

THE EFFECT OF INBREEDING ON LIFETIME PERFORMANCE OF DAIRY CATTLE

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(ABSTRACT)

Data for this study were age-adjusted linear scores on all cows scored between 1980 and 1993. Lifetime production information on these cows and their herdmates was used to calculate Relative Net Income adjusted for opportunity cost (RNIOC) for the 2,249,835 cows with an 84 month herdlife opportunity. The effect of inbreeding was analyzed using both a fixed and animal model, with little difference in results. Inbreeding depressed RNIOC by \$12.69 in a fluid market and \$11.53 in a manufacturing market per 1% increase in inbreeding. Addition of somatic cell information in the profit function had little effect. Heritabilities of profit functions were .16 and .14 for a fluid and manufacturing market, respectively. Animal model estimates of inbreeding depression were +.16 days, -6.7 days and -5.1 days for age at first freshening (AFF), days of productive life (DPL) and days in milk (TDIM), respectively. Inbreeding decreased first lactation mature equivalent milk, fat, and protein by 23.7 kg, .85 kg, and .76 kg, respectively and lifetime milk, fat, and protein production by 176.9 kg, 6.4 kg, 5.6 kg, respectively per 1% increase in inbreeding. Inbreeding had little effect on conformation traits. Effects of inbreeding were cumulative, exacting a larger effect on lifetime profit functions than on individual traits, when expressed as a percent of additive standard deviation. This study gives evidence that though not alarming, inbreeding has a deleterious effect on the lifetime performance of dairy cattle.

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Dedication

I would like to gratefully dedicate this body of work to my parents W.D. and Winnie Smith, for their unending support and faith. At those horrible moments throughout my life when I have felt like I couldn't go on you have always said the same thing....,

"you can do it."

Table of Contents

Introduction	1
Review of Literature	
Inbreeding	3
Calculation of Inbreeding Coefficients	5
Somatic Cell Information	6
Lifetime Net Income Functions	7
Relationship of Type to Lifetime Profit and Herd Life	10
Materials and Methods	12
Results	
Inbreeding	21
84 Month Age at First Freshening Data Set	24
60 Month Data Set	30
84 Month Calving Interval Data Set	34
84 Month Type Data Set	36
Conclusions	41
References	45
Vita	50

List of Tables

Table 1.	Estimates of inbreeding depression on first lactation mature equivalent milk, fat, and protein production.	4
Table 2.	Estimates of inbreeding for cows born in 1970, 1976, 1982 and 1990, using various base years.	6
Table 3.	Numbers and percentages of animals removed and those remaining after edits to the 84 month opportunity data set.	13
Table 4.	Costs and values for traits used in calculation of Relative Net Income in fluid and manufacturing markets for the 84 month data set.	14
Table 5.	Numbers and percentages of animals removed and those remaining after edits to the 60 month opportunity data set.	15
Table 6.	Costs and values for traits used in calculation of Relative Net Income in fluid and manufacturing markets for the 60 month opportunity data set.	16
Table 7.	Comparison of different methods for prediction of 84 month OC.	17
Table 8.	Characterization of all original data sets, including number of animals, herds, contemporary groups (CG), sires, dams, paternal grandsires (PGS), and maternal grandsires (MGS), before any subsampling.	19
Table 9.	Characterization of subsamples for 84AFF, 84CINT, and 84TYPE data sets.	20
Table 10.	Definitions of abbreviations used in the study.	25
Table 11.	Means and fixed model analysis of the 2,249,8335 cows in the 84 month opportunity length data set. Somatic cell information not required for profit function calculation or for inclusion in the data set.	26

Table 12.	Means, fixed model, and mixed model analysis of the 60,536 random animals in the 84AFF subsample. Somatic cell information not required for profit function calculation or for inclusion in the data set.	27
Table 13.	Researcher, year of research, and mean age at first freshening (AFF) for comparison with current study.	28
Table 14.	Estimates of inbreeding depression on first lactation mature equivalent milk, fat, and protein production, including current research.	29
Table 15.	Means, fixed model, and averaged mixed model analysis of the 199,320 animals in the 60 month opportunity length data set. Somatic cell information required in all lactations for inclusion in the data set.	31
Table 16.	Means, standard deviations, minimums, maximums, and mixed model analysis of the 57,991 animals in Sample 1 of the 60 month opportunity length data set. Somatic cell information required in all lactations for inclusion in the data set.	32
Table 17.	Means, standard deviations, minimums, maximums, and mixed model analysis of the 61,329 animals in Sample 2 of the 60 month opportunity length data set. Somatic cell information required in all lactations for inclusion in the data set.	32
Table 18.	Researcher, year of research, indication of animal or fixed model analysis, and estimates of heritability for somatic cell score (SCS).	33
Table 19.	Means and fixed model analysis of the 1,547,637 animals with 84 month herd life opportunity that initiated a second lactation.	35
Table 20.	Means, fixed model, and mixed model analysis of the 52,769 random animals in the 84CINT subsample that initiated a second lactation.	35

Table 21.	Means and fixed model analysis of the 675,098 animals with 84 month herdlife opportunity and type information.	37
Table 22.	Means, fixed model, and mixed model analysis of the 73,703 84 month opportunity animals with type data in the 84TYPE subsample.	38
Table 23.	Comparison of recent literature estimates of heritability for type traits with those in the current study.	39
Table 24.	Comparison of recent literature estimates of heritability for type traits with those in the current study.	40
Table 25.	Net losses for an average heifer due to 12.5% inbreeding, and percent of additive standard deviation.	42
Table 26.	Changes in conformation traits for an average heifer due to 12.5% inbreeding and percent of additive standard deviation.	43

List of Illustrations

- Figure 1. Mean percent inbreeding levels by year of birth for all animals having the opportunity to live for 84 months, regardless of date of death or disposal. Lines represent all animals, registered animals, grade animals, and for USDA national data. 22
- Figure 2. Linear and quadratic regressions of year born on inbreeding for the 2.2 million animals having the opportunity to live for 84 months, regardless of date of death or disposal. 23

INTRODUCTION

Inbreeding has been studied intently for many years, though the inaccessibility of large numbers of inbreeding coefficients and the difficulty of their calculation have limited large-scale studies, with few exceptions. VanRaden's (52) method of creating a small relationship matrix for each animal instead of one large matrix for the population reduced required memory and CPU time on the large national database. The recent availability of inbreeding coefficients from USDA has facilitated broad-scale inbreeding research. Small-scale research on the effects of inbreeding has resulted in various estimates of inbreeding depression on production traits. Information is more limited on the effect of inbreeding on relative net income and other traits relative to lifetime performance and longevity. The continued diversification of milk markets makes it necessary to consider profit functions calculated in the fluid market and manufacturing market as individual traits, and to investigate the impact of inbreeding in both markets.

Disease resistance is related to longevity. Mastitis is the third leading reason, behind low production and reproduction, for culling of dairy cows, and is responsible for 6 to 17% of all culling (42). Intense selection for increased milk production has increased the incidence of clinical mastitis due to a positive genetic correlation of approximately .2 between the two traits (42). Somatic cell score is used as an indicator for mastitis and little is known about the effect of inbreeding on somatic cell score. Estimation of the effect of inbreeding on disease resistance, especially for a disease as prevalent and financially destructive as mastitis, is warranted. Additionally, the implementation of somatic cell bonuses and penalties constitutes another argument for continued investigation of the impact of inbreeding on somatic cell score.

Intense selection for milk production has also resulted in increased pressure to identify quality young sires for breeding purposes. Often those bulls progeny tested by the various bull studs are sons of the same proven bulls out of many of the same cow families. In 1981, through use of partial pedigrees, Rutter and Pearson (39) found 6 bulls, with birth years from 1952 to 1965, that had direct relationships to all AI progeny test bulls then available in excess of 3%. Though the magnitude of relationship to individual animals caused little concern, the author concluded that use of the same sires over periods of 5 to 15 years could be an indication of future problems. Heavy use of popular Holstein bulls like Tomar Blackstar and Walkaway Chief Mark has contributed to their increased relationship to the breed. For example, 625 Blackstar sons were sampled in 1990 alone (21), resulting in 128 currently active AI sons (25). Heavy use of a few bulls as sires of sons, combined with the adaptation of AI, the widespread use of embryo transfer, and inaccurate record keeping has contributed to an increase in inbreeding across all dairy breeds, especially since the 1980s (45, 60).

The objectives of this study were

1. To estimate the effect of inbreeding on lifetime relative net income in both fluid and manufacturing milk markets for Holstein cattle
2. To explore the relationship between inbreeding depression and traits related to lifetime performance, such as linear type traits and final score, somatic cell score, first lactation production, age at first freshening, calving interval, and length of productive life.

REVIEW OF LITERATURE

Inbreeding

Inbreeding results from the mating of related individuals. Offspring resulting from such a mating are then said to be inbred. Another definition of inbreeding is the probability that an individual has two alleles at the same locus that are exact copies of the same original gene in a common ancestor. Inbreeding depression is the reduction of mean phenotypic value due to an increase in homozygous genotypes and a decrease in heterozygous genotypes.

One reason inbreeding may be a concern is the increasing inbreeding levels and levels of relationship in currently available AI bulls. Short, et al. (45) found that average inbreeding for Holstein bulls born in 1940 was 1.2% and increased to 3.5% for those born in 1990, with the majority of the increase occurring since 1980. In a study of AI bulls in 1987, Hudson and Van Vleck (26) found 12.1% of all AI Holstein bulls to be inbred, with an average inbreeding of 5.99%. The average inbreeding for all Holstein bulls was .17.

Young and Seykora found the mean inbreeding coefficients of registered U.S. Holsteins born in 1970, 1976, 1982, and 1990 was 4.7%, 3.85, 4.3%, and 5.1% respectively (62,63). The authors compared these results with those of Lush et al. (28) and concluded that no significant increase in inbreeding had occurred from 1931 to 1990. In contrast, Short et al. (45) found the mean inbreeding coefficient of U.S. Holstein cows had increased from .9% for animals born in 1940 to 3.5% for those born in 1990. Number of cows utilized in the study was not stated, but included all registered cows and some grade cows.

Inbreeding increases homozygosity. Decreases in physiological and reproductive efficiency have been associated with increased homozygosity. This phenomenon of decreased fitness is called inbreeding depression and many studies have estimated the depression of various production traits due to inbreeding. Wiggans et al. (60) found the mean inbreeding of all Holsteins born in 1990 to be 2.6%, corresponding to an inbreeding depression of -29.6 kg milk, -1.08 kg fat and -.97 kg protein per 1% of inbreeding. Some other estimates of inbreeding depression on production traits are found in Table 1.

Few researchers have studied the effect of inbreeding on linear type. A small, nonsignificant negative regression coefficient of type on inbreeding was found by Nelson et al. (35), who concluded that inbreeding had no certain effect on type ratings. Young, et al. (63) found inbreeding to have little or no effect on type. Regression coefficients were negative, but only a few differed significantly from zero. Thomson and Freeman (49) reported little, if any, change in type score due to inbreeding. Short et al. (45) reported a small response (-.09 for stature to .05 for udder depth) to inbreeding for linear type traits and a decline of -.02 points per 1% inbreeding for final score. The literature suggests that inbreeding will have little effect on type in this study.

Table 1. Estimates of inbreeding depression on first lactation mature equivalent milk, fat and protein production.

Researcher	Date	Breed	Inbreeding Depression Estimates		
			Milk	Fat	Protein
			————— (kg) —————		
Von Krosigk, et al. (55)	1957	H	-24.5	-.79	-
Allaire, et al. (1)	1965	H	-15.3	-.4	-
Hodges, et al. (23)	1979	H	-22.85	not signif.	-
Bonczek, et al. (9)	1980	H	-37.5	-1.47	-
Hudson, et al. (26)	1984	H	-21.1	-.78	-
Hermas, et al. (22)	1986	G	-23.8	-1.25	-
Miglior, et al. (29)	1992	J	-9.84	-.55	-
Short, et al. (45)	1992	H	-22.6	-.78	-.85

Inbreeding can also affect the length of time a cow remains in the herd, possibly shortening the amount of time she has to make a profit. Research into herd life variables such as productive life (PL) determined such variables may be economically as high as one third as important as yield (54). VanRaden and Wiggans (54) determined that yield is anywhere from 1 to 8 times as important as herd life. Having determined the economic importance of herd life traits, these researchers formulated an index (Net Merit) intended to improve economic merit by inclusion of productive life. Net Merit (NM) starts with the production economic index milk-fat-protein dollars (MFP\$) and subtracts feed costs, milk loss and losses due to milk quality, and adds value of PL. In effect, the index gives weights of 10:4:-1 for yield, PL, and SCS, respectively. The effect of inbreeding on conformation traits, if any, may be especially useful in evaluating the effectiveness of the Net Merit index, as type information is used as an indirect method of predicting PL. PL in this instance is defined as is the length of time from a cow's first freshening to death or some fixed age, with a maximum of 10 months per lactation, and is a measure of a cow's genetic ability to survive. The direct effect of inbreeding on PL is examined in the current study, along with the indirect effect on linear type information.

Less is known about the effect of inbreeding on survival or longevity. Bonczek and Young (9) found a reduction of 11.04 days of herd life per 1% increase in inbreeding. Hudson and Van Vleck (26) reported a reduction of .003 stayability points per 1% inbreeding, but concluded that, "inbreeding does not affect adversely the longevity of a cow once first calving has been reached." It is possible that the effect of inbreeding on longevity, if any, will be small because any decrease in fitness due to inbreeding could very well have expressed its largest impact prenatally or directly after birth, causing a reduction in the number of heifers surviving to first lactation. Exclusion of these animals from data sets based on lactating animals may have underestimated the effect of inbreeding.

Several studies of inbreeding have included reproductive traits. Bonczek and Young (9) found an increase of .024 services per conception, .84 days open, and .65 days in age at first freshening per 1% increase in inbreeding when studying two lines of Holsteins in Minnesota. Inbreeding increased number of services by .17 services, decreased conception rate 3.3%, and increased days open by 2.3 days in a study by Hermas, et al. (22). Age at first freshening decreased 3.7 days per 1% increase in inbreeding in the same study. Hudson and Van Vleck (26) and Hodges et al. (23) found inbreeding to increase calving interval by .09 and .196 days, respectively, per increase of 1% inbreeding. In addition, Young, et al. (63) reported that inbreeding resulted in reduced conception rates, higher services per conception, and delayed puberty. Inbred dams had fewer multipleovulations and were more likely to abort.

Miglior, et al. (30) studied the effect of inbreeding on SCS on a population of registered Holstein cows. Inbreeding coefficients ranged from 0 to .275, with an average of .017. Heritability of SCS in the narrow sense was found to be .165 and .203 in the broad sense. Inbreeding depression for lactation SCS per 1% increase of inbreeding was .012, indicating a relatively small, but deleterious change in SCS with inbreeding. Only first lactation heifers were utilized in the analysis. Production records from later parities may show an elevated inbreeding depression of SCS.

A recent study (29) compared regression of performance on inbreeding in an animal model with a fixed model containing all but the animal effects. Considering a random animal effect in a model estimating the effects of inbreeding will account for changes in inbreeding depression with changes in genetic merit for a trait. Miglior et al. (29) reported inbreeding depression of 9.84 kg of milk for each 1% of inbreeding using an animal model and 10.10 kg milk per 1% inbreeding from a fixed model analysis of the same data. The authors concluded that differences between the models were very small. Their results showed that inbreeding depression was reasonably constant across the range of genotypes in their data and that fixed models were adequate to estimate the effects of inbreeding on performance of dairy cattle.

Calculation of Inbreeding Coefficients

Inbreeding coefficients used in this study were calculated by Wiggans, et al. (60), and use a base year of 1960. Animals born before 1960 were considered to be non-inbred and unrelated. The year 1960 was chosen as the base year because around this time electronic data processing was instituted, and earlier data was believed to be unreliable or not representative of the entire dairy cattle population. There is concern that important inbreeding information is lost by exclusion of earlier pedigree data. Young and Seykora (62), calculated inbreeding coefficients using different base years. Estimates of inbreeding (Table 2) using earlier base years were significantly higher, though the authors concluded that the annual increase in inbreeding from 1976 to 1990 was not significantly different, regardless of base year used and ranged from .08 to .12%.

Wiggans, et al. (60) used VanRaden's method (52) to store all pedigree information for the Holstein breed in memory. Any incorrect or impossible identification numbers were renumbered as zeros, or unknown. Birth date information on animals was available, making it possible to process parental information before animal information. Where birth dates were unknown, birth years were estimated as 3 years prior to the earliest birth year of progeny.

Table 2. Estimates of inbreeding for cows born in 1970, 1976, 1982 and 1990, using various base years (62).

Base Year	Birth Year			
	1970	1976	1982	1990
	(% Inbreeding)			
1884	4.7	3.8	4.3	5.1
1900	3.2	2.9	3.4	4.6
1920	2.0	1.9	2.3	3.2
1940	1.2	.83	1.9	2.2
1960	.17	.17	.83	1.7

When unknown parents were encountered in a pedigree, an estimate of probable relationship between the parents was made. Birth years for unknown parents were estimated as 3 years prior to the animal in question. The relationship between a known and unknown or between two unknown parents was estimated by averaging the inbreeding coefficients for all known animals from the previous semiannual evaluation by birth year. In the event one or both parents are unknown and of different birth years, the relationship between these parents is equal to twice the average inbreeding for animals born during the birth year of the most recent parent, regardless of identification status.

The relationship between a known and an unknown or between two unknown parents may be overestimated due to the gradual increase in inbreeding over time. If an animal has two unknown parents, then multiplying the average inbreeding for the most recent parent's birth year and using that as the relationship between the parents would be using the higher of the two possible estimates. The inbreeding coefficient for the animal in question would be equal to the average inbreeding for the birth year of the most recent unknown parent.

Somatic Cell Information

Mastitis is generally recognized as the most costly disease in dairy cattle. Studies (20,41) show that mastitis accounts for approximately 50% of annual incurred health care expense and is responsible for the vast majority of mammary dysfunction. These costs are attributable to reduced milk production, discarded milk, cost of veterinary services, cost of drugs, increased

labor, decreased sale value, and increased replacement costs (6). Estimates vary on total annual expense due to mastitis, but the figure is generally agreed to be between \$140 and \$300 per cow, 70 to 80% of which is attributable to milk reduction due to nonsymptomatic, subclinical infection (37,38). As there were an estimated 9.6 million cows in the United States in 1994, the total cost due to mastitis was roughly \$1.34 to 2.88 billion dollars (34).

Intense selection for increased milk production will increase the incidence of clinical mastitis due to a positive (adverse) genetic correlation of approximately .2 between the two traits (42). In recent years genetic response to selection for milk yield has resulted in an estimated 139 kg/yr improvement, with the rate of gain increasing at an increasing rate since the late 1960s (43). Thus, incidence of clinical mastitis has increased also, though at a slower rate.

Mastitis data is difficult to collect and tends to be threshold data. The presence of a high milk somatic cell count (SCC) is an indication of clinical and subclinical infection, and due to its high correlation with mastitis incidence, SCC is used as an indicator trait. SCC is a generic term for the macrophages, neutrophils, lymphocytes, eosinophils, and various epithelial cells normally present at the sight of infection. High somatic cell count is not a cause of mastitis, rather it is a response to the presence of a bacterial infection. SCC has a low heritability of .06 (32), but a large genetic correlation with clinical mastitis of around .88 (42). SCC data is positively skewed and has markedly heterogeneous variances among groups (2). When transformed to log, base 2 equivalents, somatic cell score (SCS) becomes more normally distributed so that the mean, median and mode have the same value (2).

The heritability of SCS is about 10 to 12% (4,7,32) and its genetic correlation with clinical mastitis is .6 to .8 (43). The recommended procedure is to select on SCS rather than on mastitis resistance due to a high correlation between SCS and clinical mastitis and ease of record keeping. Approximately 84% (33) of all tested dairy cows in the United States participated in some kind of somatic cell testing program in 1994, providing the requisite data for population studies of mastitis.

The estimation of the impact of inbreeding on mastitis related traits is justified by the large economic impact of the disease. Inbreeding decreases vigor, and increases the incidence of genetic abnormalities regulated by recessive genes. Little information is available regarding the effects of inbreeding on SCS and thus on an animal's ability to resist diseases such as mastitis. The economic impact of mastitis is known, but any magnification of that cost due to inbreeding has yet to be determined.

Lifetime Net Income Functions

Selection for more profitable cows should be a goal for all commercial dairymen. As it takes 1 to 3 years of production for a dairy cow to recover rearing costs (24), selection for animals that remain in the herd for the length of time required to cover rearing costs and make a profit should

be of interest to producers. Unfortunately, the late expression of lifetime traits, such as lifetime milk production, and their relatively low heritability make direct selection unfeasible.

One way to measure lifetime performance is through profit functions which involve income and expense variables collected over the lifetime of the cow. Initially, to accurately estimate lifetime profit, very detailed income and expense information was used to describe profit functions. This kind of extensive information was normally available only on a small number of cows, such as one or two herds. Balaine, et al., (3) derived a profit function that included 5 income variables and 6 expense variables collected on 182 cows. He compared two linear net income functions comprised of income minus expense to two functions using ratios, income/expense and expense/income and concluded that the linear function expressed per time of herd life was more accurate than ratios for predicting economic efficiency. Price changes in the profit function had little effect on rank of cows based on profit per day.

Having undergone extensive research for more than 20 years, these profit functions have changed much over time, though the differences seem only to be in which variables are included in the equation. Refinement of the Relative Net Income (RNI) equation, a lifetime economic merit function, has entailed discerning which variables may be omitted, preferably those which are not recorded easily or inexpensively, while still explaining the maximum amount of variation in profit.

Gill and Allaire (15,16,17) defined a profit function using milk production, body weight, reproductive performance, herd life, and prices for feed energy, milk, calves, salvage value, and fixed costs for 933 Holstein cows. The authors concluded that this simplified function could be effective in increasing profitability. Similarly, Norman et al. (36) suggested using DHI data in a profit function called Relative Net Income (RNI). The study was performed on Jersey cows scored before 43 months of age, with a 72 month opportunity length. Opportunity length is the amount of time allowed for cows to live, regardless of culling or death and is calculated by subtracting each cow's birthdate from the last date the herd was still on test. The RNI function utilized net value of milk produced, net value of calves, net cow depreciation, and fixed cost during productive herd life.

Tigges et al., (50) compared two RNI functions, calculated using variables available through DHI, to two lifetime profit functions, calculated using detailed income and expense information. Lifetime income was calculated from product sold, live calves and salvage value. Lifetime expense included initial value, feed, mastitis treatment, breeding, and fixed costs. DHI variables needed to calculate RNI were milk and fat production, age at first freshening, number of calvings, and days of herd life (HL). All functions were expressed on a total and on a per day basis. RNI explained 85% of total variation in profit per day while the best two-variable model (milk/day of HL and total fat) explained 83% of total variation. The best three-variable model (# calves, fat/day of HL, and milk/day since 2 yrs old) explained 86%. RNI explained 95% of variation in total profit, while the best two-variable model (milk production and days of HL) explained 94% of variation, and the best three-variable model (milk, days of HL, aff) explained 95%. Adding number of calves to the model increased R^2 to 96%. The single most important variable to

predict profit per day was fat per day of herd life, accounting for 69% of total variation. Tigges (50) concluded that RNI and RNIPD were accurate predictors of cow profitability.

The effect of 11 different income/expense combinations on RNI was explored by Beaudry, et al. (5). using a 72 month opportunity length. The authors concluded though changes in economic assumptions affected mean and standard deviation of RNI, major conclusions from studies involving RNI would be valid as long as economic assumptions were reasonable.

Van Arendonk (51) suggested adjusting the lifetime profit function for opportunity cost. Opportunity Cost is defined as the profit forfeited by keeping a cow for another lactation instead of freshening an average replacement heifer. The author hypothesized that RNI was inflated due to failure to recognize this expense and, in simulation, compared total lifetime profit, profit adjusted for opportunity cost (RNIOC), and profit per day of herd life. He concluded relative value of herd life is overestimated by 260% when opportunity cost is ignored. In this study opportunity cost was calculated as the average total profit divided by the average herd life measured in days. As his example included only one herd, this OC was expressed as the average net revenue per day per cow in the herd.

This concept of opportunity cost was incorporated into a study done by Cassell, et al. (12) where three net income functions, RNI, discounted RNI (DRNI), and RNIOC were examined for 48, 60, and 72 month opportunity lengths. Calculation of opportunity cost (OC) was done by year of freshening, where OC was the ratio RNI/DPL. RNI and DPL were each regressed on overall herd means. OC was the average income per day of a heifer that freshened the same year as the animal in question and was applied to all DPL of that animal. This application of OC implies that a cow has the same opportunity cost per day across her lifetime. Means and standard deviations for all net income functions examined increased with opportunity, but less for RNIOC. RNIOC was less accurately predicted by length of PL, first lactation milk production, and age at first freshening and was less correlated with DPL than with the other two net income functions. Correlations between RNI and DRNI tended to decrease with increasing opportunity length, but RNIOC seemed unaffected by herd management factors, including opportunity cost. Variation in RNIOC increased with herd life opportunity. It was concluded that RNIOC was more useful than RNI or DRNI in evaluating profit characteristics of dairy cows.

Weigel, et al. (58) applied OC specific to each lactation, following the assumption that due to genetic trend for profitability, heifers freshening in progressive years should represent a higher opportunity cost to the unculler. Prediction factors for OC were estimated from shorter opportunity length animals. Opportunity costs estimated on a lactation basis were higher than those applying OC from year of first freshening across the lifetime of the cow, suggesting positive genetic trend for profit.

Weigel et al., (57) utilized RNIOC in predicting transmitting abilities for herd life and for estimating economic weights of indicator traits. Heritability of RNI was found to be .12, but

adjusting RNI for OC increased heritability .12 to .17 for RNIOC. Similar, high phenotypic and genetic correlations indicated that the two traits measured similar things.

Continuing diversification of milk markets, component pricing, and premium payments has necessitated further research into profit functions using information from different markets. Research by Weigel (59) derived costs of production of components based on Dado, et al. (13), determining that it costs \$0.02, \$.567, and \$1.02 to produce a kilogram of carrier, fat, and protein, respectively. Weigel used these costs to calculate RNIOC in both milk and manufacturing markets and showed a high genetic correlation of .92 between the two functions. Differences between the two functions were due to different component pricing in the two markets and the presence of a SCC premium or penalty in the manufacturing market. Adjustment in the manufacturing market for SCC was applied as a percentage increase or decrease in the value of the individual components. Selection indexes for lifetime merit in fluid market put a much higher weight on milk yield and selected against protein yield. An appropriate index in a manufacturing market placed a high weight on milk yield, while giving more weight to SCC and traits relative to productive life. SCC contributed information to the prediction of PL. Use of different selection indexes in the two markets seemed warranted.

Relationship of Type to Lifetime Profit and Herd Life

Linear type traits are used as indirect predictors of productive life in Holsteins (25) and, thus, Net Merit. Research on conformation traits relative to productive life and lifetime profit have centered upon recognition of those specific traits that lend information to prediction.

Burke, et al. (10) found linear traits accounted for 14% of explained variation for herd life after adjustment for effects of herd and production. Udder traits explained more herd-life variation than other conformation traits, with fore udder and udder depth explaining the most variation when production was included in the analyses. Intermediate curvature of the rear legs was indicative of the longest herd life in any housing type. Cows with a steeper foot angle had longer herd lives in all housing types. In a study before the conception on the linear type traits currently used, Gilmore & McDaniel (18) found that dairy character was the only physical trait significantly correlated with annualized income.

Norman et al. (36), identified final score as the type trait most useful in predicting number of lactations and net income per day of productive life (NI/DPL) in Jerseys. Mammary system and suspensory ligament were next in importance. Cassell et al. (11), found production explained more than 85% of accountable variation when discounted relative net income was regressed on PD dollars and individual type traits. Fore udder attachment, udder depth, and teat placement were the most useful type traits for prediction of DRNI. Leg set and foot angle were not useful in prediction of DRNI.

An abstract by Short & Lawlor (44) showed udder traits had the largest correlation with herd-life traits, followed by body traits and feet and leg traits. Genetic correlations between the 14 linear type traits and yield in first lactation ranged from -.48 for udder depth to .54 for dairy form. Similarly, Weigel et al., (57) also found that dairy form, along with first lactation ME milk and fat yield, had high genetic correlations with RNIOC of .48, .8, and .6 respectively, when considering cows from classified herds. Yield and HL were the two most important traits for overall lifetime merit. The authors reported an approximate reliability of predicted lifetime merit using type was .32 for sires with an effective progeny number of 80, though this estimate increased to .65 when first lactation yield and predicted months in milk were added into the prediction equation. The maximum accuracy of predicting MIM from type traits was .45, and .31 with an effective progeny number of 80. The authors concluded that prediction of MIM from type traits on registered and grade cows was less accurate than previously reported estimates using only grade animals.

Through net income functions we should be able to estimate the economic impact of inbreeding on the total lifetime performance of a cow. Little is known about the effects of inbreeding on some of the traits that are important components of lifetime performance, such as days in milk, length of productive life, calving interval and age at first freshening. Increased awareness of the long-term economic ramifications of inbreeding can only benefit the producer, as well as the industry.

MATERIALS AND METHODS

A portion of the data set for this experiment was obtained from the Holstein Association USA and contained age adjusted linear scores and breeding values for linear type data for all cows scored between 1983 and 1990. Originally, this file contained data from 27,013 herds, including 1,567,531 registered and grade cows. The file was reduced to 18,729 herds including 1,342,531 cows due to inability to cross reference certain Holstein Association herd codes to Dairy Herd Improvement herd codes. Proper herd codes were sent to USDA-Beltsville to obtain actual lifetime production data, (including calving dates, birth and ID information, days in milk, etc.), actual lactation average somatic cell data (where available) and inbreeding coefficients for all cows born since 1979 within the specified herds.

Initially the focus of this research was an 84 month opportunity length. However, we were unable to use an 84 month opportunity profit function adjusted for somatic cell information due to inadequate early somatic cell data. Thus, another data set requiring a 60 month opportunity was used to increase the number of cows with profit functions including SCC information.

Calculation of Relative Net Income (RNI)

The RNI function used in the 84 month data set was similar to that used by Weigel (56). Calculation of the 84 month opportunity used the animal's date of birth and the last date the herd was still on continuous test, i.e., the last freshening date in the data for that herd. If the difference between these two dates was greater than 2555 days, the animal was included in the data set. A production record was included in calculation of RNI if it was initiated prior to the end of the 84 month opportunity length. RNI was calculated as:

$$\text{RNI} = \sum_{i=1}^n \left[\sum_{j=1}^3 \text{Component}_{ij} (\text{Value}_j - \text{Cost}_j) \right]$$

- + (number of lactations)(net value of a calf)
- + net salvage value
- rearing cost
- (total days in milk)(maintenance, fixed, and labor cost for 2x or 3x per day in milk)
- (total days dry)(maintenance, fixed, and labor cost per day dry)

84 Month Opportunity Data Set

All edits to the 84 month data set are explained in Table 3.

Table 3. Numbers and percentages of animals removed and those remaining after edits to the 84 month opportunity data set.

INITIAL EDITS		No. of animals removed	Percent of original data	Animals remaining after edits
Edit	Explanation			
0	Original data set			7,564,030
1	Removed those animals not Holstein, not coded for genetic evaluation, those with improper birthdates, or improper calving dates.	21,841	.29	7,542,189
2	Removed those animals whose first hercodes were not identical to their last hercodes, and those calvings before 1983.	402,511	5.32	7,139,678
3	Removed those animals in herds with less than 6 calvings per year	251,326	3.32	6,888,352
4	Removed those animals with less than an 84 month opportunity	3,167,289	41.90	3,721,063
5	Removed those animals with calving intervals under 270 days or over 730 days and those animals with calving ages under 548 days or over 1096 days.	496,224	6.56	3,224,839
6	Removed those animals without protein information in all lactations within the opportunity length.	500,355	6.61	2,724,484
7	Removed those animals with intermittent somatic cell information within the 84 month opportunity length	370,352	4.90	2,354,132
8	Removed animals in herds without calvings in 3 consecutive years.	28,412	.38	2,325,720
9	Removed those animals without inbreeding coefficients.	18,125	.24	2,301,595
10	Removed animals sired by unregistered bulls.	50,410	.67	2,251,306
11	Removed animals without sires.	121	~0.0	2,251,185
12	Removed animals with sires whose registration number was less than 1000000.	1350	~0.0	2,249,835

where j is the kilograms of component (fluid, fat, protein) in the i^{th} lactation initiated before the end of the 84 month opportunity length. No adjustment was made for somatic cell information in this profit function. Values for components were the same as those used by Weigel (59). Values and costs for components in both markets are shown in Table 4. A base price of \$30.86/100kg was used in the fluid market, where no value was given to protein. A base price of \$26.46/100 kg was used in the manufacturing market. Costs of production were based on Dado, et al. (13).

Table 4. Costs and values for traits used in calculation of Relative Net Income in fluid and manufacturing markets for the 84 month data set.

Trait	Cost	Value	
		Fluid	Cheese
Fluid, per kg	0.020	.254	.1159
Fat, per kg	.567	1.28	1.28
Protein, per kg	1.02	-	3.00

Net value of a calf and net salvage were from Weigel (56) where calf value is \$100 for a bull calf and \$200 for a heifer calf. Net value of \$100 is reflected by the average of the two, minus a 10% death loss and a \$35 semen and breeding cost. A \$300 net salvage value was calculated by first assuming a \$525 initial salvage value and then subtracting a death loss and original cost of a heifer. Rearing cost was calculated as \$987.50 for the first 790 days of life, and then \$.99 per day thereafter until date of first freshening. For those animals that freshened before 26 months of age, \$.99/day was subtracted from the rearing cost for that number of days less than 790. The labor costs (\$1.34/day for dry cows and \$2.80/day for lactating cows) were from Weigel et al. (56). Adjustment was made for animals milked 3 times per day by increasing labor cost to \$3.53/day, 50% over that for animals milked twice per day. Days dry was calculated as the calving interval minus the days in milk for the previous lactation.

Inclusion of Somatic Cell Information

Somatic cell information was merged into the 60 month data set per lactation. The first step in guaranteeing proper usage of these data was to ensure that herds included in the data set had more than 2 animals freshening per year with somatic cell data and that the herd in question had at least three consecutive years of such data. Secondly, an edit removed those animals without somatic cell data and those without somatic cell information in all lactations within the 60 month opportunity length. This effectively forced animals in the data set to have not only a 60 month lifetime opportunity, but also a 60 month somatic cell opportunity.

60 Month Opportunity Data Set

All edits to the 60 month data set are shown in Table 5.

Table 5. Numbers and percentages of animals removed and those remaining after edits to the 60 month opportunity data set.

INITIAL EDITS		No. of animals removed	Percent of original data	Animals remaining after edits
Edit	Explanation			
0	Original data set			7,564,030
1	Removed those animals not Holstein, not coded for genetic evaluation, those with improper birthdates, or improper calving dates.	21,841	.29	7,542,189
2	Removed those animals whose first hercodes were not identical to their last hercodes, and those calvings before 1983.	402,511	5.32	7,139,678
3	Removed those animals in herds with less than 6 calvings per year	251,326	3.32	6,888,352
4	Removed those animals with less than a 60 month opportunity, calving intervals under 270 days or over 730 days, those animals with calving ages under 548 days or over 1096 days, and those animals without protein information in all lactations within the opportunity length..	3,040,901	40.20	3,847,451
5	Removed those animals without somatic cell information in all lactations within the 60 month opportunity length (60 month SC opportunity)	3,670,700	48.53	176,751
6	Removed those animals in herds with less than 3 animals freshening with SC data per year, and with a minimum of 3 consecutive years of freshening -	53,381	.71	123,370
7	Removed animals in herds without calvings in 3 consecutive years.	1466	~0.0	121,904
8	Removed animals with missing SC data	38	~0.0	121,866
9	Removed those animals without inbreeding coefficients.	387	~0.0	121,479
10	Removed animals sired by unregistered bulls.	2,099	~0.0	119,380
11	Removed animals without sires.	0	0	119,380
12	Removed animals with sires whose registration number was less than 1000000.	21	~0.0	119,359
13	Removed those animals without first lactationscs.	39	~0.0	119,320

Calculation of RNI

RNI in the 60 month data set was calculated similarly to the 84 month data set with the exception of an adjustment for somatic cell information. The profit function is shown below.

$$\begin{aligned}
 \text{RNI}_k = & \sum_{i=1}^n \left[\sum_{j=1}^3 \text{Component}_{ij} (\text{Value}_{ij} - \text{Cost}_{ij}) \right] + \sum_{i=1}^n (\text{kg milk}_i * \text{SCA}_{ik}) \\
 & + (\text{number of lactations})(\text{net value of a calf}) \\
 & + \text{net salvage value} \\
 & \quad - \text{rearing cost} \\
 & \quad - (\text{total days in milk})(\text{maintenance, fixed, and labor cost for 2x or 3x per day in milk}) \\
 & \quad - (\text{total days dry})(\text{maintenance, fixed, and labor cost per day dry})
 \end{aligned}$$

where j is kilograms of the component (fluid, fat, protein) in the ith lactation initiated before the end of the 60 month opportunity length with a somatic cell adjustment (SCA) for the kth market. Somatic cell adjustment in the fluid market was a two-tiered process, made per kg of milk produced. The highest premium was \$.006/kg for milk with a SCC less than 100,000 cells. The lower premium was \$.002/kg for milk with a SCC less than 250,000 cells. Adjustment for somatic cell in the cheese market was taken from Weigel (59), used a base of 500,000 cells, and gave a \$.004 bonus or penalty per kg of milk for each 100,000 cell variation from that base. All costs, values, and somatic cell penalty/premiums are shown in Table 6.

Table 6. Costs and values for traits used in calculation of Relative Net Income in fluid and manufacturing markets for the 60 month opportunity data set.

Trait	Cost (\$)	Value	
		Fluid (\$)	Cheese (\$)
Carrier, per kg	0.02	.254	.116
Fat, per kg	.567	1.28	1.28
Protein, per kg	1.02	-	3.00
SCC, per kg milk produced		.0055 (<100,000 cells)	± .0042/100,000 cells
		.0022 (<250,000 cells)	

Four different profit functions were used for the 60 month herd life opportunity data set. RNI was calculated for both fluid and manufacturing markets, with and without the somatic cell adjustment.

Calculation of OC for Years of First Freshening

OC is income forfeited by keeping a cow for another lactation instead of freshening an average heifer out of the herd. The same procedure was used to calculate OC for both herd life

opportunity lengths. Weigel et al., (58) calculated OC by regressing actual and predicted RNI and DPL means on overall herd means for both variables. Prediction of RNI and DPL was on a per cow basis for those animals too young for sufficient herdlife opportunity in his study. OC was then the ratio of regressed herd year means to regressed mean DPL.

Animals in the 84 month data set freshened for the first time between 1988 and 1991. Mean RNI and DPL for animals freshening for the first time in each of these years was calculated and regressed on overall herd mean RNI and DPL. OC per day (OCPD) was then the ratio of regressed herd mean RNI and regressed herd mean DPL for each year.

Prediction of OC

Animals freshening for the first time after 1991 do not appear in the 84 month data set due to the absence of the requisite 84 month opportunity length. However, animals with an earlier first year of freshening were still calving in those later years, years with no RNI data. To apply an OC for those later calvings it was necessary to estimate RNI and DPL. Two methods for prediction of OC were examined in this study. Method 1 predicted within herd-year mean RNI and DPL individually, and OC was then the ratio of predicted mean RNI and predicted mean DPL. Method 2 used calculated OCPD from actual years of first freshening and then predicted these ratios for later years using a linear function. OC for actual years of first freshening data would be the same, but the predicted costs were different. Both methods were calculated and the means and standard deviations for OCs resulting from both methods are in Table 7. Method 2, prediction of OC ratios, was chosen because means were very similar and standard deviations were more like those of the OCs for actual years of data. Resulting OC was then applied to each cow in each herd on a year of freshening basis.

Table 7. Comparison of different methods for prediction of 84 month OC.

Trait	Actual data years		Method 1 ³		Method 2 ⁴	
	Mean	SD	Mean	SD	Mean	SD
OCPDF, \$ ¹	1.79	.61	1.79	1.83	1.85	.95
OCPDM, \$ ²	.84	.50	.84	1.50	.89	.75

¹ OC per day in the fluid market

² OC per day in the cheese market

³ Prediction of OC through prediction of mean RNI and mean DPL

⁴ Prediction of RNI/DPL ratios

Adjustment of Relative Net Income for Opportunity Cost (RNIOC)

Once OC has been calculated for each herd-year of freshening, it must be summed over each cow's lactations in order to apply it to her lifetime RNI. Remembering that OC is on a per day basis, the equation is:

$$OC_{hi} = \sum_{j=1}^n \left[\left(DIM_j + DDRY_j \right) * OCPD_{hk} \right]$$

where OC_{hi} is the total OC for cow i of herd h , DIM is the total days in milk for her j^{th} lactation, DDRY is the total days dry preceding her j^{th} lactation and $OCPD_{hk}$ is the OC per day for the k^{th} year of the h^{th} herd. Adjustment of RNI for OC is a simple subtraction of the OC from RNI.

Estimation of Inbreeding Depression

The effect of inbreeding was analyzed on all data sets, whether original or subsamples, using both a fixed and a mixed model. The fixed model was analyzed using PROC GLM of SAS (40) and herd-year absorbed. The model was as follows:

$$y_{ij} = \alpha + hy_i + \beta F_{ij} + e_{ij}$$

where

- y_{ij} = the variable being estimated (see Table 10) on the j^{th} animal in the i^{th} herd
- hy_i = the fixed effect of herd-year
- β = the regression of the trait being examined on inbreeding
- F_{ij} = the inbreeding coefficient for the j^{th} animal in the i^{th} herd
- e_{ij} = the error associated with the j^{th} record for the i^{th} animal

A similar animal model was used to estimate heritabilities and inbreeding depression and was analyzed by MTDFREML (8). The mixed model included a random animal effect, herd year effect, and an inbreeding coefficient and was as follows:

$$y_{ij} = \alpha + hy_i + a_{ij} + \beta F_{ij} + e_{ij}$$

where

- y_{ij} = the record for the j^{th} animal freshening in the i^{th} herd-year
- hy_i = the fixed effect of the herd-year
- a_{ij} = random animal effect for cow $j \sim (0, A^{-1})$ where A is the numerator relationship matrix among cows
- β = the regression of the trait being examined on inbreeding
- F_{ij} = the inbreeding coefficient for the j^{th} animal freshening in the i^{th} herd-year
- e_{ij} = the error variable for the j^{th} animal freshening in the i^{th} herd-year

Relationships between animals were augmented by addition of paternal grandsires from the July 1996 USDA-DHIA genetic evaluation, and maternal grandsires when the animal's sire-identified dam appeared in the original data set.

Partitioning of 84 Month Data Set

After inbreeding coefficients were merged into the two data sets, the 84 month set was partitioned

into smaller data sets, based on information other than profit functions, that was being investigated. Subsetting the data was required in preparation for animal model estimation of heritability and inbreeding depression.

Restricted maximum likelihood (REML) estimation of variance components is generally regarded as the method of choice for animal breeding data. The procedure incorporates additive genetic effects for not only animals with records, but also related animals that are not included in the data set. Evidence suggests that analysis avoids small sample bias and selection bias (19). MTDFREML (8) was chosen due to accessibility of the program and availability of programming support.

Reasons for partitioning the 84AFF data set included avoiding missing data points, as mixed model analysis requires all traits to be present for all animals, and conforming to space and memory requirements of mixed model analysis. The 84AFF data set was analyzed individually and later was subset into 2 smaller data sets, with some animals appearing in more than one data set. The four data sets are characterized in Table 8. The 60 month data set did not require partitioning. Description of the four data sets is given below.

60MO - This data set included 4 profit functions, days of productive life (DPL), and first lactation somatic cell score (SCS1).

84AFF - Two profit functions were examined, along with AFF, DPL, lifetime milk, fat, and protein production, (TMILK,TFAT,TPROT), total days in milk (TDIM), and first lactation ME milk, fat and protein (MEMILK, MEFAT, MEPROT).

84CINT - The data included 2 profit functions and calving interval (CINT).

84TYPE - This data examined 2 profit functions, DPL, TDIM, 14 type traits and first lactation score.

Table 8. Characterization of all original data sets, including number of animals, herds, contemporary groups (CG), sires, dams, paternal grandsires (PGS), and maternal grandsires (MGS) before any subsampling.

Category	Name of Data Set			
	60 Month	84AFF	84CINT	84TYPE
animals	119,320	2,249,835	1,547,637	675,098
herds	5,706	18,089	18,080	14,026
CG	7,132			
sires	11,060	56,989	49,920	31,008
dams	104,886	1,577,018	1,157,952	533,879
PGS	652	2,167	2,046	1,372
MGS	10,026	37,356	32,360	19,394

¹Number of contemporary groups was calculated only in those data sets going directly into mixed model analysis

Three of the above data sets required subsampling, as they were too large for mixed model analysis to accommodate. Miglior, et al. (31) used only daughters of unproven bulls in his subsample. Of this sample, only those cows with inbreeding coefficients $> 6.25\%$ were kept, along with their herd-year-season contemporaries. We chose to use random samples from the data sets based on last and second to last numbers in herd codes. Entire herds were kept or deleted in the process.

The entire 60 month data set was analyzed randomly by splitting it in half, analyzing both halves, and averaging the results. The 84AFF data set was subsampled by taking those herds ending in 5 and with the second to last number equal to 2, 8, or 9. This gave a random sample of 60,536 cows. The last two sets (84CINT and 84TYPE) were similarly sampled. Characterization of the 3 subsamples are in Table 9.

Table 9. Characterization of subsamples for 84AFF, 84CINT, and 84TYPE data sets.

	84AFF	84CINT	84TYPE
animals	60,536	52,769	73,703
herds	473	590	1,543
CG	3,321	4,046	7,135
sires	6,782	6,266	8,072
dams	40,996	39,349	59,983
PGS	488	479	540
MGS	3,287	3,340	4,141

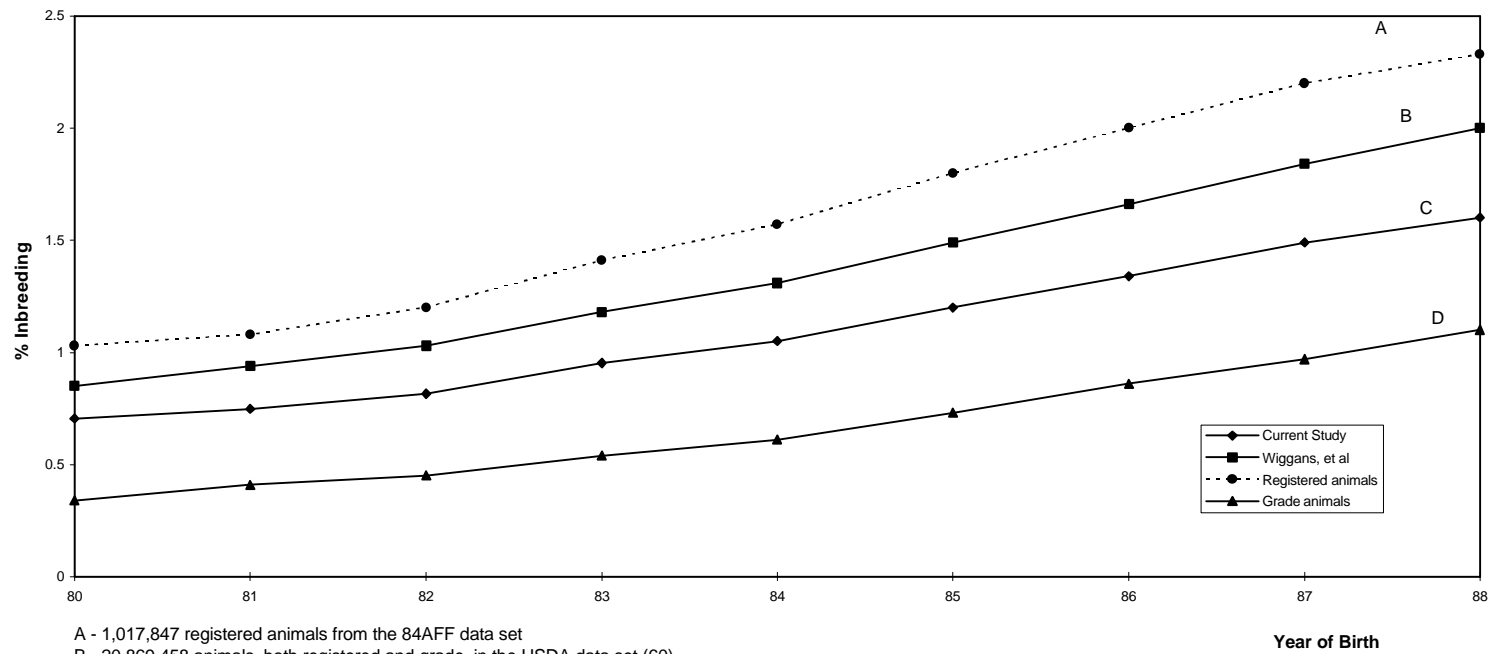
RESULTS

Inbreeding

Sire identification was required for an animal to be included in the data. Dam information was not required. Of the 2,249,835 animals in the 84 month data set, 2,057,003 had identified dams. Of those, 1,250,409 were registered animals. Thus, no animals in the data set had two unidentified parents, 91% had two identified parents, and 56% had two identified, registered parents. For those animals with only an identified sire, the relationship between the parents was estimated to be twice the average inbreeding for the youngest parent, (60), which, in many cases, would be the unknown dam. For the sire to be the more recent parent he would have to be a young sire, sampled at one year of age or possibly a bull bred on the farm and used only on that farm. Inbreeding coefficients for over half of the animals in the data set were calculated from two known parents, with the other 43% being based on one unknown parent.

Analysis of the inbreeding levels from the largest data set in the study appear in Figures 1 and 2. Figure 1 shows the mean percent inbreeding by birth year for all animals in the 84AFF data set, for registered animals, and for grade animals along with a similar graph of Wiggans, et al. (60), (personal communication). Inbreeding coefficients in the entire 84AFF data set were similar to (60) though on average a quarter of a percentage lower at each successive birth year. Registered animals, represented by the dashed line, had the highest inbreeding, averaging .26 percentage points higher than (60) and .52 percentage points higher than the entire data set. This may be a result of a more accurate estimation of inbreeding coefficients, as exact parentage is usually known for registered animals and no estimation was necessary through unknown parent groups. The grade animals in the 84AFF data set are on average .70 percentage points lower than Wiggans' data (60) and .43 percentage points lower than the entire data set. As with the registered animals, this may be due to estimation of inbreeding coefficients based on unknown parent groups.

Figure 2 depicts the linear and quadratic regressions of birth year on inbreeding for the entire 84AFF data set and shows an overall increase in inbreeding from 1980 to 1988. The corresponding linear regression coefficient was .125, indicating an increase in inbreeding of .13% per year. This increase in inbreeding is a direct result of the increase in average relationship among animals of the breed and possibly due to more complete pedigree information on animals born in most recent years. Average inbreeding has not reflected the extensive increases estimated for average inter se relationship (61), and this may be in part due to a concerted effort to avoid inbreeding in individual matings. Inbreeding may be difficult to avoid in the future.



- A - 1,017,847 registered animals from the 84AFF data set
- B - 20,869,458 animals, both registered and grade, in the USDA data set (60)
- C - 2,249,835 animals, both registered and grade, in the 84AFF data set
- D - 1,231,988 grade animals in the 844AFF data set

Figure 1. Mean percent inbreeding levels by year of birth for all animals having the opportunity to live for 84 months, regardless of date of death or disposal. Lines represent all animals, registered animals, grade animals, and for USDA national data.

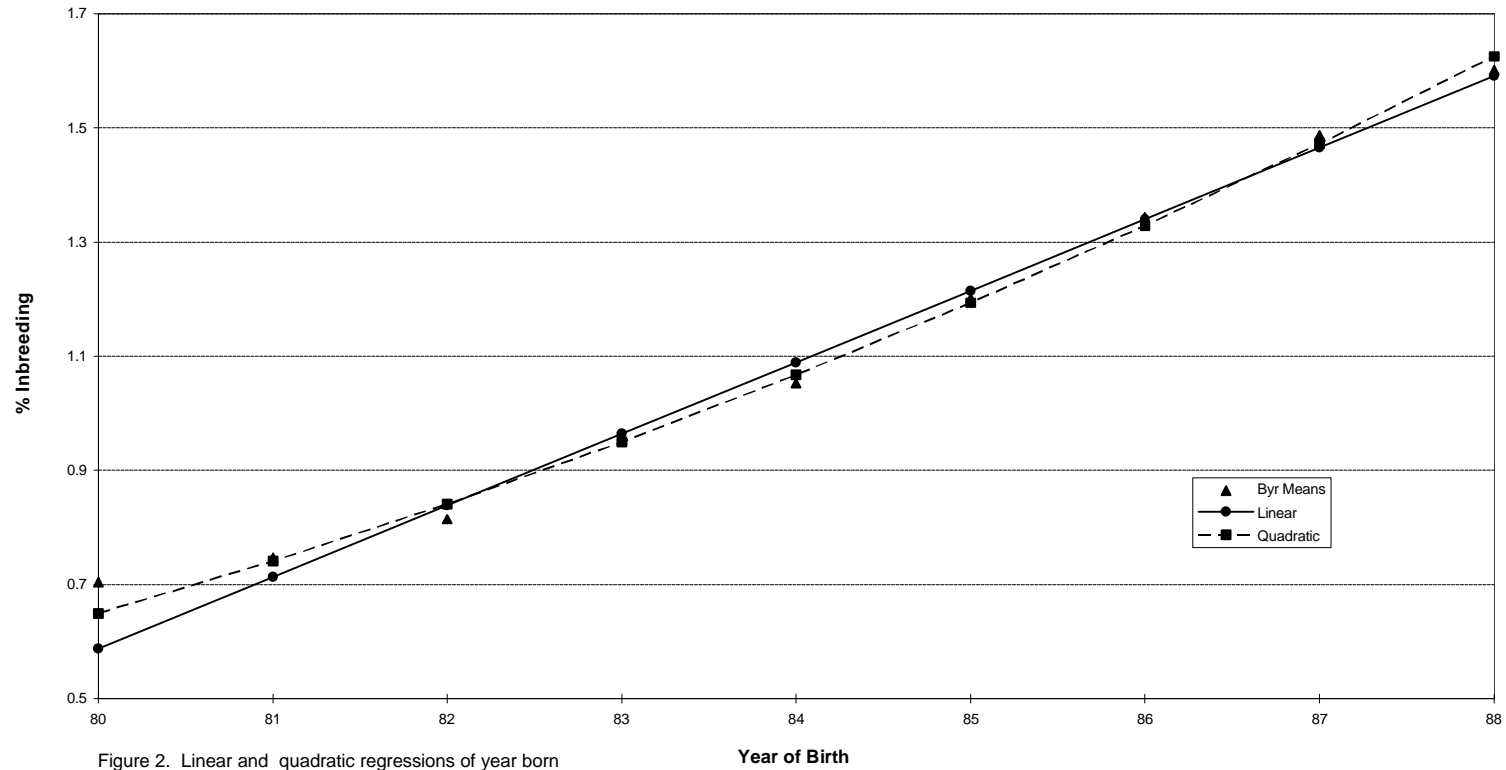


Figure 2. Linear and quadratic regressions of year born on inbreeding for the 2.2 million animals having the opportunity to live for 84 months, regardless of date of death or disposal

84AFF

Comparison of Profit Functions

Results for the 84AFF data set are found in Tables 11 and 12 (definitions of abbreviations are in Table 10) and were the intended focus of this research. Mean RNI in the fluid market was \$1637, compared to \$2572 for Weigel's (59) 84 month RNI. Mean RNIM was \$821, also compared to Weigel's \$1587. The only function that can be directly compared to other studies is the RNIOCF function, which, with a mean of \$0.40, compares to Weigel's (59) \$-118. Calculation of the profit functions was the same as (59), with the exception of inclusion of extra milk from those cows milked three times a day, and the resulting increase in corresponding labor cost. Weigel's (59) data set was composed of 52,688 classified cows, cows with type information closest to 30 months of age. Though mean DPL was not reported, cows in Weigel's study had to remain longer in the herd, while waiting for the classifier's visit. This could explain the higher values for RNI, in both fluid and manufacturing markets. Mean RNIOCs in the current data were essentially zero. Mean DPL of 831 days was lower than the 932 days in Weigel, et al. (56). This decrease in number of days of production could be affected by the inclusion of 241,000 cows milked 3x in the data set, animals removed in initial edits by Weigel, but other factors are likely involved as well. Reasons for the sharp decrease in productive life cannot be fully explained. Heritabilities for the two profit functions were .14 and .16, resembling closely Weigel's (56,59) estimates of heritability .14, .17, and .18 for 84 month profit functions.

Fixed model estimates of inbreeding depression on lifetime net income for the entire data (Table 11) were \$-10.08 in the manufactured market and \$-11.40 in the fluid market for every one percent increase in inbreeding. Fixed model analyses of the sample 60,536 animals are in Table 12, and are somewhat lower, ranging from \$-7.57 to \$-8.57. Mixed model estimates of inbreeding for the same sample data set ranged from \$-11.53 to \$-12.69 (Table 12), more closely resembling fixed model estimates for the entire data set. The similarity of estimates of inbreeding depression from the two models support Miglior's (29) conclusion that fixed model analysis of inbreeding is not greatly different from animal model analysis. In all cases, fluid market profit functions are more variable, allowing for a greater chance for differences between cows due to inbreeding.

Age at First Freshening

Mean AFF for the sample data set was 839 days, which is within the range in the literature (Table 13). Mixed model estimate of heritability was .12, which was much higher than the mixed model estimate of .02 reported by VanRaden & Klaskate (53). Fixed model analysis of the entire data set predicted an increase of .3 days in AFF for each one percent increase in inbreeding and +.1 days for the sample data set, compared with the mixed model estimate of +.16.

Table 10. Definitions of abbreviations used in the study

VARIABLE	DEFINITION
RNIF	Relative Net Income in the fluid market
RNIM	Relative Net Income in the manufacturing market
RNIOCF	Relative Net Income adjusted for opportunity cost in the fluid market
RNIOCM	Relative Net Income adjusted for opportunity cost in the manufacturing market
DPL	Days of Productive Life for the opportunity length being examined
TDIM	Total days in milk for the opportunity length being examined
TMILK	Total milk produced in the opportunity length
TFAT	Total fat produced in the opportunity length
TPROT	Total protein produced in the opportunity length
TMIM	Total months in milk for the opportunity length
SCS1	First lactation average somatic cell score
AFF	Age at first freshening
CINT1	Interval between first and second calvings
MEMILK	First lactation mature equivalent milk production
MEFAT	First lactation mature equivalent fat production
MEPROT	First lactation mature equivalent protein production
INBR	Percent inbreeding
STAT	Stature
STR	Strength
BDEPTH	Body depth
DFORM	Dairy form
RANGLE	Rump angle
TWTH	Thurl width
L(SV)	Rear leg (side view)
FA	Foot angle
FUDDATT	Fore udder attachment
UDDHT	Udder height
UDDWT	Udder width
UDDCL	Udder cleft
UDDEPTH	Udder depth
FRTPL	Front teat placement
AFS	Adjusted final score

Table 11. Means and fixed model analysis of the 2,249,835 cows in the 84 month opportunity length data set. Somatic cell information not required for profit function calculation or for inclusion in the data set.²

Variable	Fixed Model Estimates					Inbreeding Depression	SE
	Mean	SD	Minimum	Maximum			
RNIF (\$)	1637	1910	-1662	12980			
RNIM (\$)	821	1310	-1925	9329			
RNIOCF (\$)	.40	866	-4025	14510	-11.40	.30	
RNIOCM (\$)	.35	739	-3537	9654	-10.08	.26	
AFF (days)	841	97	548	1096	+ .33	.03	
DPL (days)	832	571	7	2286	-4.36	.19	
TMILK (kg)	18682	13692	36	82994	-130.91	4.65	
TFAT (kg)	677	497	1	3141	-4.84	.17	
TPROT (kg)	592	431	1	2551	-4.19	.15	
TDIM (days)	678	435	7	1830	-3.67	.15	
TMIM (mo)	23	15	.23	61	-.12	~0	
INBR (%)	1.16	2.07	0	38			
MEMILK (kg)	8723	1767	1415	21233	-18.37	.51	
MEFAT (kg)	318	64	44	967	-.70	.02	
MEPROT (kg)	276	54	45	738	-.61	.01	

¹ All estimates of inbreeding depression significant (P<.01)

² See Table 10 for definitions of abbreviations

Table 12. Means, fixed model, and mixed model analysis of the 60,536 random animals in the 84AFF subsample. Somatic cell information not required for profit function calculation or for inclusion in the data set.²

Variable	Means and Fixed Model Estimates					Mixed Model Estimates			
	Mean	SD	Minimum	Maximum	Inbreeding Depression	SE	h^2	Inbreeding Depression	SE
RNIOCF (\$)	1	866	-3544	9947	-8.57	1.92	.16	-12.69	1.96
RNIOCM (\$)	-1	735	-2268	5582	-7.57	1.64	.14	-11.53	1.68
AFF (days)	839	95	549	1096	+1.0	.17	.12	+1.16	.17
DPL (days)	839	571	7	2175	-4.19	1.23	.09	-6.65	1.26
TMILK (kg)	19059	13840	64	76575	-111.88	29.64	.10	-174.6	.3031
TFAT (kg)	694	505	2	2818	-4.03	1.08	.10	-6.38	1.10
TPROT (kg)	604	436	3	2238	-3.53	.43	.10	-5.56	.95
TDIM (days)	684	435	7	1830	-3.31	.94	.09	-5.12	.96
TMIM (mos)	23	15	.23	61	-.11	.03	.09	-.17	.32
INBR (%)	1.07	2.01	0	28.6					
MEMILK (kg)	8794	1768	2065	16813	-16.45	3.27	.31	-23.70	3.31
MEFAT (kg)	322	65	92	761	-.58	.11	.30	-.85	.11
MEPROT (kg)	278	54	66	525	-.52	.10	.26	-.76	.10

¹ Estimates of inbreeding depression on AFF not significant ($P > .01$). All other variables significant ($P < .01$)

² See Table 10 for definitions of abbreviations

Table 13. Researcher, year of research, and mean age at first freshening (AFF) for comparison with current study.

Researcher	Year of Research	Mean AFF days
Gill andAllaire, (17)	1975	856
Hermas, et al. (22)	1987	785
Lin andAllaire, (27)	1977	900
Norman, et al. (36)	1981	784
Smith, (47)	1991	860
VanRaden, et al. (53)	1993	848
Current study	1996	839

These estimates are variable, but so are estimates in the literature. Bonczek & Young (9) reported an increase of .65 days/1% increase in inbreeding for 948 Holsteins, in two line-bred groups. These results conflict with (22) in which the estimated inbreeding depression was -3.7 days for 246 registeredGuernseys. Neither researcher specified use of an animal or fixed model.

Productive Life

Mean DPL in the 84 month opportunity was 832 days and was discussed earlier. The mixed model estimate of heritability was of DPL was .09, which is slightly higher than .06 found by Weigel (56) and .07 reported by Short and Lawlor (44). Fixed model analysis of inbreeding depression was -4.36 days, compared to -6.65 in the mixed model analysis. These results are less than the reduction of 11.04 days of herd life reported by Bonczek and Young (9).

Average DIM for this data set was 678 days, compared to 755 days in (56). Heritability of DIM was estimated at .09, while fixed and animal model estimation of inbreeding depression were -4 and -5 days per 1% increase in inbreeding, respectively. MIM appears more often in the literature, with averages for an 84 month opportunity of 24.3 months and 24.6 months for VanRaden and Klaaskate (53) and Weigel, et al. (57), respectively. The mean MIM for this study is slightly less, at 22.8 months. Heritability was .09, in agreement with .085 reported by VanRaden & Klaaskate (53), but slightly higher than .06 of Weigel, et al. (57). Fixed and animal model estimations of inbreeding depression were -.12 and -.17 months per 1% increase in inbreeding, respectively.

Total production results

Average total milk and fat were 18,682 and 677 kilograms, respectively, (Table 11) compared to 19,994 and 482 kilograms in Weigel, et al. (56), who did not report total protein, nor the heritabilities of these traits. Heritabilities for total milk, fat, and protein in this study were .1. Inbreeding depression estimated from the fixed model was -131 kg milk, -5 kg fat, and -4 kg protein per 1% increase in inbreeding, compared to an inbreeding depression of -166, -6, and -5 kg estimated from a mixed model.

First lactation ME production

Means for first lactation ME milk, fat, and protein (Table 11) are somewhat higher than results of Weigel (56), though lower than estimates in another study by the same author (59). More recent data and inclusion of 3x herds could be responsible for higher estimates than those in (56). Selection of classified animals (59), a data set containing 76% registered animals, could be responsible for higher estimates of first lactation production than those in the present study. Heritabilities for these traits are in Table 12. Heritability for first lactation ME milk was .31, in agreement with .31 found by Short and Lawlor (44), and .32 reported by Weigel (56). The heritability of first lactation ME fat in this study was .30, very similar to .32 reported by Weigel (56). Fixed model estimates of inbreeding depression per 1% increase in inbreeding for the entire data (Table 11) were -18, -.7, and -.6 kg for milk, fat and protein respectively, and are higher than similar estimates for the subsample. Animal model estimates of inbreeding depression more closely resemble fixed model estimates for the entire data set, at -24, -.9, and -.8 kg for milk, fat, and protein, respectively. Table 1 has been augmented to include animal model estimates of inbreeding depression on ME milk, fat, and protein from the current research for easy comparison with other studies (Table 14).

Table 14. Estimates of inbreeding depression on first lactation mature equivalent milk, fat, and protein production, including current research.

Researcher	Date	Fixed/ Mixed	Breed	Inbreeding Depression Estimates		
				Milk	Fat	Protein
					(kg)	
Von Krosigk, et al. (55)	1957	Fixed	H	-25	-.8	-
Allaire, et al. (1)	1965	NA	H	-15	-.4	-
Hodges, et al. (23)	1979	NA	H	-23	*	-
Bonczek, et al. (9)	1980	Fixed	H	-38	-1.5	-
Hudson, et al. (26)	1984	Mixed	H	-21	-.8	-
Hermas, et al. (22)	1986	Fixed	G	-24	-1.3	-
Miglior, et al. (29)	1992	Mixed	J	-10	-.6	-
Short, et al. (45)	1992	Fixed	H	-23	-.8	-.9
Wiggans, et al. (60)	1995	Mixed	H	-30	-1.1	-1.0
Current research	1996	Mixed	H	-24	-.9	-.8

* not significant (P<.01)

Results of the current study agree well with recent estimates, both from fixed and mixed models. Most importantly, the results are similar to Wiggans, et al. (60), whose inbreeding coefficients were utilized in the study, and whose research was performed on all U.S. Holsteins, both registered and grade.

60 Month- profit functions including somatic cell information

Comparison of Profit Functions

Results for the 60 month data set are in Tables 15, 16, and 17. Table 15 shows fixed models analysis of all 119,320 animals, plus the averaged mixed model estimates from the two sample halves. Tables 16 and 17 show means and mixed model results for the two sample halves that were analyzed. Mean RNIOCs ranged from \$4 to \$10. Means were slightly higher than that found by Cassell, et al. (12) of \$-12.00 for a 60 month RNIOC. The RNIOC function used in that study, however, did not specify a milk or manufacturing market, did not adjust for somatic cell count, and assumed a constant opportunity cost across the lifetime of the animal. These results can also be compared to Weigel, et al. (56) who found a mean RNIOC of \$-20, though their function did not specify a milk or manufacturing market or adjust for somatic cell information. Weigel, et al. (59) did specify milk and manufacturing markets, and though they used an 84 month opportunity length, 60 month RNIOCF and RNIOCMS in this study, functions comparable to those used by Weigel (59) are higher and positive. These higher 60 month profit function results are in spite of a shorter opportunity for production and inclusion of the somatic cell bonus/penalty in the current fluid function, a procedure not incorporated in Weigel's study. These results may indicate a failure of registered breeders to recognize OC as an expense. They retain older cows in the herd when heifers would be more profitable, using the assumptions in RNI calculation.

Use of somatic cell information increased average values of the economic functions, indicating that in general somatic cell bonuses outweigh penalties in the data set. Means in the fluid market were higher than those in the manufacturing market, reflecting the higher milk prices and constant feed and other costs in the two markets. In comparing fluid and manufacturing functions, cheese market functions have more variation, indicating that in general a somatic cell bonus/penalty system is more profitable, but it can severely penalize a high producing/high somatic cell count cow while at the same time heavily rewarding a high producing cow with a low somatic cell count. The lowest mean in the data set was in the manufacturing market without somatic cell adjustment. Addition of somatic cell information into the profit functions increased mean net income, increased variability and decreased heritability.

Fixed model estimates of inbreeding depression for the complete data set (Table 15) range from \$-7.74 to \$-8.56 for every one percent increase in inbreeding. Also in Table 15 are the mixed model estimates of inbreeding depression, averages of the two sample halves of the data. These estimates range from \$-10.14 to \$-11.86. Differences between the two methods of estimating inbreeding depression range from \$1.58 to \$3.35. These results confirm those of Miglior, et al. (29), that differences between fixed model and animal model analysis of inbreeding depression are small. Averaged mixed model estimates of heritability are also in Table 15, and range from .09 to .11, compared to a heritabilities ranging from .14 to .18 in two of Weigel's studies (56,59) for 84 month RNIOC. The addition of somatic cell information to RNI calculations lowered heritability of lifetime net income in 60 month opportunity cows slightly. As with the 84 month opportunity data, heritability was higher for fluid market profit functions than for manufacturing due to a

Table 15. Means, fixed model, and mixed model analysis of the 199,320 animals in the 60 month opportunity length data set. Somatic cell information required in all lactations for inclusion in the data set.^{1,2}

Variable	—————Means and Fixed Model Estimates—————						Averaged —Mixed Model Estimates—		
	Mean	SD	Minimum	Maximum	Inbreeding depression	SE	h ²	Inbreeding depression	SE
RNIOCF (\$)	9	701	-2535	12903	-8.51	1.04	.11	-11.86	1.62
RNIOCFS (\$)	10	711	-2601	13228	-8.56	1.06	.09	-10.14	1.5
RNIOCM (\$)	4	606	-1809	8206	-7.74	.91	.10	-10.71	1.425
RNIOCMS (\$)	6	648	-2083	9561	-7.84	.97	.09	-11.16	1.52
INBR (%)	1.77	2.25	0	29.7					
DPL (days)	540	362	7	1477	-2.91	.52	.06	-4	.80
SCS1	2.68	1.49	.02	9.76	-.004	.002	.10	+.004	.003

1. Estimates of inbreeding depression on SCS1 not significant (P>.01), all others significant (P<.01)

2. See Table 10 for definitions of variables.

Table 16. Means, standard deviations, minimums, maximums, and mixed model analysis for the 57,991 animals in Sample 1 of the 60 month opportunity length data set. Somatic cell information required in all lactations for inclusion in the data set^{1,2}

Variable	— Means, etc. —				—Mixed Model Estimates—		
	Mean	SD	Minimum	Maximum	h ²	Inbreeding depression	SE
RNIOCF (\$)	7	706	-2351	12903	.10	-11.75	1.64
RNIOCFS (\$)	8	716	-2393	13228	.07	-8.19	1.38
RNIOCM (\$)	3	608	-1652	8206	.09	-10.54	1.44
RNIOCMS (\$)	5	651	-2083	9561	.09	-10.84	1.53
INBR (%)	1.79	2.27	0	28.9			
DPL (days)	540	363	7	1477	.05	-4.10	.80
SCS1	2.69	1.50	.02	9.76	.10	+.003	.003

1. Estimates of inbreeding depression on SCS1 not significant (P>.01), all others significant (P<.01)

2. See Table 10 for definitions of variables.

Table 17. Means, standard deviations, minimums, maximums and mixed model analysis for the 61,329 animals in Sample 2 of the 60 month opportunity length data set. Somatic cell information required in all lactations for inclusion in the data set^{1,2}

Variable	— Means, etc. —				—Mixed Model Estimates—		
	Mean	SD	Minimum	Maximum	h ²	Inbreeding depression	SE
RNIOCF (\$)	10	697	-2535	9117	.11	-11.97	1.60
RNIOCFS (\$)	11	707	-2601	9420	.11	-12.09	1.62
RNIOCM (\$)	5	604	-1809	5553	.10	-10.88	1.41
RNIOCMS (\$)	7	645	-2037	6776	.09	-11.47	1.50
INBR (%)	1.76	2.23	0	29.7			
DPL (days)	540	361	7	1469	.06	-3.90	.79
SCS1	2.67	1.49	.02	9.6	.10	+.005	.003

1. Estimates of inbreeding depression on SCS1 not significant (P>.01), all others significant (P<.01)

2. See Table 10 for definitions of variables.

higher emphasis on production traits, traits with fairly high heritabilities. The higher price given per kg of milk in the fluid market places more emphasis on production, while the manufacturing market places a higher emphasis on longevity or stayability traits, traits with lower heritabilities.

Days of productive life results

Mean days of productive life (DPL) was 540 days, contrasting sharply with mean DPL in (12) which was 796 days for a 60 month opportunity length. A more similar 60 month opportunity mean DPL of 720 days was found by Weigel. (56). As with the 84 month opportunity data set, reasons for the sharp decrease in productive life are unknown. The mixed model estimate of heritability for DPL was .06, agreeing with Weigel's (56,59) estimate of .06, and slightly lower than .07 reported by Short and Lawlor (44). Inbreeding depression per 1% increase in inbreeding for DPL was -3 and -4 days for fixed and mixed models, respectively, both of which are less than half the 11.04 day reduction in herd life reported by Bonczek and Young (9).

SCS results

Mean first lactation somatic cell score (SCS1) for the data set was 2.68, and was slightly higher than the 2.33 reported by Miglior, et al. (30) and lower than the 2.99 reported by Schutz et al., (46). Heritability was estimated as .1, and agrees with estimates reported in recent literature, (Table 18).

Table 18. Researcher, year of research, indication of animal or fixed model analysis, and estimates of heritability for somatic cell score (SCS).

Researcher	Year of Research	Mixed/Fixed Model	SCS Heritability
Banos, et al. (4)	1990	Mixed	.12
Boettcher, et al. (7)	1992	Fixed	.08 - .16
Emanuelson, et al. (14)	1988	Mixed	.12
Miglior, et al. (30)	1994	Mixed	.165
Monardes, et al. (32)	1984	Mixed	.06 - .14
Schutz, et al. (46)	1990	Mixed	.1
Current research	1996	Mixed	.1

Fixed model and mixed model estimation of inbreeding depression for SCS1 resulted in estimates of -.004 and +.004 SCS units per 1% increase in inbreeding, respectively. The only other estimate reported in the literature is +.012 by Miglior, et al. (30) for 65,491 first lactation Canadian Holsteins. Results from these two studies indicate that inbreeding has very little effect on somatic cell score.

84CINT Results

Comparison of profit functions

Of the 2.2 million animals in the 84AFF data set, only 1.5 million survived to calve a second time. These animals are represented in the 84CINT data set and results are found in Tables 19 and 20. Requiring a second calving for inclusion in this data set selected animals with longer productive lives. Of all data sets examined, these animals had the highest mean profit function results, over \$230 higher than the 84AFF data set. If an animal is required to remain in the herd to calve a second time, she will initiate a second lactation and in all probability she would not be culled early in that lactation, providing additional opportunity to cover her initial costs and generate a positive RNI. To illustrate this, mean DPL for these data was 1116 days, 284 days longer than for the 84AFF data set. These animals also produced on average 6303 kg more milk, 228 kg fat, and 200 kg protein over their lifetimes, adding explanation to higher profit function means. Mixed model estimates of heritability increased over the 84AFF data set to .19 for RNIOCF and .16 for RNIOCM. This could be due to the later expression of traits related to longevity. At the same time, many cows with short days of productive life may add only error and little additive variation to lifetime traits. Estimates of inbreeding depression using the animal model were \$-16.27 and -\$13.84 for RNIOCF and RNIOCM respectively, and were higher than estimates using the fixed model for either the whole data set or for the subsample.

Calving Interval

Mean calving interval for the 84CINT data set was 401 days, and agrees with findings of Smith (47) of 397 days. There was very little difference between fixed and animal model analysis of inbreeding depression on calving interval, with all estimates rounding to an increase of .4 or .5 days per 1% increase in inbreeding. Results were higher than estimates of .1 days by Hudson and Van Vleck (26) and of .2 days by Hodges, et al. (23). Heritability was estimated at .04, an estimate not available in other literature reviewed.

Table 19. Means and fixed model analysis of the 1,547,637 animals with 84 month herd life opportunity that initiated a second lactation.

Means and Fixed Model Analysis						
Variable	Mean	SD	Minimum	Maximum	Inbreeding Depression	SE
RNIOCF (\$)	233	943	-4025	14510	-12.88	.41
RNIOCM (\$)	237	772	-3537	9654	-10.98	.34
INBR (%)	1.12	2.02	0	37.5		
CINT1 (days)	400	67	274	730	+43	.03
DPL (days)	1116	461	285	2286	-2.71	.20
TMILK (kg)	24985	11916	372	82994	-108.44	5.06
TFAT (kg)	905	435	15	3141	-4.06	.18
TPROT (kg)	792	373	13	2551	-3.49	.16

1 All estimates of inbreeding depression significant (P<.01)

2 See Table 10 for definitions of variables

Table 20. Means, fixed model, and mixed model analysis of the 52,769 random animals in the 84CIN3 subsample that initiated a second lactation.

Variable	Means and Fixed Model Estimates					Mixed Model Estimates			
	Mean	SD	Minimum	Maximum	Inbreeding Depression	SE	h ²	Inbreeding Depression	SE
RNIOCF (\$)	244	957	-3544	11352	-12.17	2.39	.19	-16.27	2.43
RNIOCM (\$)	243	782	-2455	7454	-10.08	1.96	.17	-13.84	2.00
INBR (%)	1.08	1.91	0	27.8					
CINT1 (days)	401	68	276	730	+49	.17	.04	+40	.17
DPL (days)	1108	458	332	2201	-2.88	1.13			
TMILK (kg)	24840	11878	921	78589	-107.79	28.94			
TFAT (kg)	899	432	40	2817	-3.75	1.05			
TPROT (kg)	787	371	31	2238	-3.44	.90			

1. All mixed model estimates of inbreeding depression significant (P<.01)

2. See Table 10 for definitions of variables

84TYPE Results- Analysis of conformation data

Results from fixed model analysis of the complete 84TYPE data set are in Table 21. Fixed and mixed model analysis of the subsample are in Table 22. As with the 84CINT data set, mean profit function values for the 84TYPE data set were higher than those of the 84AFF data set. These animals had to remain in the herd long enough to be scored, eliminating cows culled or dying shortly after first freshening. 84TYPE animals remained in the herd on average 130 days longer than 84AFF animals and 184 days less than 84CINT animals, thus explaining the intermediate mean values for lifetime net merit. Estimates of inbreeding depression on conformation traits, whether using a fixed or animal model are higher than those in all other data sets, though not exceedingly so. Mixed model estimates of heritability for RNIOCF and RNIOCM are higher for this data set than for any other, again probably due to more additive genetic information being contributed from the longer period of productive life.

Heritabilities and both fixed and mixed model estimates of inbreeding depression for DPL, TDIM, and TMIM closely resemble those for the 84AFF data set. Means for TMILK, TFAT, and TPROT were higher than corresponding means in the 84AFF data set, though most likely due to the culling of short-lived animals during the extended period of production while waiting for the classifier to visit the herd.

Type trait results

Fixed model estimates of inbreeding depression on all type traits for the entire 84TYPE data set are in Table 21 and range from -.15 pts (bdepth) to +.11 (udder depth, front teat placement). Fixed model estimates of inbreeding depression on the subsample were very similar, though the range was smaller (-.14 to +.1). Very few estimates vary far from zero and the initial premise that inbreeding would have little effect on type seems to be appropriate, agreeing with conclusions by Nelson, et al. (35), Young et al. (63), and Thomson and Freeman (49). Mixed model analysis produced inbreeding depression estimates that were similar to fixed model estimates (Table 22).

Short and Lawlor (personal communication) estimated inbreeding depression on type traits for 301,996 Holstein cows, both registered and grade, representing a random 10% of all classified animals. These estimates are shown in Table 23, along with corresponding estimates from this study for comparison. Their model included a fixed herd-year-round of classification effect, age and stage of lactation, inbreeding coefficient, the animal's additive and dominance effects, herd x sire, and permanent environmental effect.

Table 21. Means and fixed model analysis of the 675,098 animals with 84 month herd life opportunity and type information.^{1,2}

Variable	Means/Fixed models Estimates					
	Mean	SD	Minimum	Maximum	Inbreeding Depression	SE
RNIOCF (\$)	116	909	-3692	11352	-15.38	.56
RNIOCM (\$)	119	768	-2905	7454	-13.48	.48
DPL (days)	962	551	8	2273	-5.32	.33
TDIM (days)	777	416	8	1830	-4.47	.25
TMILK (kg)	21666	13392	64	80504	-165.57	7.98
TFAT (kg)	787	489	2	3141	-6.17	.29
TPROT (kg)	687	421	3	2452	-5.30	.25
TMIM (mo)	26	14	.3	61	-.15	.01
INBR (%)	1.42	2.15	0	31.4		
STAT (pts)	30.8	8.7	1.1	71.4	-.08	~0
STR (pts)	29.1	7.8	1.1	69.7	-.13	~0
BDEPTH (pts)	30.9	8.0	1.1	73.7	-.15	~0
DFORM (pts)	29.8	7.6	1.0	61.6	+.02	~0
RANGLE (pts)	25.4	5.6	.9	52.0	+.01	~0
TWTH (pts)	28.0	7.5	1.1	69.5	-.09	~0
LSV (pts)	27.6	7.2	1.0	56.7	+.03	~0
FA (pts)	23.8	7.0	1.0	50.5	~0	~0
FUDDATT (pts)	23.9	7.4	.9	54.1	+.10	~0
UDDHT (pts)	26.0	7.7	.9	58.0	+.05	~0
UDDWT (pts)	25.7	7.8	.8	60.0	+.01	~0
UDDCL (pts)	26.9	6.1	.9	51.2	+.07	~0
UDDEPTH (pts)	23.7	5.2	.7	54.9	+.11	~0
FRTPL (pts)	24.1	6.7	.9	53.3	+.11	~0
AFS (pts)	80.4	3.9	50.5	94.0	~0	~0

¹Estimates of inbreeding depression on RANGLE, FA, UDDWT, and AFS not significant (P>.01), all others significant (P<.01)

²See Table 10 for definitions of variables

Table 22. Means, fixed model, and mixed model analysis of the 73,703 84 month opportunity animals with type data in the 84TYPE subsample.^{1,2}

Variable	—Means/Fixed models Estimates—				—Mixed Model Estimates—		
	Mean	SD	Inbreeding Depression	SE	h ²	Inbreeding Depression	SE
RNIOCF (\$)	121	908	-18.23	1.68	.22	-21.73	1.72
RNIOCM (\$)	124	770	-15.74	1.43	.20	-18.89	1.46
DPL (days)	966	550	-6.95	.99	.08	-9.05	1.01
TDIM (days)	781	415	-5.69	.74	.09	-7.23	.76
TMILK (kg)	21755	13380	-207.68	23.96			
TFAT (kg)	791	490	-7.53	.88			
TPROT (kg)	689	421	-6.50	.75			
TMIM (mo)	26	14	-.19	.02			
INBR (%)	1.43	2.17					
STAT (pts)	31.1	8.7	-.08	.01	.39	-.01	.15
STR (pts)	29.2	7.8	-.11	.01	.26	-.01	.01
BDEPTH (pts)	31.1	8.0	-.14	.01	.30	-.13	.01
DFORM (pts)	29.9	7.6	~0	.01	.25	-.02	.01
RANGLE (pts)	25.4	5.5	-.01	.01	.32	-.03	.01
TWTH (pts)	28.1	7.5	-.09	.01	.22	-.08	.01
LSV (pts)	27.6	7.2	+.04	.01	.20	+.03	.01
FA (pts)	24.0	7.0	+.02	.01	.13	0.00	.01
FUDDATT (pts)	24.2	7.4	+.10	.01	.21	+.05	.01
UDDHT (pts)	26.1	7.8	+.05	.01	.20	0.00	.01
UDDWT (pts)	25.9	7.8	~0	.01	.17	-.03	.01
UDDCL (pts)	27.0	6.1	+.05	.01	.14	+.01	.01
UDDEPTH (pts)	23.8	5.2	+.10	.01	.29	+.07	.01
FRTPL (pts)	24.3	6.7	+.08	.01	.23	+.03	.01
AFS (pts)	80.5	3.9	~0	.01	.28	-.02	.01

¹ Estimates of inbreeding depression on DFORM, RANGLE, FA, UDDWT, AFS not significant (P>.01), all others significant (P<.01)

² See Table 10 for definitions of variables

Table 23. Comparison of recent literature estimates of inbreeding depression on type traits with those in the current study.³

Type Trait	—Estimates of Inbreeding Depression—		
	Short, (personal communication) ¹	———Current study ² ———	
		Fixed Model	Animal Model
STAT (pts)	-.07	-.08	-.01
STR (pts)	-.07	-.11	-.01
BDEPTH (pts)	-.07	-.14	-.13
DFORM (pts)	-.04	~0	-.02
RANGLE (pts)	+.01	-.01	-.03
TWTH (pts)	-.05	-.09	-.08
LSV (pts)	+.05	+.04	+.03
FA (pts)	-.02	+.02	~0
FUDDATT (pts)	~0	+.10	+.05
UDDHT (pts)	-.03	+.05	~0
UDDWT (pts)	-.04	~0	-.03
UDDCL (pts)	~0	+.05	+.01
UDDEPTH (pts)	+.03	+.10	+.07
FRTPL (pts)	~0	+.08	+.03
AFS (pts)	-.07	~0	-.02

1. Estimates based on 301,996 Holstein cows, 1996

2. Estimates based on 73,703 Holstein cows, 1996

3. See Table 10 for definitions of variables

General conclusions of the two studies are the same: inbreeding has only small effects on linear type traits. Estimates of heritability for the 14 type traits and final score are found in Table 22 and compare well to estimates in the literature (Table 24). High heritability traits were stature, body depth, rump angle, udder depth, and adjusted final score, while low heritability traits were udder cleft, udder width, and foot angle.

Table 24. Comparison of recent literature estimates of heritability for type traits with those in the current study³.

Type Trait	Estimates of Heritability		
	Short and Lawlor, (44) ¹	Smothers (48) ²	Current study
STAT (pts)	.34	.36	.39
STR (pts)	.22	.28	.26
BDEPTH (pts)	.28	.33	.30
DFORM (pts)	.23	.27	.25
RANGLE (pts)	.29	.37	.32
TWTH (pts)	.23	.26	.22
LSV (pts)	.13	.19	.20
FA (pts)	.09	.13	.13
FUDDATT (pts)	.21	.24	.21
UDDHT (pts)	.17	.23	.20
UDDWT (pts)	.16	.20	.17
UDDCL (pts)	.16	.17	.14
UDDEPTH (pts)	.25	.31	.29
FRTPL (pts)	.23	.27	.23
AFS (pts)	.26	.21	.28

¹ Estimates based on 128,601 Holstein cows, both registered and grade, 1992

² Estimates based on 112,077 Holstein cows, 1989

³ See Table 10 for definitions of variables

Additional analyses

Initially, another subset of the 84AFF data set was created in order to examine all 84 month opportunity animals that also had first lactation somatic cell information. The average DPL for the data set was 300 days lower than that of the 84AFF data, indicating a severe shortening of herdlife for these 84 month opportunity animals with first lactation somatic cell information. Infrequent and sporadic data collection for the late 1980s and early 1990s may be responsible. Conclusions regarding first lactation somatic cell score were drawn from Table 15 as the 60 month data was considered more useful.

CONCLUSIONS

The goal of any mating is to produce the most superior animal possible. The genetic superiority of the mating must be balanced however, against the inbreeding depression that it generates. Losses due to inbreeding can easily be minimized through careful attention to identification. However, as the quadratic regression line in Figure 2 indicated, inbreeding in the Holstein population is increasing at a slightly increasing rate. As the average relationship in the population increases also, it becomes more difficult to make those mating decisions that avoid inbreeding. A misidentified cow, accidentally bred to a half sib bull produces a calf with 12.5% inbreeding. This calf, if female, would be expected to incur the losses depicted in Tables 25 and 26. Table 25 shows the production losses and Table 26 the conformation losses an average heifer would incur due to 12.5% inbreeding. Both tables also depict inbreeding depression per 1% increase in inbreeding as a percentage of additive standard deviation in order to identify those traits realizing the most severe impact of inbreeding. Genetically, RNIOCMS suffers the most from inbreeding, with an inbreeding depression of almost 6% of the additive standard deviation for the trait. However, the profit function realizing the largest impact from inbreeding is RNIOCF. This is due to the larger emphasis placed on production in fluid markets and the overall impact of inbreeding on milk production. Inbreeding has a smaller impact on many of the components involved in calculation of RNI than it does on the function itself. Cumulative effects of inbreeding on lifetime performance of dairy cows is often greater than effects on the individual traits themselves. This is exemplified in the effect of inbreeding on first lactation ME milk as compared to the same effect on lifetime milk production. Expressed as a percent of additive standard deviation, inbreeding has a 60% greater effect on lifetime milk production as it does on first lactation ME milk production.

Table 25. Net losses for an average heifer due to 12.5% inbreeding, and percent of additive standard deviation³.

Trait	Impact of 12.5% Inbreeding	% σ_a /1% Inbreeding
RNIOCF(\$) ¹	-159	3.6
RNIOCM(\$) ¹	-143	4.1
RNIOCF(\$) ²	-127	4.8
RNIOCMS(\$) ²	-140	5.8
DPL (days) ¹	-83	4.1
DIM (days) ¹	-5	3.8
AFF (days) ¹	+11	.5
CINT (days) ¹	+5	3.0
SCS1 (scores) ²	+.05	1.8
MEMILK (kg) ¹	-296	2.4
MEFAT (kg) ¹	-11	2.8
MEPROT (kg) ¹	-10	3.7
TMILK (kg) ¹	-2077	4.0
TFAT (kg) ¹	-77	3.8
TPROT (kg) ¹	-67	4.3

¹Derived from animal model estimates for 84 month opportunity animals

²Derived from animal model estimates for 60 month opportunity animals

³See Table 10 for definitions of variables

Table 26. Changes in conformation traits for an average heifer due to 12.5% inbreeding and percent of additive standard deviation².

Conformation Trait	Impact of 12.5% Inbreeding ¹ — (pts) —	% σ_a /1% Inbreeding
STAT	-.13	.2
STR	-.13	.3
BDEPTH	-1.63	3.0
DFORM	-.25	.5
RANGLE	-.38	1.0
TWTH	-1.0	2.3
LSV	+.38	.9
FA	0.0	0.0
FUDDATT	+.63	1.5
UDDHT	0.0	0.0
UDDWT	-.38	.9
UDDCL	+.13	.4
UDDEPTH	+.88	2.5
FRTPL	+.38	.8
AFS	-.25	1.0

1. Derived from animal model estimates for 84 month opportunity animals

2. See Table 10 for definitions of variables

Genetically and phenotypically the conformation traits exhibiting the largest effect due to inbreeding are body depth, thurl width, fore udder attachment, and udder depth. More highly inbred cows have more shallow ribs, narrower thurls, a smoother fore udder attachment and a shallower udder. For the udder traits such changes are not detrimental. However, inbreeding causes lower milk production, with udder structure that matches the level of production.

Inbreeding levels in Holstein cows are not alarming at the present time. The most important factors in avoiding inbreeding are maintenance of proper breeding records and accurate identification of the animals. In a registered herd identification is mandatory. For the commercial producer, it may be necessary to identify animals for DHIA testing purposes, but avoiding inbreeding could be the only economic reason to maintain identification records. In the event that breeding records are kept and a choice of bulls has to be made, a net loss of \$127 to \$159 on the lifetime of a cow is expensive, but not so much as to justify outcross matings that retard genetic progress. A portion of this potential lost revenue could be well spent in identification programs, such as the Holstein Association or possibly in enrollment in a mating program, which actively avoids inbreeding past a certain percentage when choosing bulls to mate to specific cows. Inbreeding level cutoffs and costs vary between programs, with 12.5% inbreeding the highest allowed by any program and \$3.00/cow/year the highest cost. (Tom Bruenig, American Breeders

Service, personal communication). The potential loss in lifetime profit justifies some investment in a good identification program. Avoidance of inbreeding is a clear economic benefit to mating programs designed for such a purpose. Mating programs cannot be beneficial, however, if the animal in question has no pedigree information available. Proper initial identification of the mating involved in producing an animal, combined with careful attention to potential matings can minimize inbreeding and the losses associated with it. Avoiding inbreeding will continue to become more difficult as average inbreeding and relationship increase every year.

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