{-6}
PD Fat yield	1	633.529	$>10^5$	2.92×10^{-3}	5.35×10^{-6}
CI Stature	1	0.304	143.06	6.66×10^{-4}	5.57×10^{-5}
PD Stature	1	0.744	350.46	1.11×10^{-4}	5.90×10^{-6}
CI Strength	1	4.297	2023.24	5.09×10^{-3}	1.13×10^{-4}
PD Strength	1	1.747	822.69	3.33×10^{-4}	1.16×10^{-5}
CI Dairy Character	1	0.458	215.60	2.19×10^{-3}	1.49×10^{-4}
PD Dairy Character	1	0.652	306.94	2.38×10^{-4}	1.38×10^{-5}
CI Foot shape (angle)	1	2.620	1233.91	4.50×10^{-3}	1.28×10^{-4}
PD Foot shape (angle)	1	6.623	3119.15	5.27×10^{-4}	9.94×10^{-6}
CI Rear legs (side view)	1	0.484	227.85	-2.04×10^{-3}	1.35×10^{-4}
PD Rear legs (side view)	1	0.777	365.90	-1.39×10^{-4}	7.24×10^{-6}
CI Pelvic angle	1	11.785	5549.65	-5.16×10^{-3}	6.92×10^{-5}
PD Pelvic angle	1	15.022	7073.86	-5.99×10^{-4}	7.12×10^{-6}
CI Thurl width	1	2.223	1046.70	-2.60×10^{-3}	8.04×10^{-5}
PD Thurl width	1	0.972	457.86	-2.00×10^{-4}	9.37×10^{-6}
CI Fore udder attachment	1	7.289	3432.44	5.80×10^{-3}	9.90×10^{-5}
PD Fore udder attachment	1	11.864	5586.97	6.55×10^{-4}	8.77×10^{-6}
CI Rear udder height	1	3.557	1674.80	5.17×10^{-3}	1.26×10^{-4}
PD Rear udder height	1	5.511	2597.22	5.75×10^{-4}	1.13×10^{-5}
CI Rear udder width	1	0.348	163.78	1.69×10^{-3}	1.32×10^{-4}
PD Rear udder width	1	0.004	1.67 *	2.13×10^{-5}	1.64×10^{-5}
CI Udder depth	1	0.615	289.42	-1.57×10^{-3}	9.21×10^{-5}
PD Udder depth	1	2.721	1281.37	-4.62×10^{-4}	1.29×10^{-5}
CI Suspensory ligament	1	1.468	691.19	2.05×10^{-3}	7.81×10^{-5}
PD Suspensory ligament	1	1.980	932.36	2.56×10^{-4}	8.39×10^{-6}
CI Teat placement	1	0.183	86.06	9.68×10^{-4}	1.04×10^{-4}
PD Teat placement	1	2.373	1117.30	1.98×10^{-4}	5.93×10^{-6}
Crossproducts $PD_i \times CI_i$					
Milk yield	1	4.844	2281.17	-0.00×10^{-5}	0.22×10^{-6}
Fat yield	1	0.930	43.79	-0.14×10^{-5}	0.22×10^{-6}
Stature	1	0.214	100.76	-2.84×10^{-5}	2.83×10^{-6}
Strength	1	0.003	1.25 *	-0.81×10^{-5}	7.23×10^{-6}
Dairy Character	1	0.025	11.65	3.98×10^{-5}	1.17×10^{-5}
Foot shape (angle)	1	0.003	1.38 *	1.87×10^{-5}	1.60×10^{-5}
Rear legs (side view)	1	0.016	7.67	3.74×10^{-5}	1.35×10^{-5}
Pelvic angle	1	0.003	1.27 *	-0.66×10^{-5}	5.88×10^{-6}
Thurl width	1	0.0001	0.08 *	0.18×10^{-5}	6.25×10^{-6}
Fore udder attachment	1	0.287	135.18	-8.11×10^{-5}	6.98×10^{-6}
Rear udder height	1	0.142	66.68	8.98×10^{-5}	1.10×10^{-5}
Rear udder width	1	0.011	4.96 *	3.03×10^{-5}	1.36×10^{-5}
Udder depth	1	1.210	569.95	-2.38×10^{-4}	9.95×10^{-6}
Suspensory ligament	1	0.411	193.69	8.94×10^{-5}	6.42×10^{-6}
Teat placement	1	0.001	0.34 *	-0.45×10^{-5}	7.74×10^{-6}

* non-significant ($P > .01$)

placement did not significantly ($P > .01$) affect predicted RNI/DPL. Regressions for crossproducts ranged from 8.98×10^{-5} for rear udder height to -8.11×10^{-5} for fore udder attachment. Estimates for dairy character, foot angle, rear legs (side view), thurl width, rear udder height, rear udder width, and suspensory ligament were positive. Estimates for milk yield, fat yield, stature, strength, pelvic angle, fore udder attachment, udder depth, and teat placement were negative.

Regressions of offspring RNI/DPL on estimates of parental transmitting abilities should reflect the mathematical relationships used to predict offspring RNI/DPL from expected offspring trait values. Since expected offspring trait values were linear functions of parental transmitting abilities, significant regression for RNI/DPL on crossproducts between transmitting abilities of parents are reflections of non-linear associations between trait values and RNI/DPL. Although several regressions for crossproduct terms were statistically significant, their magnitude generally was much less than regressions on PD or CI (the latter were 10 to 4500 times the former). These results are consistent with the previous conclusion that non-linear relationships between RNI/DPL and the individual production and type traits measured, are of minor importance when compared with corresponding linear effects.

Summary and Conclusions

Data for this study consisted of 921,915 simulated offspring from all possible matings (made from genetic estimates) of 20,487 cows and 45 active AI sires. Predicted trait values for the offspring (milk yield, fat yield, and 13 linear type traits) were used to predict RNI/DPL.

Predicted RNI/DPL of all potential offspring had a mean of 0.288 (dollars per day) and ranged from -4.081 to 2.091 with a standard deviation of 0.753. Herd averages ranged from -3.102 to 1.828 with a standard deviation of 0.773 and mean of 0.271.

Five different methods of assigning sires to dams were evaluated when sire usage was restricted by limits imposed by this study. Each used the same data set composed of all possible predicted offspring, with the goal to achieve the maximum possible predicted RNI/DPL in herds while using a reasonable amount of computer time.

The first method of assignment of sires to cows with restricted use was accomplished using LP techniques. LP achieved the maximum possible RNI/DPL of potential offspring (0.459). LP techniques however used from 5.75 to 88.88 times as much computer time per herd (for herd sizes of 25 and 252 respectively) as the second method of

pairing. Results of the LP were used as a comparison to test the efficacy of the other four methods.

In the second method of mate pairing all possible offspring in a herd were sorted by their predicted RNI/DPL and mates were assigned to cows from highest to lowest. This method achieved the third highest RNI/DPL (0.456) but was not significantly different ($P > .01$) than the LP method.

The third method of mate selection utilized deviations from the mean of all potential progeny for each dam. Pairings were made within herds by choosing the highest deviations first and moving toward the lowest. (All methods were subject to limits imposed on sires and dams.) This method achieved the second highest mean herd average (0.458) which was not significantly different ($P > .01$) than the LP method. This method of pairing did however use approximately 1.5 times as much computer time as the second method (LP used 3.92 to 59.2 times as much time per herd as this method).

In the forth method of mate pairing potential offspring were deviated from the next highest offspring of each dam. Pairings were again made by choosing the highest deviation first and working toward the lowest. This method of pairing achieved the lowest mean herd average (0.312) and on average used slightly more computer time than the third method.

The fifth method employed selection of sires based on their TA for RNI/DPL (calculated in this study) and randomly mated to dams. This method of mate pairing was significantly different from the LP method, but it still achieved a mean herd average of 0.453. Computational time was not recorded on random pairing. Although sire selection with random pairing was significantly different from LP pairing, the similarity of results from the two methods indicates that although non-linear relationships between individual traits and RNI/DPL exist, they are not very important in prediction of RNI/DPL.

Analysis of variance for predicted RNI/DPL (all possible offspring) indicated herd, dam within herd, sire and inbreeding class to be significant ($P > .01$) variables in determining RNI/DPL. However, the sire by dam within herd interaction did not to significantly affect RNI/DPL, again indicating non-linear relationships between traits and RNI/DPL are not very important.

A final analysis determined the relative importance of genetic evaluations for individual traits of sires, dams, and their crossproducts by regressing PD's, CI's, and their crossproducts for milk yield, fat yield and 13 linear type traits while herd was absorbed. All linear regressions except that for PD rear udder width were significantly differently from zero. Estimates of linear regression ranged from 5.80×10^{-3} for CI for udder attachment to -2.60×10^{-2} for CI for thurl width. With the exception of fat yield, absolute values of linear regressions for CI were larger than those for PD, probably due to the smaller variation in CI compared to PD. The overriding importance of production in the determination of RNI/DPL was indicated by the magnitude of the F values for milk and fat yield ($F > 10^5$). Although nine of 15 crossproducts between PD's and CI's were significant the magnitude of the F values were much lower than those for linear regressions on PD's and CI's, showing the linear effects of parental genetic evaluations to be of much greater importance.

Although non-linear relations between individual traits and RNI/DPL do exist they are of minimal value in determining RNI/DPL. Selection, not pairing, should be of primary importance to the breeder. However, since many breeders are interested in "scientifically" choosing mates for their cows, computerized methods of pair selection could be made available which detract little from genetic progress and which may contribute to the selection of better bulls and avoidance of inbreeding.

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