An Udder Health Index for Sire Selection Based on Somatic Cell Score, Udder Conformation, and Milking Speed

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Abstract

An udder health index for use in sire selection was developed for an aggregate genotype that included subclinical mastitis in lactations 1 and ≥ 2 , clinical mastitis in lactations 1 and ≥ 2 , and milking time. Respective economic weights were -12, -31, -15, -59, and -11 \$ per genetic standard deviation. Traits in the selection index were milking speed, udder conformation, and somatic cell score in first and later parities. Genetic correlations between milking speed and somatic cell score were moderately high and positive, indicating that faster milking was associated with increased somatic cell score. Greatest genetic correlations were with udder depth for somatic cell score (deeper udders = higher somatic cell scores) and with width of rear udder attachment for milking speed (wider udders = slower milking). Standardized weights for a simple index for sires based on EBV from 50 daughter records were 5.5, -1.2, 3.5, -3.9, and -8.7 for udder depth, front teat length, milking speed, and somatic cell scores in first and later parities. Accuracy of the index was 0.776, an increase of 15% over an index with only somatic cell scores.

1. Introduction

In Canada, dairy sires receive EBV for a selection index of overall economic merit. The index is called Total Economic Value (TEV) and the aggregate genotype includes production, longevity, and udder health. The TEV is based on combining sub-indexes associated with the three components in the aggregate genotype (Dekkers, 1995). Currently, the aggregate genotype for udder health includes susceptibility to clinical and subclinical mastitis and the corresponding index includes EBV for somatic cell scores (SCS) in lactations 1, 2, and 3 (Reents et al., 1995). However, other aspects of the udder, including milking speed (MS) or milking time, are also of economic importance. Increased MS is associated with decreased milking labor time and labor is a significant expense in the harvest of milk. Decreased milking time per cow implies decreased costs for electrical power and decreased wear on milking equipment. Unfortunately, increased MS may also be associated with increased mastitis.

Sires with daughters in Canada are currently evaluated for a subjective assessment of MS (Meyer and Burnside, 1987; Banos and Burnside, 1992). Producers evaluate their cows for MS and sires with greater EBV have faster milking daughters. The EBV for MS will be used most efficiently when incorporated into a selection index that considers the positive and negative aspects of increased MS.

Udder conformation (UC) traits are also evaluated in Canada. Several researchers (Sevkora and McDaniel, 1985; Rogers et al., 1991; Lund et al., 1994) have reported genetic associations between UC and mastitis or SCS. Observed relationships were generally favorable. Others (Batra and McAllister, 1984; Seykora and McDaniel, 1985) have examined relationships between UC traits and different measures of MS. Results have been somewhat variable, but genetic correlations between UC traits and MS tended to be favorable. Because genetic relationships exist between UC, SCS or mastitis, and MS, the accuracy of an udder health index may be increased by

including UC traits.

The objective of this study was to develop and compare sire selection indexes for an aggregate genotype that included mastitis resistance and decreased milking time.

2. Material and methods

The aggregate genotype for the udder health index included five traits. The five traits were subclinical mastitis in first lactation and in lactations two and greater, clinical mastitis (CM) in lactation 1, CM in lactations two and greater, and total milking time (TMT) in all lactations. Traits in the selection index were SCS in lactations 1 and 2, MS and up to 12 UC traits. The 12 UC traits were objectively measured traits and subjective composites for fore udder, rear and leg, and mammary system. Genetic and phenotypic parameters were not available for all traits in the index and aggregate genotype. Thus, several assumptions about parameters were made. First, subclinical mastitis and SCS were assumed to be the same trait within the same lactation. Second, correlations between UC and CM were assumed to be the same as correlations between UC and SCS. Finally, correlations with MS were assumed to be the same as correlations with TMT. Genetic correlations between mastitis traits and milking time and the selection index traits are in Table 1. Most of the correlations with mastitis and milking time were estimated by Boettcher et al. (1997). Genetic correlations are also given for production. Most of the parameters for production were from a study by Liu, Jairath, and Dekkers (1994, unpublished data).

Effects on the index of using two different sets of correlations between UC and mastitis (SCS and CM) were examined. The first set assumed that correlations between UC traits and mastitis were as estimated for SCS in first lactation and applied to later lactations. The second set used greater correlations for mastitis in second and later lactations with UD, fore udder, and fore udder attachment (-0.50, -0.33, and -0.37, respectively). These correlation were estimated by Liu and Dekkers (1994, unpublished data).

Economic values used for traits in the aggregate genotype are in Table 2. The marginal value was the change in profit per animal per lactation expected from a single unit change in the respective trait. Differences in TMT were expressed in each lactation, but differences in SCS and CM were defined and expressed only in specific lactations. Therefore, marginal values were multiplied by the number of discounted expressions for each trait. A discount rate of 5% and planning horizon of 15 years was used when determining the number of discounted expressions.

Economic values for TMT considered the costs of milking labor, electrical power to drive the milking equipment, and effects of wear on the milking equipment. For the base index, the economic value of TMT was derived by assuming a situation in which cows were milked in groups of eight. The main consequence of this assumption was that an increase in average TMT of 1 minute per cow resulted in costs for an additional 1/8 minute in labor, electricity, and wear to equipment per cow. Hourly costs for labor, electricity, and equipment wear were assumed to be \$10, \$0.66, and \$1, respectively.

Economic values for SCS were the same as used in the current TEV index and were based exclusively on the decreases in cheese yield that accompany increases in SCS. These values were originally derived by Kolstad and Dekkers (1994, unpublished data) and were described in more detail by Dekkers (1995). Increased SCS decreases cheese yield in two ways: 1) by decreasing the amount of casein as a percentage of total protein in milk; and 2) by decreasing the efficiency of conversion of casein into cheese. Increased SCS is also associated with losses resulting from decreased milk production, but these losses were not accounted for in the sub-index for udder health. Losses in production associated with increased SCS were accounted for by the sub-index for production in the TEV and would be "double counted" if also considered in the sub-index for udder health.

Economic values for clinical mastitis were also based on results of Kolstad and Dekkers, as described by Dekkers (1995). Clinical mastitis was modeled as a discrete variable based on cases of CM per lactation. Costs of veterinary treatment, drugs, extra labor, and discarded milk were considered. Costs associated with decreased production and increased involuntary culling were not included because these losses are accounted for by other subindexes in TEV.

Several series of indexes were derived using these economic values. All indexes were designed for sire selection and assumed that sires had 50 daughters with records for all traits. The first series of indexes was designed to determine which UC traits were necessary for the udder health index and whether these traits differed according to the genetic correlations used for UC in second and later The series started by calculating lactations. accuracies of 12 indexes, which each included a single UC trait along with MS and SCS. The UC trait that gave the greatest accuracy was then added to the index and 11 new indexes were derived, each containing the most important udder trait and one of the remaining 11. This operation was repeated 12 times, sequentially adding the UC trait that yielded the greatest marginal increase in accuracy. The goal was to identify a simple index with fewer than 12 UC traits, but with reasonable accuracy. A selection index with MS, SCS, and the UC traits considered under international harmonization (UD, FTL, median suspensory ligament, fore udder attachment, front teat placement, and rear udder height) was also calculated for comparison.

Finally, to examine the relative importance of the udder health index and production, a series of indexes that included production were examined also. For these indexes, production was expressed in dollars and assumed to have a genetic standard deviation of \$150. The standardized economic value of production was approximately 12.5 times that of TMT and was based on results of Gibson et al. (1992). The indexes examined were those including all UC traits, the international UC traits, simple indexes with the most important UC traits, no UC traits, only SCS and production (i.e. similar to the current index), and production only.

3. Results and discussion

Table 3 lists the UC traits in order of importance for two udder health indexes. For Index 1, genetic correlations between a given UC trait and mastitis (both clinical and subclinical) were assumed to be the same for all lactations. For Index 2, genetic correlations with mastitis traits in second and later lactations were increased in magnitude for fore udder, UD, and fore udder attachment. Also shown in Table 3 are the signs of the coefficients for each UC trait in each index, the accuracy of the indexes following sequential addition of each UC trait, and the marginal increase in accuracy associated with the addition of each UC trait. Several results are worth noting. For both indexes, UD was easily the most important UC trait. This was not particularly surprising, because UD was the UC trait most

highly correlated genetically with SCS and had the second greatest genetic correlation with milking speed (Table 1). Other scientists (DeJong and Lansbergen, 1996; Rogers, 1996) also reported that UD was the most important UC trait for selection for increased udder health. Front teat length was the second most important UC trait for both indexes, but its importance was much less than UD. For both indexes, when a third UC trait was added, the coefficient for that trait was negative.

Assuming increased correlations in later lactations had several effects on the indexes (Table 3). Accuracy of the index was increased markedly. The order of importance for UC traits was also affected by changing the correlations. In particular, the subjective composite traits for fore udder, rear udder, and mammary system became much more important when genetic correlations were increased. After UD, FTL, and three composites, the remaining UC traits were of little importance for either index.

Based on the results in Table 3, indexes with only the most important UC traits were examined further. One index included only UD and FTL, another index also included the three composite traits. In subsequent comparisons of these indexes, genetic correlations were assumed to be greater for fore udder, UD, and fore udder attachment in second and later lactations than in first lactation.

Results from a comparison of four udder health indexes are in Table 4. Expected genetic response in daughters to one standard deviation of selection among sires for all udder health traits are given for each index. The first index included all UC traits. The second index included five traits: UD, FTL, and the three composite traits. The third index included the six international UC traits. The final index included only UD and FTL. Accuracies for the four indexes were 0.808, 0.801, 0.778, and 0.776, respectively. Differences among indexes were relatively minor for traits in the aggregate genotype. The more accurate indexes, those including all UC traits or the five most important traits, produced greater response for mastitis resistance in lactations 2 and greater, but less response in first lactation. Responses in MS were nearly the same for all indexes. Essentially no discernable advantage in terms of accuracy was obtained by using all international udder traits versus just UD and FTL. Ironically, the index that included only UD and FTL was associated with the most favorable expected responses in all UC traits. This result occurred because several UC traits had negative index

weights when added to an index that also included UD and FTL.

Table 5 gives expected genetic responses to selection on five indexes for simultaneous selection for both production and udder health. The five indexes included: 1) all available udder health traits; 2) MS, SCS, UD, FTL, and the three composites; 3) same as 2 but without the composite traits; 4) SCS only (similar to the current situation); and 5) only production. Corresponding accuracies for the five indexes were 0.886, 0.884, 0.881, 0.876, and 0.866, respectively. Production was clearly the dominant trait; genetic responses in SCS and CM were unfavorable regardless of which udder health index was used. Differences between indexes in response for udder health traits were quite small. Adding MS and UC traits to the udder health index led to a small increase in response for TMT, when compared to the index that included SCS only. Response in CM was also slightly more favorable when MS and UC were included and the deterioration of UC traits was decreased. Some response in production was sacrificed for the incremental gains in MS and UC traits. Among the three indexes that included MS and UC traits, differences in responses for traits in the aggregate genotype were minimal.

4. Conclusions

Based on results of these studies, two udder health indexes seemed to be the most practical. The first index included SCS in first and second and later lactations, MS, UD, and FTL. The respective standardized index weights for these traits were -3.9, and -8.7, 3.5, 5.5, and -1.2, respectively. The second index also included fore udder, rear udder, and mammary system composites. Index weights for SCS1, SCS2, MS, UD, FTL, fore udder, rear udder, and mammary system were -5.5, -6.4, 3.7, 6.4, -1.3, 13.5, 13.6, and -25.4, respectively. Each of these indexes has some advantages over the other. The first index is more simple, containing fewer traits. Furthermore, both UD and FTL can be measured objectively, in contrast to the composite traits, and are they among the six internationally recognized UC traits. Also, the signs of the index coefficients for UD and FTL are the same as the signs of their genetic correlations with mastitis resistance. In contrast, the coefficient for mammary system is negative in the second index even though higher scores are associated with increased resistance to mastitis. Because of the negative coefficient for mammary system, responses in UC traits are expected to be more favorable when using the first index. The second index produced greater selection accuracy for the aggregate genotype, however, primarily by improving mastitis resistance in second and later lactations.

Differences among alternative udder health indexes were quite small when selection for production was considered, but indexes that include MS and some UC traits excelled over the current Canadian udder health index, which includes SCS only, by increasing response in TMT and decreasing the expected deterioration in UC that accompanies selection for production.

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 Table 1. Genetic correlations between somatic cell score in first lactation, milking speed, and production with other traits in the aggregate genotype and selection index.

| Trait ^a | SCS1 | MS | MILK | |
|--------------------|-------------------|------------|-------|--|
| SCS1 | 0.13 ^b | 0.43 | 0.20 | |
| SCS2 | 0.86 | 0.25 | 0.20 | |
| CM1 | 0.65 | 0.43 | 0.20 | |
| CM2 | 0.55 | 0.25 | 0.20 | |
| MS | 0.43 | 0.14^{b} | -0.07 | |
| TMT | 0.20 | -0.90 | 0.00 | |
| FU | -0.21 | 0.03 | -0.29 | |
| RU | -0.18 | -0.11 | -0.03 | |
| MAM | -0.21 | -0.03 | -0.17 | |
| UD | -0.26 | 0.18 | -0.41 | |
| UT | 0.04 | 0.18 | -0.07 | |
| MSL | 0.01 | -0.02 | 0.01 | |
| FUA | -0.24 | 0.03 | -0.38 | |
| FTP | 0.00 | 0.11 | -0.09 | |
| FTL | 0.05 | -0.18 | 0.00 | |
| RAH | -0.14 | -0.12 | -0.03 | |
| RAW | -0.13 | -0.24 | 0.16 | |
| RTP | 0.07 | 0.03 | -0.04 | |

MILK = production, SCS1 = somatic cell score in lactation 1, SCS2 = somatic cell score in lactations ≥2, CM
 1 = clinical mastitis in lactation 1, CM2 = clinical mastitis in lactations ≥2, FU = fore udder, RU = rear udder, MAM = mammary system, UD = udder depth, UT = udder texture, MSL = median suspensory ligament, FUA
 = fore udder attachment, FTP = front teat placement, FTL = front teat length, RAH = rear udder attachment height, RAW = rear udder attachment width, RTP = rear teat placement.

^b Heritability.

| Trait ^a | Genetic SD | Marginal Value (\$/cow/yr) | Discounted expressions ^b (No.) | Economic value ^c (\$/cow/yr) | Standardized economic value ^d |
|--------------------|------------|----------------------------------|---|--|--|
| TMT | 0.86 | -15 | 0.63 | -9.5 | 1.00 |
| SCS1 | 0.45 | -26 | 0.21 | -5.6 | 0.21 |
| SCS2 | 0.45 | -29 | 0.47 | -13.8 | 0.51 |
| CM1 | 0.32 | -22 | 0.21 | -4.7 | 0.18 |
| CM2 | 0.35 | -44 | 0.47 | -20.6 | 0.88 |

Table 2. Economic values for traits in the aggregate genotype for udder health.

^a Units for traits are minutes for TMT (total milking time), linear score units for SCS1 and SCS2 (somatic cell scores in lactations 1 and ≥2 respectively), and phenotypic standard deviations for CM1 and CM2 (clinical mastitis in lactations 1 and ≥2, respectively).

^b Discounted expressions of 1 unit of genetic superiority of sires over 15 years at 5% interest.

^c Economic value is product of marginal value and discounted expressions.

^d Economic value per 1 genetic SD, relative to 1 for TMT.

Table 3. The 12 udder conformation (UC) traits listed in the order that they were added to udder health indexes that assumed the same (Index1) or different^a (Index2) correlations between UC and somatic cell score in lactations 1 and 2 along with the sign of the coefficient for each UC trait and the accuracy and marginal increase in accuracy of the respective indexes following the addition of each UC trait.

| Index 1 | | | Index2 | | | | |
|----------------|-------------------|----------|--------------------------|----------------|------|----------|--------------------------|
| Udder trait | ^b Sign | Accuracy | Marginal increase (%) | Udder trait | Sign | Accuracy | Marginal increase (%) |
| None | | 0.7205 | ··· | None | | 0.7205 | |
| UD | + | 0.7394 | 2.62 | UD | + | 0.7730 | 7.29 |
| FTL | - | 0.7423 | 0.40 | FTL | - | 0.7756 | 0.36 |
| MSL | - | 0.7431 | 0.12 | MAM | - | 0.7782 | 0.36 |
| UT | + | 0.7436 | 0.07 | FU | + | 0.7820 | 0.53 |
| RAH | - | 0.7442 | 0.08 | RU | + | 0.8008 | 2.61 |
| RU | + | 0.7448 | 0.09 | RAH | + | 0.8034 | 0.36 |
| RAW | - | 0.7451 | 0.03 | UT | + | 0.8054 | 0.28 |
| RTP | - | 0.7452 | 0.02 | FTP | - | 0.8064 | 0.14 |
| FUA | + | 0.7453 | 0.01 | FUA | - | 0.8080 | 0.22 |
| FU | - | 0.7454 | 0.01 | MSL | - | 0.8080 | < 0.01 |
| MAM | + | 0.7455 | 0.01 | RAW | - | 0.8080 | < 0.01 |
| FTP | + | 0.7455 | < 0.01 | RTP | + | 0.8080 | < 0.01 |

^a Genetic correlations with somatic cell score for fore udder, udder depth, and fore udder attachment were increased from -0.21, -0.26, and -0.24, respectively, in first lactation to -0.33, -0.50, and -0.37, respectively, in second lactation.

^b FTP = front teat placement, FTL = front teat length, FU = fore udder, FUA = fore udder attachment, MAM = mammary system, MSL = median suspensory ligament, RAH = rear udder attachment height, RAW = rear udder attachment width, RTP = rear teat placement, RU = rear udder, UD = udder depth, and UT = udder texture.

| | Udder conformation traits in index | | | | | |
|--------------------|------------------------------------|---------|--------|------------|--|--|
| Trait ^c | All | 5 trait | INT | UD and FTL | | |
| SCS1 | -0.127 | -0.130 | -0.139 | -0.140 | | |
| SCS2 | -0.218 | -0.217 | -0.210 | -0.210 | | |
| CM1 | -0.058 | -0.060 | -0.065 | -0.064 | | |
| CM2 | -0.107 | -0.105 | -0.096 | -0.096 | | |
| TMT | -0.017 | -0.016 | -0.016 | -0.017 | | |
| MS | 0.019 | 0.019 | 0.019 | 0.020 | | |
| FU | 2.020 | 2.104 | 2.141 | 2.268 | | |
| RU | 0.903 | 0.834 | 0.961 | 1.044 | | |
| MAM | 1.476 | 1.464 | 1.546 | 1.660 | | |
| UD | 3.368 | 3.408 | 3.549 | 3.551 | | |
| UT | 0.058 | -0.077 | 0.021 | 0.170 | | |
| MSL | -0.114 | -0.110 | -0.188 | 0.058 | | |
| FUA | 2.371 | 2.434 | 2.467 | 2.506 | | |
| FTP | 0.347 | 0.496 | 0.333 | 0.576 | | |
| FTL | -0.817 | -0.837 | -0.086 | -0.868 | | |
| RAH | 1.197 | 1.044 | 1.274 | 1.274 | | |
| RAW | 0.199 | 0.191 | 0.226 | 0.264 | | |
| RTP | -0.407 | -0.337 | -0.467 | -0.233 | | |

Table 4. Genetic changes expected in daughters to one standard deviation of sires based on 50 daughter records in all index and aggregate genotype traits when udder health index includes all udder conformation traits, five traits^a, international udder traits^b (INT), and only udder depth and front teat length (UD and FTL).

^a Five traits were udder depth (UD), front teat length (FTL), fore udder (FU), rear udder (RU), and mammary system (MS).

^b International udder traits include FUA, FTP, FTL, MSL, RAH, and UD.

^c SCS1 = somatic cell score in lactation 1, SCS2 = somatic cell score in lactations \geq 2, CM 1 = clinical mastitis in lactation 1, CM2 = clinical mastitis in lactations \geq 2, FU = fore udder, RU = rear udder, MAM = mammary system, UD = udder depth, UT = udder texture, MSL = median suspensory ligament, FUA = fore udder attachment, FTP = front teat placement, FTL = front teat length, RAH = rear udder attachment height, RAW = rear udder attachment width, RTP = rear teat placement.

| Table 5. | Genetic changes expected in daughters to one standard deviation of sires based on 50 daughter records |
|----------|---|
| | in the traits for several udder health indexes when production is included in the index and aggregate |
| | genotype. |

| | Udder health traits in index | | | | | | |
|--------------------|-------------------------------|---|-------------------------|-------|-------|--|--|
| Trait ¹ | All UC traits, MS, and SCS | FU, RU, MAM, UD, FTL, MS, and SCS | UD, FTL, MS, and SCS | SCS | None | | |
| Production | 37.80 | 37.81 | 37.87 | 38.12 | 38.97 | | |
| SCS1 | 0.02 | 0.02 | 0.02 | 0.02 | 0.04 | | |
| SCS2 | 0.00 | 0.01 | 0.01 | 0.01 | 0.05 | | |
| CM1 | 0.02 | 0.02 | 0.02 | 0.02 | 0.03 | | |
| CM2 | 0.01 | 0.01 | 0.01 | 0.02 | 0.03 | | |
| TMT | 0.00 | 0.00 | 0.00 | 0.01 | 0.00 | | |
| MS | 0.02 | 0.02 | 0.02 | 0.03 | 0.02 | | |
| FU | -1.07 | -1.04 | -0.91 | -1.13 | -1.34 | | |
| RU | -0.03 | -0.07 | 0.07 | -0.03 | -0.15 | | |
| MAM | -0.60 | -0.62 | -0.48 | -0.66 | -0.80 | | |
| UD | -1.28 | -1.28 | -1.27 | -1.60 | -1.93 | | |
| UT | -0.45 | -0.48 | -0.33 | -0.38 | -0.35 | | |
| MSL | -0.06 | -0.07 | 0.06 | 0.03 | 0.04 | | |
| FUA | -1.40 | -1.38 | -1.31 | -1.53 | -1.77 | | |
| FTP | -0.46 | -0.42 | -0.32 | -0.44 | -0.44 | | |
| FTL | -0.20 | -0.21 | -0.22 | -0.03 | 0.00 | | |
| RAH | 0.09 | 0.03 | 0.14 | -0.04 | -0.14 | | |
| RAW | 0.80 | 0.76 | 0.85 | 0.84 | 0.75 | | |
| RTP | -0.36 | -0.31 | -0.21 | -0.22 | -0.17 | | |

 $SCS1 = somatic cell score in lactation 1, SCS2 = somatic cell score in lactations <math>\geq 2$, CM1 = clinical mastitis in lactation 1, CM2 = clinical mastitis in lactations ≥ 2 , FU = fore udder, RU = rear udder, MAM = mammary system, UD = udder depth, UT = udder texture, MSL = median suspensory ligament, FUA = fore udder attachment, FTP = front teat placement, FTL = front teat length, RAH = rear udder attachment height, RAW = rear udder attachment width, RTP = rear teat placement.