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Are there too many traits in our selection indices?

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ABSTRACT

Selective breeding has been practiced since domestication, but early breeders commonly selected on appearance (e.g., coat color) rather than performance traits (e.g., milk yield). A breeding index converts information about several traits into a single number, typically representing total economic merit, that can be used for selection or to predict an animal's own performance. The first USDA selection index released in 1971 included only milk and fat yield, whereas the 2025 revision of the Lifetime Net Merit (NM\$) index includes 17 traits and composites (weighted averages of other traits). Many dairy farmers, semen salespeople, sire analysts, and genetics consultants (expressed in personal communications) are concerned that, as the number of traits in the index grows, it becomes less effective because selection response is "diluted" (the efficiency of the index decreases). What actually happens is that the response in individual traits changes, but the overall index response (total economic merit) does not. Correlated response to selection for 24 traits and composites currently evaluated by the Council on Dairy Cattle Breeding (Bowie, MD) and Holstein Association USA (Brattleboro, VT) was calculated for 12 USDA selection indices and their changes over time were examined. Indices including only yield (milk, fat, and protein) traits had the highest heritabilities (0.272–0.290), whereas NM\$ had heritabilities ranging from 0.188 in 2010 to 0.243 in 2025. Rates of genetic gain have changed over time but are in favorable directions for most traits. Although selection response has slowed for some traits (e.g., production) as new traits were added to the index, they remain favorable (positive). Other traits, most notably fertility, now have favorable trends when they had unfavorable (negative) trends in earlier versions of the selection index. There is some

reranking within birth year cohorts for both genetic merit and reliabilities because older animals were selected using different criteria than contemporary animals. Rank correlations are high across indices, ranging from 0.8746 to 0.9994, meaning that sires rank similarly despite the increasing complexity of the index. Selection gains for fat, protein, productive life, and BW composite have the greatest economic value regardless of how responses are calculated. These results show that properly constructed selection indices produce desirable rates and directions of gain for many traits at once.

Key words: breeding program, genetic improvement, selection indices

INTRODUCTION

Selection indices are important tools in dairy cattle breeding because they allow information about many traits of importance to be combined into a single value for ranking animals and making breeding decisions. The need for such a tool was recognized very early in the history of modern animal breeding, when Hazel and Lush (1942) applied the method of Smith (1934) to the improvement of economically important traits of livestock. The ideal breeding objective for dairy cattle remains a popular topic, and has been reviewed periodically (Hazel et al., 1994; Philipsson et al., 1994; VanRaden, 2004; Miglior et al., 2005; Shook, 2006), but there is no single selection objective that is best for all populations or all herds within a population. The construction of selection indices in the United States is complex and involves many participants (Cole et al., 2021). The first economic index for US dairy cattle was constructed in 1971 and included only milk and fat yield in the selection criterion, and the portfolio of traits included has evolved steadily over time to include 17 individual traits and composites in the most recent revision of the index (Table 1). It is clear that the number of traits included in selection indices will continue to increase as the number of economically and socially important phenotypes increases (Cole and Van-

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The list of standard abbreviations for JDS is available at adsa.org/jds-abbreviations-25. Nonstandard abbreviations are available in the Notes.

Raden, 2018; Cole et al., 2020), but many in the industry are concerned that the addition of too many traits to the selection objective will reduce the efficiency of the index, resulting in rates of gain that are not as fast as those seen before the new traits were added. Users of the index worry that the continual addition of new traits will result in lower rates of gain for some core set of traits that, in their eyes, has the greatest economic value. Although the mathematics show clearly that the fastest rates of gain for total economic merit are achieved when the index includes all traits that affect lifetime profitability (e.g., Gjedrem, 1972; Yamada et al., 1975), mathematical arguments are not persuasive to everyone.

The goal of this paper is to compare attributes of USDA selection indices used over the last 50 yr to address the concern—expressed by many professionals in the breeding industry and by farmers alike—that there are now so many traits included in modern selection indices that they are no longer useful as tools for population improvement. Correlated responses to selection, index heritability, and correlations among predicted transmitting abilities (PTA) and reliabilities (REL) will be examined for 12 indices, including the April 2025 revision to Lifetime Net Merit (NMS₂₀₂₅). These values will be used to address (1) the idea that selection pressure has been “diluted,” (2) the genetic progress we can expect from selection on the index, and (3) how changes in the index affect the ranking of bulls over time.

MATERIALS AND METHODS

The correlated response to selection for 24 traits and type composites included in NMS₂₀₂₅ (VanRaden et al., 2025) and gestation length (GL) from selection on earlier indices was computed for 12 different selection goals used in the United States from 1971 to the present: predicted difference dollars (PDS; Dickinson et al., 1971), milk-fat-protein dollars (Norman et al., 2010), cheese yield dollars (CY\$; Norman, 1986), 1994 Lifetime Net Merit (NMS₁₉₉₄; VanRaden and Wiggans,), 2000 Lifetime Net Merit (NMS₂₀₀₀; VanRaden, 2000), 2006 Lifetime Net Merit (NMS₂₀₀₆; VanRaden and Multi-State Project S-1008, 2006), 2010 Lifetime Net Merit (NMS₂₀₁₀; Cole et al., 2010), 2014 Lifetime Net Merit (NMS₂₀₁₄; VanRaden and Cole, 2014), 2017 Lifetime Net Merit (NMS₂₀₁₇; VanRaden, 2017), 2018 Lifetime Net Merit (NMS₂₀₁₈; VanRaden et al., 2018), 2021 Lifetime Net Merit (NMS₂₀₂₁; VanRaden et al., 2021), and NMS₂₀₂₅ (VanRaden et al., 2025). The 2003 version of Lifetime Net Merit (VanRaden and Seykora, 2003) was not included in this study because correlations were available only for the calving ability (CA\$) composite

and not the individual calving ease and stillbirth traits used to compute CA\$.

The traits included in the analysis were milk, fat, and protein yields (all measured in pounds), productive life (PL; mo), SCS (log₂), body weight composite (BWC; includes stature, strength, body depth, rump width, and dairy form), udder composite (UDC; includes fore udder attachment, udder cleft, rear teat placement, rear udder height, udder depth, teat length, rear udder width, front teat placement, and stature), foot and leg composite (FLC; includes foot angle, rear legs rear view, feet and legs score, stature, and rear legs side view), daughter pregnancy rate (DPR; %), calving traits dollars (\$), heifer conception rate (HCR; %), cow conception rate (CCR; %), cow livability (LIV; %), GL (d), health dollars (HTH\$; \$), residual feed intake (RFI; pounds), milk fever (MFEV; %), displaced abomasum (%), ketosis (%), clinical mastitis (%), metritis (%), retained placenta (%), early first calving (EFC, d), and heifer livability (%). Detailed information about each trait is available from CDCB (2025).

Prediction of Response to Selection

The initial construction of the Lifetime Net Merit (NMS) index is described in VanRaden et al. (2004), and its periodic revisions have been documented in detail (VanRaden, 2000, 2017; VanRaden and Seykora, 2003; VanRaden and Multi-State Project S-1008, 2006; Cole et al., 2010; VanRaden and Cole, 2014; VanRaden et al., 2018, 2021, 2025). The portfolio of 24 traits and type composites included in NMS₂₀₂₅, which makes up the selection objective (the traits being improved), was fixed for all indices. In the case of health traits (Parker Gaddis et al., 2020), both the HTH\$ subindex and the 6 traits that make up the index are included in this list. Residual feed intake and GL are also included in the list of traits because they are included in the portfolio of Council on Dairy Cattle Breeding evaluations. Selection criteria (the traits included in the index) varied, ranging from only milk and fat yield for PD\$ to the 24 traits and type composites included in NMS₂₀₂₅.

Selection Index Responses. Correlated responses to selection were calculated using an extension of the well-known breeder's equation (e.g., Cameron, 1997):

$$\mathbf{CR} = i \times \frac{\mathbf{b}'\mathbf{G}}{\sqrt{\mathbf{b}'\mathbf{P}^*\mathbf{b}}}, \quad [1]$$

where **CR** is a vector of correlated responses to selection of the traits in the selection objective in response to selection on the selection criterion, *i* is the expected annual

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Table 1. Traits included in USDA selection indices and the relative emphasis placed on each, 1971—2025

Trait ^{2,3}	Relative emphasis on traits ¹ (%)													
	PD\$ (1971)	MFP\$ (1976)	CY\$ (1984)	NM\$ ₁₉₉₄	NM\$ ₂₀₀₀	NM\$ ₂₀₀₃	NM\$ ₂₀₀₆	NM\$ ₂₀₁₀	NM\$ ₂₀₁₄	NM\$ ₂₀₁₇	NM\$ ₂₀₁₈	NM\$ ₂₀₂₁	NM\$ ₂₀₂₅	
h ²	0.272	0.283	0.290	0.217	0.223	—	0.196	0.188	0.221	0.201	0.192	0.240	0.243	
Milk	52	27	-2	6	5	0	0	0	-1	-1	-1	0	3	
Fat	48	46	45	25	21	22	23	19	22	24	27	22	25	
Protein	—	27	53	43	36	33	23	16	20	18	17	17	11	
PL	—	—	—	20	14	11	17	22	19	13	12	15	12	
SCS	—	—	—	-6	-9	-9	-9	-10	-7	-7	-4	-3	-3	
BSC/BWC ³	—	—	—	—	-4	-3	-4	-6	-5	-6	-5	-9	-11	
UC	—	—	—	—	7	7	6	7	8	7	7	3	1	
FLC	—	—	—	—	4	4	3	4	3	3	3	1	1	
DPR	—	—	—	—	—	7	9	11	7	7	7	5	3	
SCE	—	—	—	—	—	-2	—	—	—	—	—	—	—	
DCE	—	—	—	—	—	-2	—	—	—	—	—	—	—	
CAS\$	—	—	—	—	—	—	6	5	5	5	5	3	3	
HCR	—	—	—	—	—	—	—	—	1	1	1	1	1	
CCR	—	—	—	—	—	—	—	—	2	2	2	1	2	
LIV	—	—	—	—	—	—	—	—	—	7	7	4	6	
HTHS	—	—	—	—	—	—	—	—	—	—	2	2	2	
RFI	—	—	—	—	—	—	—	—	—	—	—	-12	-14	
EFC	—	—	—	—	—	—	—	—	—	—	—	1	1	
LLIV	—	—	—	—	—	—	—	—	—	—	—	1	1	

¹Index abbreviations are: PD\$ = Predicted Difference Dollars, MFP\$ = Milk-Fat-Protein Dollars, CY\$ = Cheese Yield Dollars, NM\$₁₉₉₄ = 1994 Lifetime Net Merit, NM\$₂₀₀₀ = 2000 Lifetime Net Merit, NM\$₂₀₀₆ = 2006 Lifetime Net Merit, NM\$₂₀₁₀ = 2010 Lifetime Net Merit, NM\$₂₀₁₄ = 2014 Lifetime Net Merit, NM\$₂₀₁₇ = 2017 Lifetime Net Merit, NM\$₂₀₁₈ = 2018 Lifetime Net Merit, NM\$₂₀₂₁ = 2021 Lifetime Net Merit, and NM\$₂₀₂₅ = 2025 Lifetime Net Merit.

²PL = productive life, UC = udder composite, FLC = foot and leg composite, BSC = body size composite, BWC = body weight composite, DPR = daughter pregnancy rate, SCE = sire calving ease, DCE = daughter calving ease, CAS = calving ability dollars, HCR = heifer conception rate, CCR = cow conception rate, LIV = cow livability, HTHS = health dollars, RFI = residual feed intake, EFC = early first calving, and HLIV = heifer livability.

³BSC was replaced with BWC in April 2017.

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selection differential for NM\$₂₀₂₅ (0.35; VanRaden et al., 2025), **b** is a vector of index weights (inflation-adjusted dollar values per unit of PTA) for the traits in the selection criterion, **P*** is a weighted phenotypic (co)variance matrix for the traits in the selection criterion weighted to account for differences in information available for each trait (discussed below), and **G** is a matrix of genetic (co)variances among the traits in the criterion and the objective. Responses in **CR** were divided by 2.2 yr, the average generation interval for Holstein bulls born in 2017 (Guinan et al., 2023), to convert from changes per generation to changes per year. This equation shows that the correlated response is a function of the genetic and phenotypic correlations among the traits in the objective and the criterion and the index weights. Phenotypic and genetic SD for each trait are shown in Table 2.

In the case of the PD\$ index, for example, the matrices **b** and **P** contain the following values:

$$\mathbf{b} = \begin{bmatrix} 0.423 \\ 8.52 \end{bmatrix}, \mathbf{P} = \begin{bmatrix} 10,163,387.59 & 233,426.72 \\ 233,426.72 & 13,992.05 \end{bmatrix},$$

and the weighted phenotypic (co)variance matrix, **P***, contains the following values:

$$\mathbf{P}^* = \begin{bmatrix} 6,485,324.99 & 148,748.31 \\ 148,748.31 & 8,904.12 \end{bmatrix}.$$

The matrix **G**, which contains the (co)variances of the traits in the selection criterion with the traits in the selection objective, is of dimension 2 × 24 and has the following values:

$$\mathbf{G} = \begin{bmatrix} 2,032,677.52 & 30,092.81 & 44,023.81 & \cdots & 442.54 \\ 30,092.81 & 2,798.41 & 1,156.14 & \cdots & 16.42 \end{bmatrix}.$$

In this example, the rows of **G** represent milk and fat, respectively, whereas the columns are the (co)variances of milk, fat, protein, and heifer livability with milk and fat (intervening columns [traits] were omitted for legibility). The resulting genetic (co)variance matrix is available in Supplemental Table 1 (see Notes).

Solving Equation [1] for the correlated response to selection gives a 1 × 24 matrix, **CR**, which is the response to selection for each trait in the selection objective:

$$\mathbf{CR} = [104.666 \quad 3.429 \quad 2.670 \quad \cdots \quad 0.031].$$

There are 17 traits and type composites included in NM\$₂₀₂₅; however, correlated responses to selection

Table 2. Genetic¹ and phenotypic SD of traits included in USDA selection indices; note that genetic SD are on a breeding value basis.^{2,3,4}

Trait name	SD	
	Genetic	Phenotypic
Milk yield (lb)	1,425.72	3,192.57
Fat yield (lb)	52.90	118.29
Protein yield (lb)	36.98	82.69
Productive life (mo)	4.40	15.91
Somatic cell score (log ₂)	0.40	1.15
BW composite	2.12	3.35
Udder composite	1.68	3.23
Feet and legs composite	1.82	4.69
Daughter pregnancy rate (%)	4.72	23.10
Calving ability (\$)	35.28	105.83
Heifer conception rate (%)	4.70	47.60
Cow conception rate (%)	5.64	39.31
Cow livability (%)	4.44	38.94
Gestation length (d)	2.86	8.62
Health (\$)	22.00	170.00
Residual feed intake (lb)	438.00	1,117.15
Milk fever (%)	0.40	5.16
Displaced abomasum (%)	1.00	9.53
Ketosis (%)	1.00	9.13
Mastitis (%)	3.40	19.31
Metritis (%)	1.60	13.52
Retained placenta (%)	0.80	8.00
Early first calving (d)	5.50	33.47
Heifer livability (%)	1.60	19.12

¹The genetic SD are the SD of true transmitting abilities for each trait multiplied by 2 to place them on a breeding value basis.

²Milk, fat, and protein are expressed in pounds in the service documentation published by CDCB and USDA-AGIL, but values in this table have been converted to kilograms.

³Gestation length is not included in the selection index but is included here because there are official genetic evaluations for the trait and the correlated response to selection was included in this study.

⁴The 6 individual health traits are included in the selection index as part of the health dollars (HTH\$) subindex, not individually, but they are included here because there are official genetic evaluations for each trait, and their correlated responses to selection were included in this study.

were calculated for 24 traits: 17 from NM\$₂₀₂₅, the 6 individual traits included in the HTH\$ subindex, and GL.

Economic values for the traits in each index were adjusted to 2017 dollars using conversion factors provided by Sahr (2018). The entries in each vector of economic values were divided by the 2017\$ CF factor in column Z of Sahr (2018) for the year in which each index was originally published. For example, the vector used for NM\$₁₉₉₄ was:

$$\mathbf{b}_{1994} = [0.011 \quad 1.049 \quad 1.365 \quad 11.670 \quad -29.130].$$

The adjustment factor of 0.605 needed to convert from 1995 dollars to 2017 dollars is found in row 254, column Z of Sahr (2018), and the resulting values are:

$$\mathbf{b}_{1994-2017} = [0.015 \quad 1.734 \quad 2.256 \quad 19.289 \quad -48.148].$$

Values were adjusted to 2017 dollars, because that was the most recent year for which conversion factors were available.

Phenotypic and Genetic (Co)variance Matrices. The genetic and phenotypic correlations used in this study were those computed for the NM\$₂₀₂₅ (VanRaden et al., 2025; <https://web.archive.org/web/20250404053357/https://www.ars.usda.gov/arsuserfiles/80420530/publications/arr/NMcorrelations2025.txt>). Genetic correlations among all 24 traits and type composites were estimated from correlations among PTA of Holstein bulls with high REL for productive life ($REL \geq 0.85$) because REML estimates were not available between all traits. Ideally, a multiple-trait model would be used to estimate all correlations simultaneously, but in practice convergence of such models can be achieved only for subsets of traits. Phenotypic correlations were similarly estimated using yield deviations for cows with records included in the August 2024 US genomic evaluations calculated by the Council on Dairy Cattle Breeding (Bowie, MD). The correlation matrices along with the SD of true transmitting abilities (TTA) and heritabilities are available from the Animal Genomics and Improvement Laboratory (Beltsville, MD; <https://web.archive.org/web/20250404053357/https://www.ars.usda.gov/arsuserfiles/80420530/publications/arr/NMcorrelations2025.txt>).

Genetic SD (Table 3) were approximated by multiplying the TTA by 2 to convert from a transmitting ability to a breeding value basis. Phenotypic SD for each trait were then computed by dividing the trait's genetic SD by the square root of the trait heritability (e.g., Falconer, 1989):

$$SD_{\text{phenotypic}} = \frac{SD_{\text{genetic}}}{h} = \frac{2 \times SD_{\text{TTA}}}{h},$$

where $SD_{\text{phenotypic}}$ and SD_{genetic} are the respective phenotypic and genetic SD, SD_{TTA} is the SD of the TTA, and h is the square root of the heritability.

The genetic and phenotypic (co)variance matrices were constructed from their respective correlation matrices and SD as:

$$\mathbf{S} = \mathbf{d}'\mathbf{R}\mathbf{d},$$

where $\mathbf{S}$ is the genetic (phenotypic) (co)variance matrix, $\mathbf{d}$ is a diagonal matrix of genetic (phenotypic) standard deviations, and $\mathbf{R}$ is a matrix of genetic (phenotypic) correlations. The elements of $\mathbf{d}$ were calculated as described above and $\mathbf{R}$ were provided by the USDA Animal Genomics and Improvement Laboratory.

Phenotypic (Co)variance Weights. The elements of the phenotypic (co)variance matrix, $\mathbf{P}$, were then weighted by the average reliabilities of genomic PTA for Holstein

cows born in 2023 by taking the Hadamard (elementwise) product of $\mathbf{P}$ with the matrix of reliabilities as follows:

$$\mathbf{P}^* = \begin{bmatrix} P_{11} & \dots & P_{1n} \\ \vdots & \ddots & \vdots \\ P_{n1} & \dots & P_{nn} \end{bmatrix} \odot \begin{bmatrix} \text{Rel}(1) & \dots & \sqrt{\text{Rel}(1) \times \text{Rel}(n)} \\ \vdots & \ddots & \vdots \\ \sqrt{\text{Rel}(n) \times \text{Rel}(1)} & \dots & \text{Rel}(n) \end{bmatrix},$$

where $\mathbf{P}^*$ is the phenotypic (co)variance matrix where each element is adjusted to account for the information available for each trait, P_{tt} are variances and (co)variances from $\mathbf{P}$, and $\text{Rel}(t)$ is the average reliability of the PTA of trait t for Holstein cows born in 2023. This group of cows was selected to match the population used for computing expected genetic progress in VanRaden et al. (2025). The resulting phenotypic (co)variance matrix is available in Supplemental Table 2 (see Notes).

Index Heritability. The heritability of each index, h_1^2 , was calculated after Lin and Allaire (1977) as:

$$h_1^2 = \frac{\mathbf{b}'\mathbf{G}_c\mathbf{b}}{\mathbf{b}'\mathbf{P}_c^*\mathbf{b}},$$

where $\mathbf{b}$ is a $1 \times t$ vector of index weights for the t traits in the selection criterion, $\mathbf{P}_c^*$ is a $t \times t$ phenotypic (co)variance matrix for the t traits in the selection criterion accounting for differing average reliabilities among traits, and $\mathbf{G}_c$ is a $t \times t$ matrix of genetic (co)variances among the traits in the selection criterion. Only the traits included in the selection objective were used in this calculation.

Expected Genetic Progress. Alternative estimates of genetic gain were computed following the approach described in the 2025 Lifetime Net Merit documentation (VanRaden et al., 2025). Expected genetic progress for each trait was calculated using its correlation with NM\$₂₀₂₅, SD of individual PTA, and the expected annual trend in SD of NM\$ (0.35) as:

$$ER_t = r_{\text{PTA}}(t, \text{NM}\$_{2025}) \times SD_{\text{PTA}}(t) \times 0.35, \quad [2]$$

where ER_t is the expected response of trait t to selection for NM\$₂₀₂₅, $r_{\text{PTA}}(t, \text{NM}\$_{2025})$ is the correlation of genomic PTA for trait t with PTA for NM\$₂₀₂₅ for Holstein females born in 2023, $SD_{\text{PTA}}(t)$ is the SD of PTA for trait t , and 0.35 is the expected annual trend in SD of NM\$₂₀₂₅. This approach was applied to each of the indices included in this study. Similar to VanRaden et al. (2025), input data were PTA for genotyped US

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Table 3. Traits included in USDA selection indices¹ and the economic value (\$) per PTA unit placed on each, 1971–2025; all economic values have been adjusted to 2017 dollars to allow comparisons over time

Trait ²	PD\$ (1971)	MFP\$ (1976)	CY\$ (1984)	NM\$ ₁₉₉₄	NM\$ ₂₀₀₀	NM\$ ₂₀₀₆	NM\$ ₂₀₁₀	NM\$ ₂₀₁₄	NM\$ ₂₀₁₇	NM\$ ₂₀₁₈	NM\$ ₂₀₂₁	NM\$ ₂₀₂₅
Milk	0.0745	0.016	-0.0021	0.0112	0.018	—	-0.001	-0.006	-0.004	-0.004	0.002	0.022
Fat	1.50	1.50	1.899	1.049	2.14	2.70	2.89	3.22	3.56	4.03	4.18	5.01
Protein	—	1.95	1.646	1.365	4.76	3.55	3.41	4.14	3.81	3.53	4.67	3.33
PL	—	—	—	11.67	28.00	29.00	35.00	29.00	21.00	19.00	34.00	30.00
SCS	—	—	—	-29.13	-154.00	-150.00	-182.00	-122.00	-117.00	-72.00	-74.00	-74.00
BSC/BWC ³	—	—	—	—	-14.00	-14.00	-23.00	-16.00	-20.00	-18.00	-45.00	-57.00
UC	—	—	—	—	29.00	28.00	32.00	31.00	31.00	31.00	19.00	8.00
FLC	—	—	—	—	15.00	13.00	15.00	10.00	10.00	10.00	3.00	3.00
DPR	—	—	—	—	—	21.00	27.00	11.00	11.00	11.00	11.00	6.00
CAS	—	—	—	—	—	1.00	1.00	1.00	1.00	1.00	1.00	1.00
HCR	—	—	—	—	—	—	—	2.30	2.20	2.40	1.10	1.50
CCR	—	—	—	—	—	—	—	2.20	2.20	2.80	2.20	4.30
LIV	—	—	—	—	—	—	—	—	12.00	12.00	9.80	14.30
HTH\$	—	—	—	—	—	—	—	—	—	1.00	1.00	1.00
RFI	—	—	—	—	—	—	—	—	—	—	-0.30	-0.35
EFC	—	—	—	—	—	—	—	—	—	—	2.10	2.00
HLIV	—	—	—	—	—	—	—	—	—	—	5.00	8.20

¹PD\$ = Predicted Difference Dollars, MFP\$ = Milk-Fat-Protein Dollars, CY\$ = Cheese Yield Dollars, NM\$₁₉₉₄ = 1994 Lifetime Net Merit, NM\$₂₀₀₀ = 2000 Lifetime Net Merit, NM\$₂₀₀₆ = 2006 Lifetime Net Merit, NM\$₂₀₁₀ = 2010 Lifetime Net Merit, NM\$₂₀₁₄ = 2014 Lifetime Net Merit, NM\$₂₀₁₇ = 2017 Lifetime Net Merit, NM\$₂₀₁₈ = 2018 Lifetime Net Merit, NM\$₂₀₂₁ = 2021 Lifetime Net Merit, and NM\$₂₀₂₅ = 2025 Lifetime Net Merit.

²PL = productive life, UC = udder composite, FLC = foot and leg composite, BSC = body size composite, BWC = body weight composite, DPR = daughter pregnancy rate, CAS = calving ability dollars, HCR = heifer conception rate, CCR = cow conception rate, LIV = cow livability, HTH\$ = health dollars, RFI = residual feed intake, EFC = early first calving, and HLIV = heifer livability.

³BSC was replaced with BWC in April 2017.

Holstein cows born in 2023 from the April 2025 genetic evaluations.

Trends in Predicted Transmitting Abilities and Reliabilities

Results from the April 2025 US national genomic evaluations were used to compute PTA and REL for each of the 12 selection indices studied. Individual PTA for each bull were read from the Format 38 (“All domestic and foreign bulls with official evaluations”; <ftp://ftp.uscdcb.com/pub/bulls/38alloff.zip>) and Format CT (“Calving traits evaluations”; <ftp://ftp.uscdcb.com/pub/bulls/CT.itb.zip>) files distributed by the Council on Dairy Cattle Breeding (Bowie, MD). Standardized transmitting abilities and REL for type (conformation) traits were obtained from Holstein Association USA (Brattleboro, VT).

Reliabilities of the various indices were calculated as the variance of the predicted index values divided by the variance of the true index values:

$$\text{Rel}(\text{index}) = \frac{\mathbf{r}'\mathbf{G}\mathbf{r}}{\mathbf{v}'\mathbf{G}\mathbf{v}},$$

where $\mathbf{r}$ contains the relative economic values (Table 1) multiplied by the square root of REL for each PTA trait (ranges from 2×1 for PD\$ to 17×1 for NM\$₂₀₂₅), $\mathbf{G}$ contains the genetic correlations among the traits (ranges from 2×2 for PD\$ to 17×17 for NM\$₂₀₂₅), and $\mathbf{v}$ contains the relative economic values for the traits (ranges from 2×1 for PD\$ to 17×1 for NM\$₂₀₂₅) (VanRaden et al., 2025). Relative economic values were calculated as:

$$\mathbf{v} = \frac{\mathbf{b} \odot \mathbf{d}}{\sum_t |\mathbf{b}_t \times \mathbf{d}_t|},$$

where $\mathbf{b}$ is a vector of economic values defined above, $\mathbf{d}$ is a vector of SD of true transmitting abilities of the traits in the index, and $|\mathbf{b}_t \times \mathbf{d}_t|$ is the absolute value of the economic value of trait t multiplied by the SD of the TTA of trait t .

Reliability of RFI

The PTA and reliability of RFI were obtained by back-solving from PTA and reliabilities for BWC and feed saved (FSAV) as:

$$\text{PTA}(\text{RFI}) = -\text{PTA}(\text{FSAV}) - 151.8 \times \text{PTA}(\text{BWC}),$$

$$\text{REL}(\text{RFI}) = \frac{\text{REL}(\text{FSAV}) - 0.367 \times \text{REL}(\text{BWC})}{0.633}.$$

Holstein Association USA was responsible for the calculation and distribution of BWC (Holstein Association USA, 2023). VanRaden et al. (2021) described in detail how FSAV is computed from BWC and RFI.

Visualizing Differences Among Indices

Rates of gain for each of the 24 traits and type composites were plotted for each of the selection indices. Distributions of reliabilities for each of the 12 selection indices were also computed and plotted. Spearman's (rank) correlations were calculated among PTA and REL of each index in 10-yr birth cohorts (≤ 1950 , 1960–1969, 1970–1979, 1980–1989, 1990–1999, 2000–2009, and ≥ 2010). Animals were also grouped into quartiles across all birth year cohorts based on their April 2025 ranking for NM\$₂₀₂₅. Heatmaps of the correlation matrices were visualized to identify patterns among changes in correlations as indices changed over time.

Economic Value of Selection Responses

The economic value of the selection response for a trait was calculated as the product of either the correlated response to selection or expected selection response for that trait and the value per PTA unit used in the NM\$₂₀₂₅ calculation. Values for each trait were divided by the total value of the respective index to convert them to a percentage basis, allowing for easier comparisons across indices.

Availability of Software and Data

The IPython notebooks used for the calculations described above are available on GitHub at <https://github.com/wintermind/toomanytraits> under a Creative Commons CC0 1.0 Universal license. Code used for data preparation is included in the notebook “Cole Selection Index Data Preparation.ipynb.” The SD, heritabilities, and correlations used in these calculations are included in the notebook “Cole Selection Index Correlated Responses NM25.ipynb,” as are individual selection index calculations and visualizations of correlated responses to selection. Reliabilities and correlation matrices were visualized using code in the notebook “Cole Selection Index Graphics.ipynb.” Expected genetic progress calculations are documented in the notebook “Cole Expected Genetic Progress NM25.ipynb.”

The data used in the calculations are not stored on GitHub and must be obtained from the original data providers. The PTA for production, health, fitness, and calving traits used in this study may be downloaded from the Council on Dairy Cattle Breeding (<ftp://ftp.uscdcb.com/>). Genetic evaluations for conformation (type) traits may be requested from Jason Graham, Genetic Evaluation and Research Scientist, Holstein Association USA (jgraham@holstein.com).

Calculations were performed using Python 3.11.7 (Van Rossum and Drake, 2009), NumPy 1.26.4 (Oliphant, 2006), Pandas 2.2.2 (McKinney, 2010), and JupyterLab 4.0.11 (Huebner, 2018), running on macOS 14.6.1. Figures were prepared using Seaborn version 0.13.2 (Waskom, 2021).

RESULTS

Changes in the Heritability of the Index

The heritability of each of the 12 indices studied are presented in Table 1 and range from 0.188 in 2010 (NM\$₂₀₁₀) to 0.290 in 1984 (CY\$). Heritabilities were highest for those with heavy emphasis on yield traits, which have heritabilities of 0.20 in this population, and lowest for indices with greater emphasis on health and fitness traits, such as DPR ($h^2 = 0.04$), CCR ($h^2 = 0.01$), and HCR ($h^2 = 0.02$). The heritability of NM\$₂₀₂₅ is 0.243, which is lower than the yield-based indices but higher than all other versions of the lifetime net merit index. The average difference between the 2 groups of indices is 0.069, smaller than might be expected given the low heritabilities of many of the traits added to the indices in the last 20 yr and reflects the genetic and phenotypic correlations among traits. Heritabilities would also be lower if an unweighted phenotypic (co)variance matrix was used. Importantly, this shows the addition of new traits to the index has not notably affected the heritability of the overall selection goal, which is total economic merit.

This makes sense because the goal of the index is to predict an animal's genetic merit for lifetime profitability, which is not measured directly. Profitability depends on economic conditions that are not static, and changes over time are not guaranteed to be consistent in direction; for example, the futures price for milkfat can be higher in one 5-yr period than another. The heritability of the predictor will also change as traits with differing heritabilities and genetic and phenotypic correlations are added to—or removed from—the index. Although it has long been accepted as a useful concept, perhaps lifetime profitability can only be computed retrospectively and attempts to predict it will be unsatisfying. If this is true, then small changes in the properties of the index over time are to be expected.

Changes in Correlated Rates of Gain

The correlated responses to selection and expected genetic progress of all 24 traits from selection on each of the 12 selection indices studied are shown in Table 4 and Figure 1, and Table 5 and Figure 2, respectively. Trends were favorable for most traits (e.g., production traits, PL), although for some traits (e.g., SCS, MFEV) trends are minimal. It should also be noted that although the rates of gain for milk, fat, and protein have decreased over time, they remain favorable, reflecting the economic importance of these traits; the trend has stayed positive, although the overall rate of increase has slowed. Reduced rates of gain for some traits are expected as others are added to the index, but some phenotypes exhibit increased rates of gain as new traits are added. The average PTA for the type composites—BWC, UDC, and FLC—are decreasing slightly, which is due to selection for more moderate body size, but these traits likely have intermediate optima, so a small change in sign is not cause for alarm. The expected genetic responses shown in Table 5 differ from those presented in VanRaden et al. (2025) because the same estimation procedure was used, but the PTA for the animals included have been updated since December 2024. It is also possible that some animals that were not genotyped in December 2024 have since received genotypes and entered the dataset.

Several traits that have not been included in the selection index until recently, such as LIV and HTH\$, show desirable long-term trends, probably due to their favorable correlations with PL, which has been included in the selection criterion since 1994 when NM\$ was introduced by USDA's Animal Improvement Programs Laboratory (VanRaden and Wiggans, 1995). The fertility traits DPR, HCR, and CCR show similar relationships, but the trend for EFC has remained constant over time. This is expected because EFC has much lower genetic correlations with DPR and CCR, and the phenotype is more closely associated with rate of growth than ability to conceive when bred. Traits with greater economic values and higher heritabilities will typically contribute more to the economic objective than traits with low heritabilities and low economic values. A trait that has strong, desirable correlations with others in the index may also produce larger changes than those expected from only its heritability or economic value. Should larger-than-expected gains persist for some traits, the selection index can be restricted to keep changes within desirable limits (e.g., Mancin et al., 2022).

Although the general trends estimated by the 2 methods (Equations 1 and 2) are generally similar, the rates of genetic change differ substantially in some cases. These differences are relatively modest when expressed as SD of PTA (Supplemental Table 3, see Notes; "Difference

Table 4. Correlated response to selection (PTA change/year) for traits and composites included in USDA selection indices, 1971–2025^{1,2,3}

Trait ³	PD\$ (1971)	MFP\$ (1976)	CY\$ (1984)	NM\$ ₁₉₉₄	NM\$ ₂₀₀₀	NM\$ ₂₀₀₆	NM\$ ₂₀₁₀	NM\$ ₂₀₁₄	NM\$ ₂₀₁₇	NM\$ ₂₀₁₈	NM\$ ₂₀₂₁	NM\$ ₂₀₂₅
Milk	104.67	91.245	78.097	71.079	71.155	41.998	34.967	52.399	46.299	44.478	52.643	51.717
Fat	3.43	3.869	4.247	2.996	2.819	2.348	2.075	2.867	2.770	2.837	2.820	2.915
Protein	2.67	2.849	2.648	2.222	2.218	1.493	1.266	1.827	1.653	1.611	1.790	1.719
PL	0.0449	0.047	0.044	0.183	0.189	0.234	0.243	0.220	0.214	0.200	0.231	0.221
SCS	0.0054	0.005	0.004	-0.005	-0.006	-0.009	-0.010	-0.007	-0.006	-0.005	-0.004	-0.003
BSC/BWC ³	-0.0260	-0.023	-0.022	-0.028	-0.033	-0.032	-0.036	-0.037	-0.041	-0.039	-0.064	-0.072
UC	0.0080	0.005	0.005	0.004	0.024	0.015	0.013	0.018	0.013	0.013	0.004	-0.001
FLC	-0.0122	-0.013	-0.011	-0.010	0.005	0.001	0.000	0.000	-0.002	-0.001	-0.008	-0.010
DPR	-0.1402	-0.130	-0.122	-0.008	-0.018	0.106	0.129	0.063	0.065	0.056	0.064	0.042
CA\$	0.4831	0.549	0.596	0.815	0.795	1.176	1.155	1.181	1.132	1.099	1.205	1.184
HCR	-0.0454	-0.046	-0.039	0.014	0.016	0.080	0.091	0.069	0.066	0.062	0.061	0.058
CCR	-0.0992	-0.086	-0.078	0.056	0.046	0.178	0.201	0.140	0.136	0.125	0.133	0.120
LIV	-0.0697	-0.066	-0.060	0.058	0.047	0.105	0.121	0.084	0.104	0.097	0.121	0.124
GL	-0.0619	-0.064	-0.061	-0.058	-0.055	-0.047	-0.043	-0.054	-0.051	-0.051	-0.059	-0.058
HTH\$	0.0847	0.153	0.200	0.641	0.676	0.841	0.868	0.793	0.772	0.769	0.776	0.733
RFI	-0.5683	-0.521	-0.597	-1.053	-1.299	-0.730	-0.741	-1.229	-1.405	-1.385	-10.839	-12.115
MFEV	0.0021	0.003	0.003	0.004	0.004	0.004	0.004	0.004	0.004	0.004	0.003	0.003
DSAB	0.0141	0.016	0.017	0.028	0.029	0.030	0.030	0.031	0.031	0.031	0.035	0.035
KETO	0.0178	0.025	0.026	0.034	0.036	0.037	0.036	0.038	0.036	0.036	0.036	0.034
MAST	-0.0554	-0.052	-0.046	0.030	0.041	0.069	0.077	0.053	0.051	0.046	0.040	0.034
METR	0.0236	0.029	0.031	0.043	0.042	0.051	0.050	0.051	0.049	0.050	0.050	0.047
REPL	-0.0025	-0.003	-0.002	0.004	0.004	0.009	0.009	0.007	0.007	0.008	0.007	0.006
EFC	0.1272	0.135	0.124	0.148	0.135	0.149	0.144	0.152	0.142	0.135	0.157	0.149
HLIV	0.0307	0.029	0.028	0.043	0.044	0.046	0.045	0.047	0.044	0.043	0.047	0.046

¹PD\$ = Predicted Difference Dollars, MFP\$ = Milk-Fat-Protein Dollars, CY\$ = Cheese Yield Dollars, NM\$₁₉₉₄ = 1994 Lifetime Net Merit, NM\$₂₀₀₀ = 2000 Lifetime Net Merit, NM\$₂₀₀₆ = 2006 Lifetime Net Merit, NM\$₂₀₁₀ = 2010 Lifetime Net Merit, NM\$₂₀₁₄ = 2014 Lifetime Net Merit, NM\$₂₀₁₇ = 2017 Lifetime Net Merit, NM\$₂₀₁₈ = 2018 Lifetime Net Merit, NM\$₂₀₂₁ = 2021 Lifetime Net Merit, and NM\$₂₀₂₅ = 2025 Lifetime Net Merit.

²Trait abbreviations are: PL = productive life, UC = udder composite, FLC = foot and leg composite, BSC = body size composite, BWC = body weight composite, DPR = daughter pregnancy rate, CA\$ = calving ability dollars, HCR = heifer conception rate, CCR = cow conception rate, LIV = cow livability, GL = gestation length, HTH\$ = health dollars, RFI = residual feed intake, MFEV = milk fever, DSAB = displaced abomasum, KETO = ketosis, MAST = clinical mastitis, METR = metritis, REPL = retained placenta, EFC = early first calving, and HLIV = heifer livability.

³BSC was replaced with BWC in April 2017.

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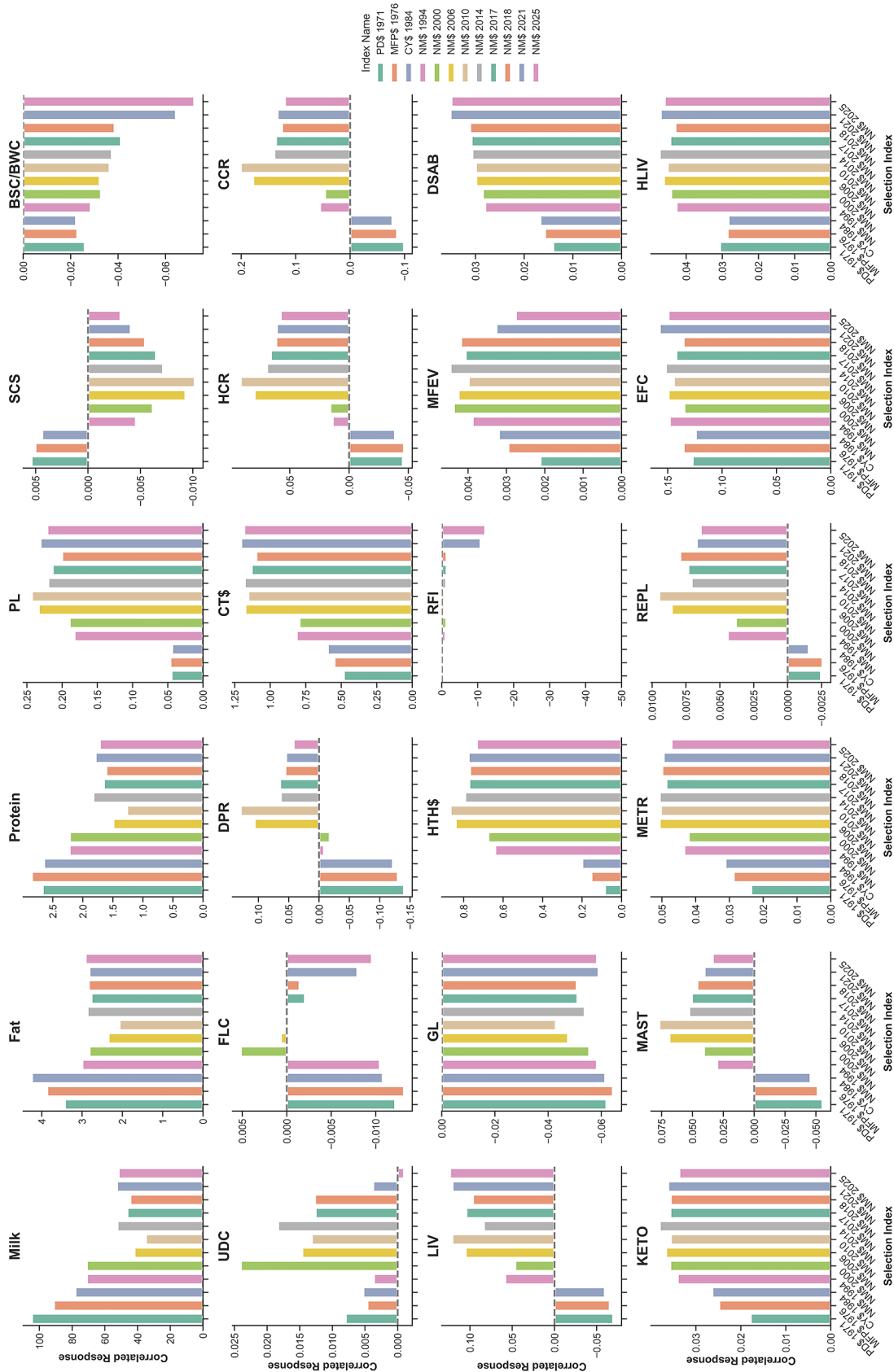


Figure 1. Correlated response to selection (PTA change/yr) for traits included in 2025 Lifetime Net Merit from selection on USDA selection indices, 1971–2025. PD\$ = predicted difference dollars, MFP\$ = milk-fat-protein dollars, CY\$ = cheese yield dollars, NMS₁₉₉₄ = 1994 Lifetime Net Merit, NMS₂₀₀₀ = 2000 Lifetime Net Merit, NMS₂₀₀₆ = 2006 Lifetime Net Merit, NMS₂₀₁₀ = 2010 Lifetime Net Merit, NMS₂₀₁₄ = 2014 Lifetime Net Merit, NMS₂₀₁₇ = 2017 Lifetime Net Merit, NMS₂₀₁₈ = 2018 Lifetime Net Merit, NMS₂₀₂₁ = 2021 Lifetime Net Merit, and NMS₂₀₂₅ = 2025 Lifetime Net Merit. Trait abbreviations: PL = productive life, BSC = body size composite, BWC = body weight composite, UDC =udder composite, FLC = foot and leg composite, DPR = daughter pregnancy rate, CT\$ = calving traits dollars, HCR = heifer conception rate, CCR = cow conception rate, LIV = cow livability, GL = gestation length, HTH\$ = health dollars, MFEV = milk fever, DSAB = displaced abomasum, KETO = ketosis, MAST = clinical mastitis, METR = metritis, REPL = retained placenta, EFC = early first calving, and HLIV = heifer livability. BSC was replaced with BWC in April 2017. The values used to create these plots are provided in Table 4.

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Table 5. Expected genetic progress (PTA change/year) for traits and composites included in USDA selection indices, 1971–2025¹

Traits ²	PD\$ (1971)	MFP\$ (1976)	CY\$ (1984)	NM\$ ₁₉₉₄	NM\$ ₂₀₀₀	NM\$ ₂₀₀₆	NM\$ ₂₀₁₀	NM\$ ₂₀₁₄	NM\$ ₂₀₁₇	NM\$ ₂₀₁₈	NM\$ ₂₀₂₁	NM\$ ₂₀₂₅
Milk	162.79	126.33	100.43	110.79	109.79	71.73	62.17	80.10	72.73	69.74	80.50	79.50
Fat	7.54	8.57	9.09	8.14	7.72	7.52	7.17	8.03	8.09	8.26	7.80	7.93
Protein	4.65	4.79	4.42	4.47	4.45	3.71	3.42	3.96	3.80	3.76	3.82	3.69
PL	0.1106	0.1352	0.1401	0.3009	0.3135	0.3788	0.4035	0.3425	0.3498	0.3388	0.3577	0.3461
SCS	0.0035	0.0009	-0.0001	-0.0107	-0.0128	-0.0171	-0.0190	-0.0140	-0.0138	-0.0127	-0.0124	-0.0114
BSC/BWC ³	-0.0628	-0.0534	-0.0526	-0.0691	-0.0688	-0.0737	-0.0825	-0.0762	-0.0852	-0.0819	-0.1115	-0.1239
UC	0.0237	0.0277	0.0281	0.0328	0.0621	0.0569	0.0560	0.0560	0.0473	0.0464	0.0286	0.0176
FLC	-0.0211	-0.0133	-0.0099	-0.0147	0.0038	0.0038	0.0034	0.0010	-0.0040	-0.0032	-0.0195	-0.0258
DPR	-0.2165	-0.1891	-0.1748	-0.0936	-0.0881	0.0246	0.0561	-0.0236	-0.0153	-0.0195	-0.0195	-0.0311
CAS	0.8337	1.017	1.0655	1.4275	1.3746	1.8504	1.8911	1.7569	1.8260	1.8098	1.8911	1.8870
HCR	0.0043	0.0115	0.0182	0.0674	0.0726	0.1247	0.1390	0.1123	0.1137	0.1118	0.1171	0.1137
CCR	-0.1403	-0.1067	-0.0933	0.0168	0.0212	0.1447	0.1794	0.0944	0.1023	0.0961	0.1017	0.0894
LIV	-0.0986	-0.0617	-0.0401	0.0931	0.0801	0.1757	0.2084	0.1362	0.1837	0.1775	0.1979	0.2053
GL	-0.0729	-0.0797	-0.0748	-0.0789	-0.0721	-0.0714	-0.0683	-0.0736	-0.0767	-0.0763	-0.0831	-0.0831
HTH\$	0.1065	0.3460	0.4311	0.9713	1.0086	1.3146	1.4024	1.1656	1.2002	1.2162	1.2162	1.1576
RFI	-0.2274	-0.0568	0.2274	-1.6769	-1.8190	-2.1601	-2.4159	-1.9327	-2.0464	-1.8759	-5.5707	-5.8549
MFEV	0.0014	0.0021	0.0027	0.0043	0.0040	0.0052	0.0055	0.0048	0.0054	0.0056	0.0051	0.0052
DSAB	0.0111	0.0154	0.0168	0.0336	0.0328	0.0395	0.0417	0.0364	0.0388	0.0400	0.0425	0.0419
KETO	-0.0044	0.0116	0.0109	0.0439	0.0486	0.0560	0.0629	0.0516	0.0516	0.0521	0.0513	0.0442
MAST	-0.0732	-0.0289	-0.0080	0.0871	0.1050	0.1612	0.1811	0.1299	0.1314	0.1274	0.1199	0.1080
METR	0.0625	0.0783	0.0819	0.1070	0.1045	0.1225	0.1251	0.1167	0.1197	0.1228	0.1236	0.1213
REPL	-0.0102	-0.0073	-0.0059	0.0032	0.0025	0.0099	0.0119	0.0060	0.0073	0.0088	0.0083	0.0073
EFC	0.2733	0.2800	0.2673	0.3093	0.2943	0.3078	0.3040	0.3093	0.3070	0.3040	0.3333	0.3288
HLIV	0.0042	0.0009	0.0003	0.0147	0.0166	0.0195	0.0217	0.0169	0.0177	0.0161	0.0195	0.0195

¹PD\$ = Predicted Difference Dollars, MFP\$ = Milk-Fat-Protein Dollars, CY\$ = Cheese Yield Dollars, NM\$₁₉₉₄ = 1994 Lifetime Net Merit, NM\$₂₀₀₀ = 2000 Lifetime Net Merit, NM\$₂₀₀₆ = 2006 Lifetime Net Merit, NM\$₂₀₁₀ = 2010 Lifetime Net Merit, NM\$₂₀₁₄ = 2014 Lifetime Net Merit, NM\$₂₀₁₇ = 2017 Lifetime Net Merit, NM\$₂₀₁₈ = 2018 Lifetime Net Merit, NM\$₂₀₂₁ = 2021 Lifetime Net Merit, and NM\$₂₀₂₅ = 2025 Lifetime Net Merit.

²PL = productive life, U/C = udder composite, FLC = foot and leg composite, BSC = body size composite, BWC = body weight composite, DPR = daughter pregnancy rate, CAS = calving ability dollars, HCR = heifer conception rate, CCR = cow conception rate, LIV = cow livability, GL = gestation length, HTH\$ = health dollars, RFI = residual feed intake, MFEV = milk fever, DSAB = displaced abomasum, KETO = ketosis, MAST = clinical mastitis, METR = metritis, REPL = retained placenta, EFC = early first calving, and HLIV = heifer livability.

³BSC was replaced with BWC in April 2017.

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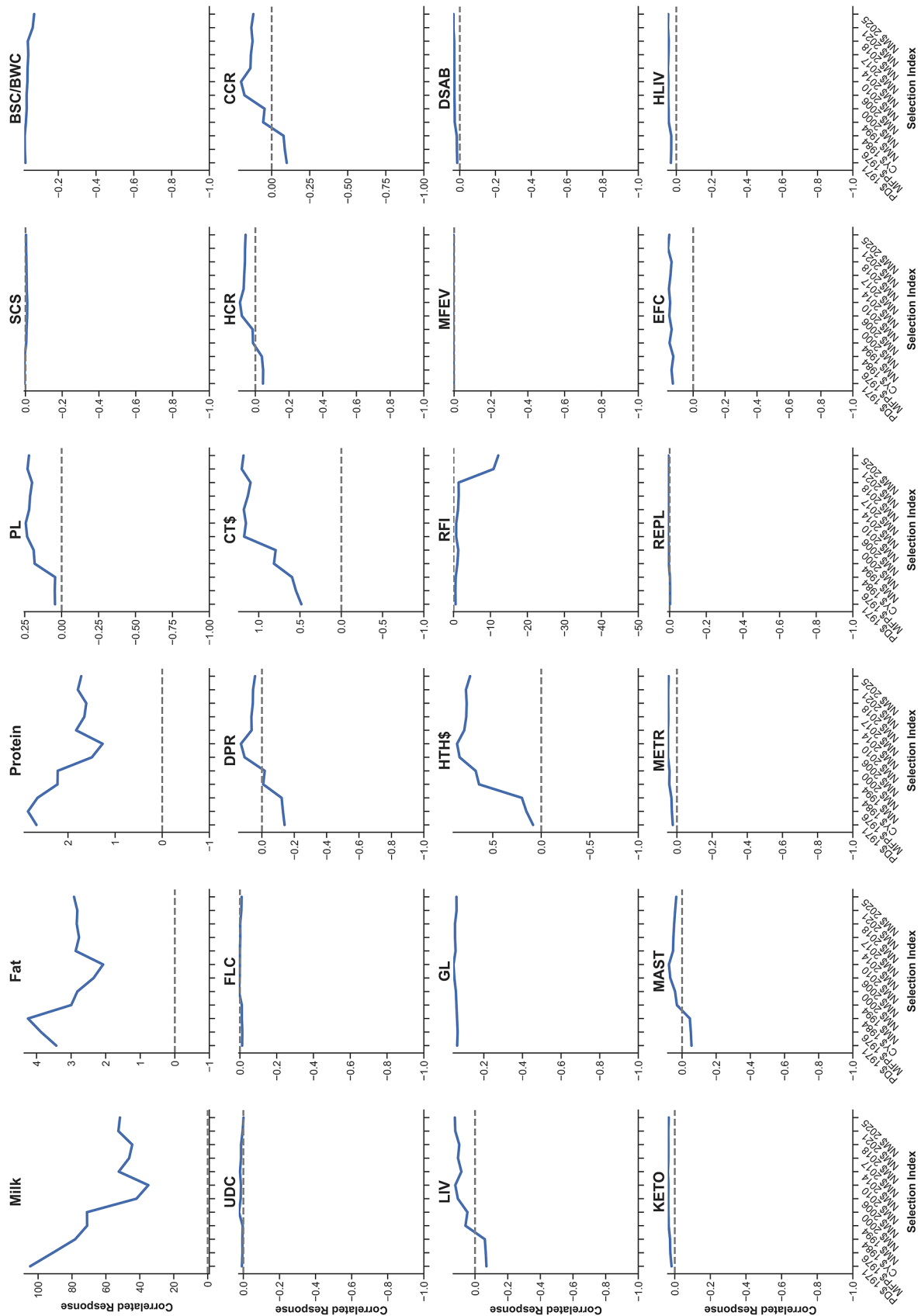


Figure 2. Expected genetic progress (PTA change/yr) for traits included in 2025 Lifetime Net Merit from selection on USDA selection indices, 1971–2025. Index abbreviations: PD\$ = predicted difference dollars, MFPS\$ = milk-fat-protein dollars, CY\$ = cheese yield dollars, NMS₁₉₉₄ = 1994 Lifetime Net Merit, NMS₂₀₀₀ = 2000 Lifetime Net Merit, NMS₂₀₀₆ = 2006 Lifetime Net Merit, NMS₂₀₁₀ = 2010 Lifetime Net Merit, NMS₂₀₁₄ = 2014 Lifetime Net Merit, NMS₂₀₁₇ = 2017 Lifetime Net Merit, NMS₂₀₁₈ = 2018 Lifetime Net Merit, NMS₂₀₂₁ = 2021 Lifetime Net Merit, and NMS₂₀₂₅ = 2025 Lifetime Net Merit. Trait abbreviations: PL = productive life, BSC = body size composite, BWC = body weight composite, UDC = udder composite, FLC = foot and leg composite, DPR = daughter pregnancy rate, CT\$ = calving traits dollars, HCR = heifer conception rate, CCR = cow conception rate, LIV = cow livability, GL = gestation length, HTH\$ = health dollars, MFEV = milk fever, DSAB = displaced abomasum, KETO = ketosis, MAST = clinical mastitis, METR = metritis, REPL = retained placenta, EFC = early first calving, and HLIV = heifer livability. BSC was replaced with BWC in April 2017. The values used to create these plots are provided in Table 5.

in Response” worksheet). For example, the 27.79-pound difference in $NM\$_{2025}$ Milk between the 2 methods is equivalent to only about 5% (0.049) SD. The smallest difference in $NM\$_{2025}$ responses, representing the closest concordance of the methods, was 0.003 for RETP, whereas the largest was 0.185 for fat. This is not said to minimize the importance of estimation—larger-than-expected differences between predictions and observed performance undermine confidence in selection tools—but it is not clear which estimate is the “best” in the sense of producing the smallest difference when compared with actual lifetime production.

Changes Among Individual Bull Rankings

Heatmaps of the rank correlations among bull PTA for each selection index are shown in Figure 3. There is little reranking for the youngest cohorts of bulls (born 2010–2019 and 2020–2025). The highest degree of reranking was consistently seen for $NM\$_{2006}$ and $NM\$_{2010}$, which had less emphasis on protein production and more emphasis on fertility and longevity than other indices. Over time, there is also less reranking because younger cohorts are the product of selection for earlier versions of the index, which included emphasis on fertility and longevity that older birth year groups were not exposed to. Although these young animals also show higher reranking for $NM\$_{2006}$ and $NM\$_{2010}$ than the other indices, the degree of reranking is much lower than for earlier cohorts of bulls. As Lush (1945, p. 145) noted, “the animal is the smallest unit that can be selected or rejected at any one time,” and these bulls might be viewed as proof that selection works.

There are clear differences between index PTA for bulls in the top quartile and the bottom quartile (Figure 4), with bulls in the top quartile changing rank more often than bulls in the bottom quartile. This suggests that there are many ways that a bull can achieve a desirable ranking on the index as the traits in the selection criterion change—through high components or outstanding daughter fertility, for example—but poor-performing bulls rank low regardless of the index. This provides breeders with many choices to suit their own circumstances and meet their breeding objectives.

Changes in Reliability of the Index

Distributions of traditional and genomic bull reliabilities for each of the 12 selection indices are shown in Figure 5. Very general patterns can be seen in these plots, such as cohorts of young bulls with relatively low reliabilities on the left side of each plot, with separation into groups with higher reliabilities representing different cohorts of bulls with daughter records. There is a

“flattening” of the distributions beginning with $NM\$_{2006}$, which corresponds to generally lower weights on production and increased weights on traits with lower heritability, such as DPR and PL. As expected (e.g., Schaeffer, 2006; Dekkers et al., 2021), genomic reliabilities were consistently higher than traditional values. These results are consistent with predictions of Pszczola et al. (2012), as virtually all reference animals have actual or imputed genotypes, and the index has a moderate heritability.

Heatmaps of the rank correlations among reliabilities of genomic PTA for each selection index are shown in Figure 6. There are no notable differences when all animals are visualized together (“All Birthyears” subplot), meaning that there is little reranking, but there is reranking among bulls born in the 1950s, 1960s, and 1970s. The correlations among reliabilities of different indices for these animals are difficult to interpret, but their reliabilities for traits other than milk, fat, and protein are relatively low because they will have no or very few daughters phenotyped for traits other than production. This leads to reranking when the index changes, particularly as weight is placed on traits with low reliabilities. Correlations are generally high among indices with similar composition, and low with dissimilar indices for which bulls have few daughters with records. There are few differences among bulls born in the 1980s or later. Animals in the top and bottom quartiles of PTA for each index showed little reranking (data not shown).

Correlations Among Indices

Rank correlations are high across indices, ranging from 0.875 to 0.999, suggesting that sires rank similarly despite the increasing complexity of the index over time (Supplemental Table 4, see Notes). This implies that more complex indices do not, in general, lead to notably different selection decisions (e.g., Legarra et al., 2007). For example, the correlation of $NM\$_{1994}$ with the other versions of $NM\$$ ranges from 0.973 with $NM\$_{2010}$, to 0.993 with $NM\$_{2000}$. It is possible that genetic progress in the population is more affected by variation in the accuracy of genetic parameters, difficulties in estimating economic value estimates, and low reliabilities for new traits of economic significance than by the index used to rank bulls for selection. An unintended consequence of changes in the index producing relatively small changes in animal rankings is that modern management practices in the United States that seek to minimize labor costs rather than maximize rates of genetic gain have only small effects on realized selection gains. Although the theory is clear that all traits affecting an animal’s lifetime economic performance should be included in the index, the marginal value of adding new traits may be relatively

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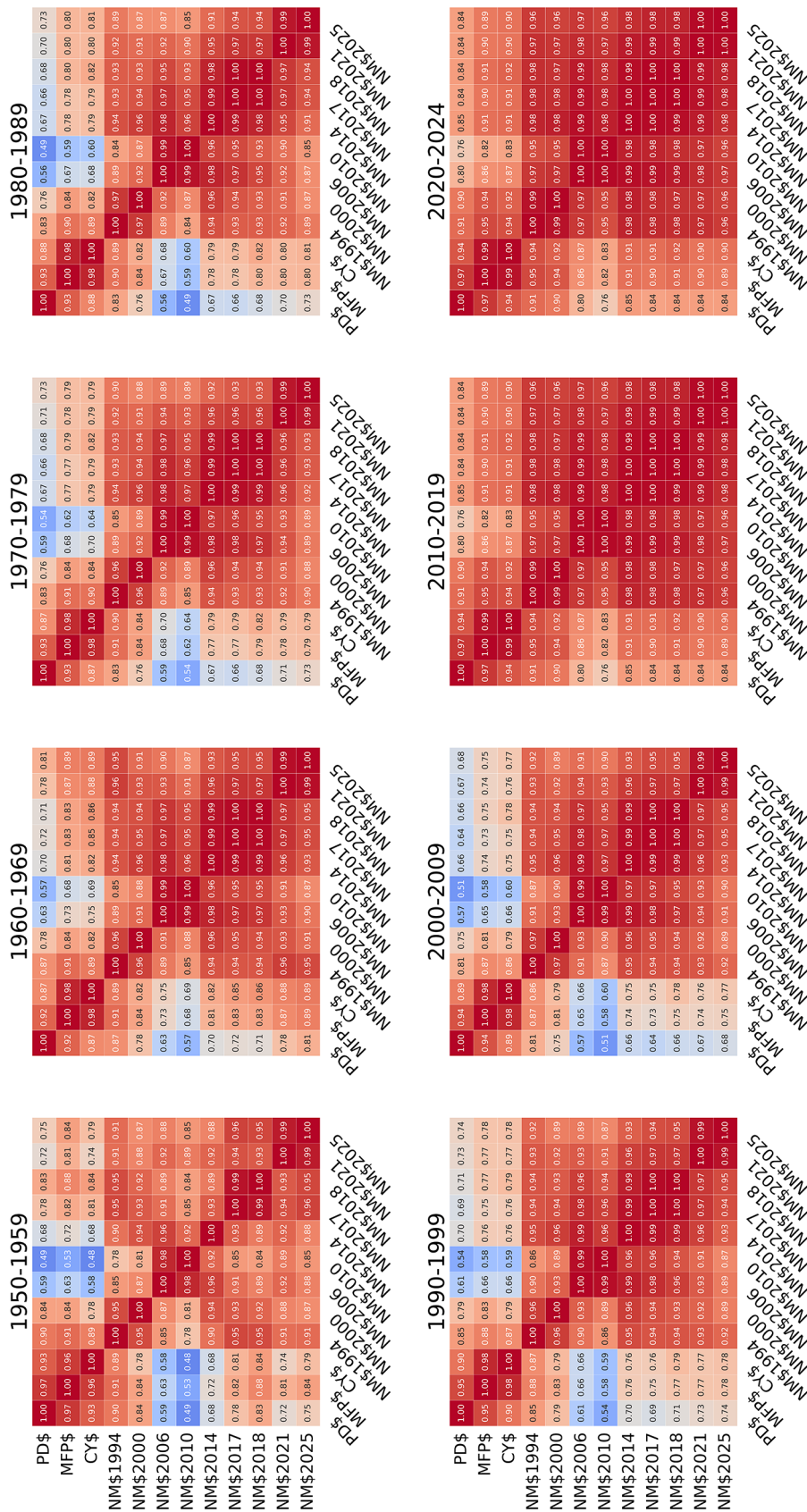


Figure 3. Correlations among USDA selection index values for all Holstein bulls with evaluations in the April 2025 Format 38 (“All domestic and foreign bulls with official evaluations”) in 10-year birth cohorts. Index abbreviations: PD\$ = predicted difference dollars, MFP\$ = milk-fat-protein dollars, CY\$ = cheese yield dollars, NM\$₁₉₉₄ = 1994 Lifetime Net Merit, NM\$₂₀₀₀ = 2000 Lifetime Net Merit, NM\$₂₀₀₃ = 2003 Lifetime Net Merit, NM\$₂₀₀₆ = 2006 Lifetime Net Merit, NM\$₂₀₁₀ = 2010 Lifetime Net Merit, NM\$₂₀₁₄ = 2014 Lifetime Net Merit, NM\$₂₀₁₇ = 2017 Lifetime Net Merit, NM\$₂₀₁₈ = 2018 Lifetime Net Merit, NM\$₂₀₂₁ = 2021 Lifetime Net Merit, and NM\$₂₀₂₅ = 2025 Lifetime Net Merit. No correlations of one index with another (the off-diagonal elements) were equal to 1 in the “all birthyears” group, but the software used to draw the figure rounded off-diagonal values >0.99 to 1.0. The underlying data are provided in Supplemental Table 2 (see Notes).

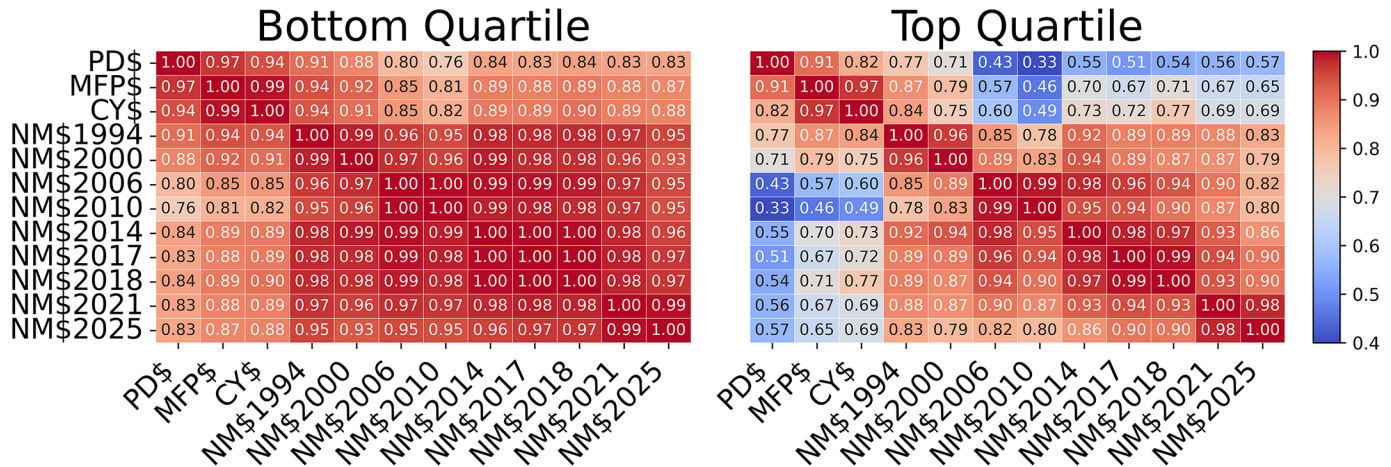


Figure 4. Correlations among USDA selection index values for all Holstein bulls with evaluations in the April 2025 Format 38 (“All domestic and foreign bulls with official evaluations”) that fall in the bottom and top quartiles of the population.¹ Index abbreviations are: PD\$ = predicted difference dollars, MFP\$ = milk-fat-protein dollars, CY\$ = cheese yield dollars, NM\$₁₉₉₄ = 1994 Lifetime Net Merit, NM\$₂₀₀₀ = 2000 Lifetime Net Merit, NM\$₂₀₀₃ = 2003 Lifetime Net Merit, NM\$₂₀₀₆ = 2006 Lifetime Net Merit, NM\$₂₀₁₀ = 2010 Lifetime Net Merit, NM\$₂₀₁₄ = 2014 Lifetime Net Merit, NM\$₂₀₁₇ = 2017 Lifetime Net Merit, NM\$₂₀₁₈ = 2018 Lifetime Net Merit, NM\$₂₀₂₁ = 2021 Lifetime Net Merit, and NM\$₂₀₂₅ = 2025 Lifetime Net Merit.

small once production, longevity, and efficiency are included in the index.

Economic Value of Selection Responses

Economic values, expressed as the percent of total response for an index accounted for by a trait, are shown in in Tables 6 and 7 for correlated responses to selection and expected selection response, respectively (economic values in dollars may be found in Supplemental Tables 2 and 3). Although there are small differences among the correlated responses and expected responses, fat, protein, PL, BWC, and LIV consistently have the highest values across indices and calculation methods. Residual feed intake shows considerable value in NM\$₂₀₂₁ and NM\$₂₀₂₅. Calving ability and HTH\$ are less consistent, showing greater value for correlated selection response than expected selection response. It is encouraging to consistency among the prediction methods because the same traits should have similar economic values regardless of how selection responses are calculated. It should be noted that assuming linearity of economic values also assumes that the relationship between traits remains constant (e.g., that the value of fat relative to protein is the same over time). Although this is not strictly correct, selection indices are generally robust to modest errors in economic values (e.g., Cole and VanRaden, 2017).

DISCUSSION

Changes in (Co)variances over Time

The assumption that the same genetic and phenotypic (co)variance matrices can be used over a 5-yr period is not consistent with theory or practice, but it was necessary. Except for a handful of phenotypes—milk, fat, and protein yields—the data needed to estimate all (co)variances for 24 traits and type composites at, e.g., 10-yr intervals simply do not exist. The genetic correlation of productive life with protein yield decreased from 0.47 to 0.12 between 1993 and 2004 (VanRaden and Tooker, 2005). Tsuruta et al. (2004) also reported that genetic correlations of PL with milk, fat, and protein yields and body size composite decreased between 1979 and 1993, approaching 0 in some cases and changing signs to slightly negative in others. Cole and VanRaden (2018) showed that selection indices are insensitive to some changes in parameters, but it is not known how sensitive indices are to widespread errors in (co)variances. It is important to periodically recalculate the correlation and (co)variance matrices in the population under selection.

Differences Among Predictors

Although the trends shown in Figures 1 and 2 are broadly similar, they are hardly identical. These differences likely stem from 2 different sources: (1) the use of different estimation procedures, and (2) the use of different populations. In the selection index method

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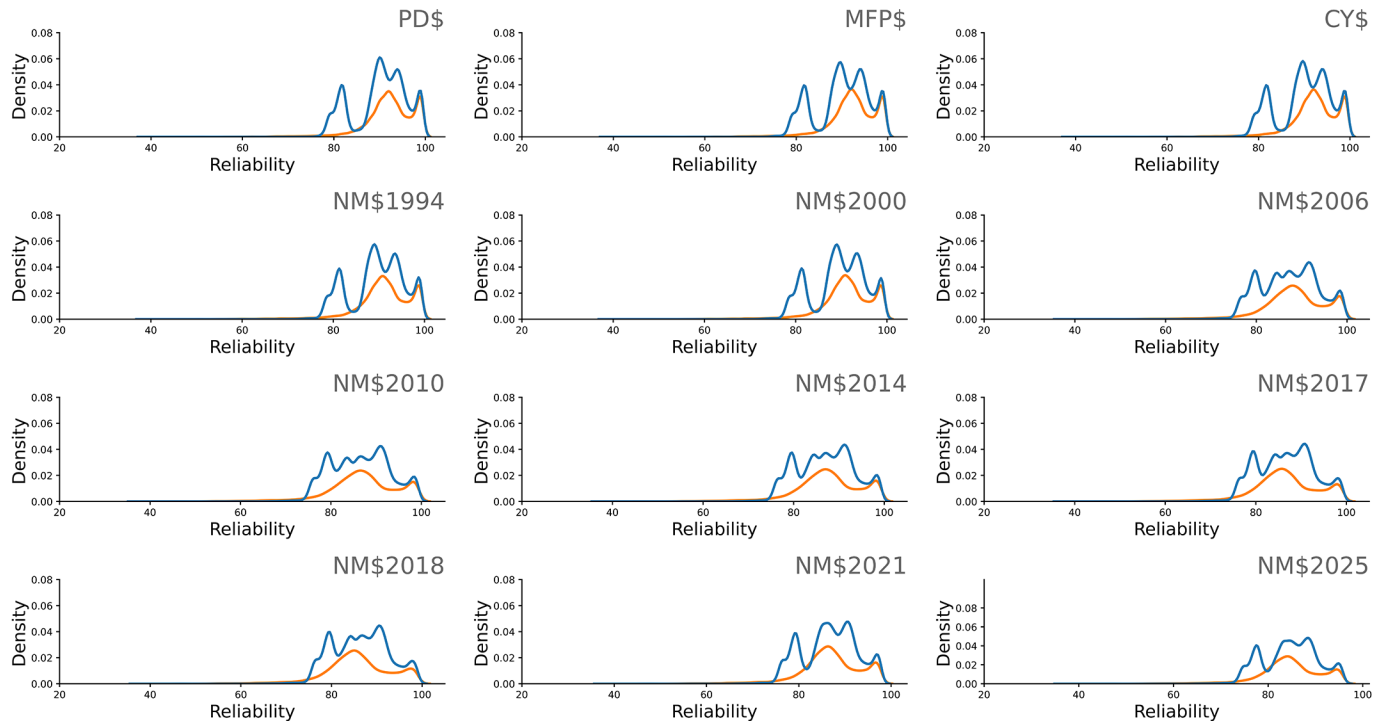


Figure 5. Distributions of traditional and genomic reliabilities of USDA selection index values for all Holstein bulls with evaluations in the April 2025 genetic evaluation run. Blue lines include genomic information and were computed from the 38alloff.zip file (“All domestic and foreign bulls with official evaluations”), and orange lines represent traditional evaluations and were computed from the 38all.trad.zip file (“Unofficial traditional only [no genomics] evaluations”). PD\$ = predicted difference dollars, MFP\$ = milk-fat-protein dollars, CY\$ = cheese yield dollars, NM\$₁₉₉₄ = 1994 Lifetime Net Merit, NM\$₂₀₀₀ = 2000 Lifetime Net Merit, NM\$₂₀₀₆ = 2006 Lifetime Net Merit, NM\$₂₀₁₀ = 2010 Lifetime Net Merit, NM\$₂₀₁₄ = 2014 Lifetime Net Merit, NM\$₂₀₁₇ = 2017 Lifetime Net Merit, NM\$₂₀₁₈ = 2018 Lifetime Net Merit, NM\$₂₀₂₁ = 2021 Lifetime Net Merit, and NM\$₂₀₂₅ = 2025 Lifetime Net Merit. These files are available by public FTP from the Council on Dairy Cattle breeding: <ftp://ftp.uscdcb.com/pub/bulls/>.

used to calculate the correlated responses to selection, genetic trends are estimated from population parameters, including the genetic (co)variances in $\mathbf{G}$ and the weighted phenotypic (co)variances in $\mathbf{P}^*$. The values in $\mathbf{P}$ were based on records of Holstein cows, the reliabilities used to compute $\mathbf{P}^*$ were those of genotyped Holstein heifers born in 2023, and the values in $\mathbf{G}$ were based on PTA correlations for Holstein bulls with reliabilities of at least 0.85. In contrast, expected genetic progress was based on PTA of genotyped Holstein heifers born in 2023. In the latter case, the economic values in $\mathbf{b}$ were applied to PTA that are regressed toward the population average, rather than to individual records or averages of progeny performance as is the case in selection index (e.g., Schneeberger et al., 1992). This could explain, in part, why predictions from the 2 methods differ. It has already been noted that the parameters used in the selection index calculations were estimated using slightly different populations, but it is not always clear which population should be used. For example, dairy bulls are the principal drivers of genetic gains in the commercial cow population, but the young Holstein

heifers used to calculate expected selection responses represent the current generation of cows, whereas their sires may represent the previous generation. A more sophisticated method is probably needed to properly account for the different sources of information available. For example, separate $\mathbf{P}$ and $\mathbf{G}$ matrices could be constructed for each path of selection, and the estimates for each path combined to produce a weighted average response. This is similar in some respects to the method implemented by Rutten et al. (2002) to predict selection response for overlapping generations in the SelAction software package.

Efficiency of Selection for Multiple Traits

Hazel and Lush (1942) showed that, when selection is for t traits using an index (“total score,” in their language), progress for any one trait is $1/\sqrt{t}$ times as great as single-trait selection alone (Figure 2 in Hazel and Lush, 1942). This appears to support the intuition of many people that an index should not include too many

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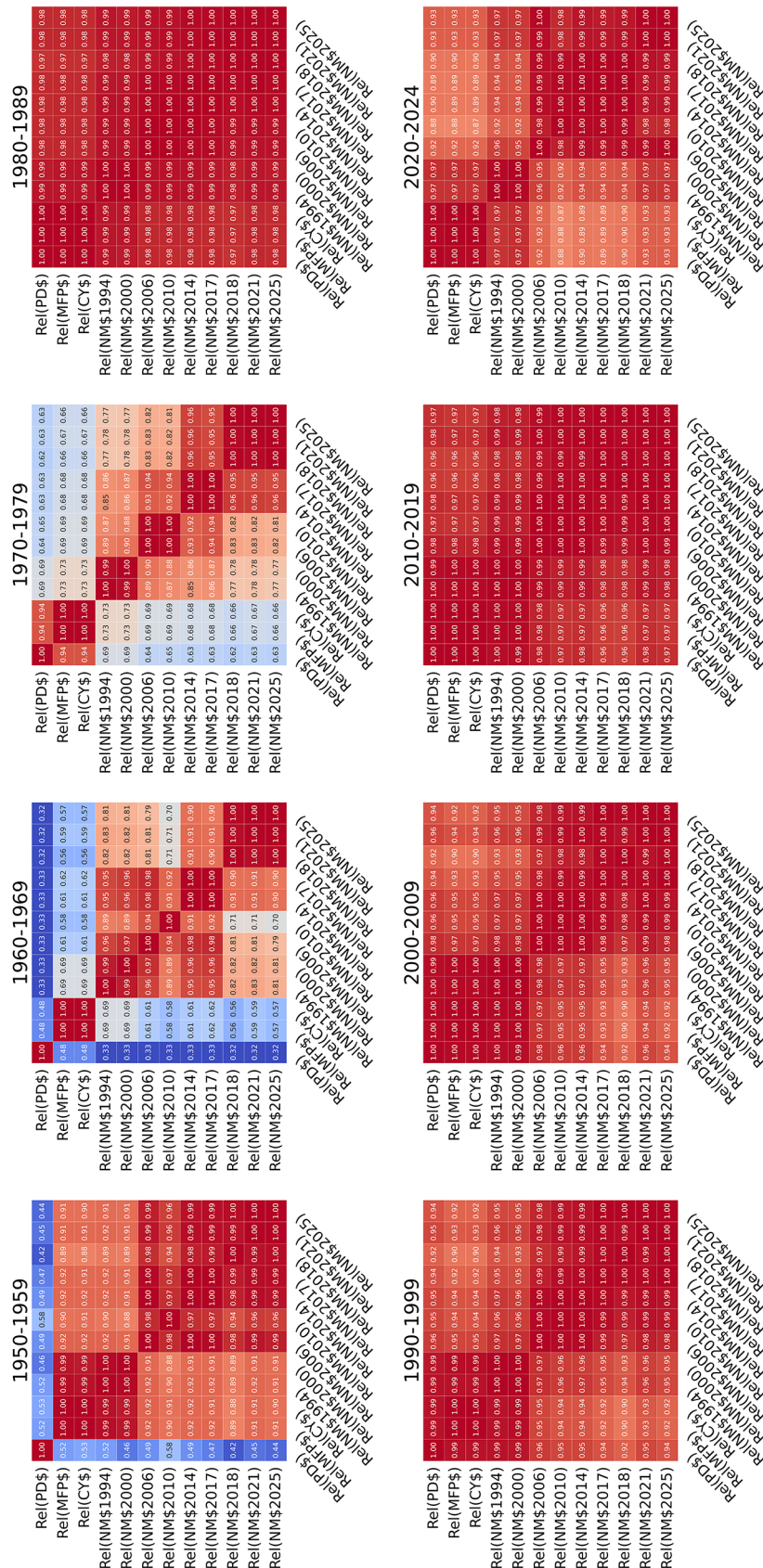


Figure 6. Correlations among genomic reliabilities of predicted transmitting abilities for USDA selection index values for all Holstein bulls with evaluations in the April 2025 Format 38 (“All domestic and foreign bulls with official evaluations”) across all birthyears and in 10-year cohorts. PD\$ = predicted difference dollars, MFP\$ = milk-fat-protein dollars, CY\$ = cheese yield dollars, NM\$₁₉₉₄ = 1994 Lifetime Net Merit, NM\$₂₀₀₀ = 2000 Lifetime Net Merit, NM\$₂₀₀₃ = 2003 Lifetime Net Merit, NM\$₂₀₀₆ = 2006 Lifetime Net Merit, NM\$₂₀₁₀ = 2010 Lifetime Net Merit, NM\$₂₀₁₄ = 2014 Lifetime Net Merit, NM\$₂₀₁₇ = 2017 Lifetime Net Merit, NM\$₂₀₁₈ = 2018 Lifetime Net Merit, NM\$₂₀₂₁ = 2021 Lifetime Net Merit, and NM\$₂₀₂₅ = 2025 Lifetime Net Merit. No correlations of one index with another (the off-diagonal elements) were equal to 1 in the “all birthyears” group, but the software used to draw the figure rounded off-diagonal values >0.99 to 1.0. The underlying data are provided in Supplemental Table S3.

Table 6. Value of correlated responses to selection as a proportion of total index response for traits and composites included in USDA selection indices, 1971–2025¹

Traits ²	PD\$ (1971)	MFPS (1976)	CY\$ (1984)	NM\$ ₁₉₉₄	NM\$ ₂₀₀₀	NM\$ ₂₀₀₆	NM\$ ₂₀₁₀	NM\$ ₂₀₁₄	NM\$ ₂₀₁₇	NM\$ ₂₀₁₈	NM\$ ₂₀₂₁	NM\$ ₂₀₂₅
Milk	0.0652	0.0534	0.0450	0.0445	0.0449	0.0278	0.0240	0.0317	0.0288	0.0283	0.0280	0.0271
Fat	0.4866	0.5155	0.5567	0.4276	0.4054	0.3537	0.3248	0.3952	0.3930	0.4110	0.3415	0.3484
Protein	0.2518	0.2523	0.2307	0.2108	0.2120	0.1495	0.1317	0.1674	0.1559	0.1551	0.1441	0.1365
PL	0.0381	0.0375	0.0345	0.1564	0.1628	0.2110	0.2277	0.1816	0.1818	0.1735	0.1675	0.1582
SCS	0.0113	0.0098	0.0077	0.0105	0.0127	0.0200	0.0231	0.0143	0.0126	0.0107	0.0072	0.0053
BSC/BWC ³	0.0420	0.0349	0.0328	0.0455	0.0540	0.0348	0.0641	0.0580	0.0662	0.0643	0.0882	0.0979
UC	0.0018	0.0011	0.0010	0.0009	0.0055	0.0036	0.0032	0.0040	0.0029	0.0030	0.0008	0.0002
FLC	0.0010	0.0010	0.0009	0.0009	0.0004	0.0001	0.0000	0.0000	0.0002	0.0001	0.0006	0.0007
DPR	0.0238	0.0207	0.0192	0.0031	0.0031	0.0191	0.0242	0.0104	0.0097	0.0110	0.0078	0.0060
CAS	0.0137	0.0146	0.0156	0.0232	0.0228	0.0354	0.0361	0.0325	0.0321	0.0318	0.0291	0.0282
HCR	0.0019	0.0018	0.0015	0.0006	0.0007	0.0036	0.0043	0.0028	0.0027	0.0028	0.0022	0.0021
CCR	0.0121	0.0098	0.0088	0.0069	0.0057	0.0230	0.0270	0.0166	0.0166	0.0155	0.0138	0.0123
LIV	0.0282	0.0251	0.0224	0.0236	0.0193	0.0451	0.0541	0.0330	0.0421	0.0401	0.0418	0.0423
HTHS	0.0024	0.0041	0.0052	0.0183	0.0194	0.0253	0.0271	0.0218	0.0219	0.0222	0.0188	0.0175
RFI	0.0056	0.0048	0.0055	0.0105	0.0131	0.0077	0.0081	0.0118	0.0139	0.0140	0.0917	0.1011
EFC	0.0072	0.0072	0.0065	0.0084	0.0078	0.0090	0.0090	0.0084	0.0080	0.0078	0.0076	0.0071
HLIV	0.0071	0.0063	0.0060	0.0100	0.0104	0.0113	0.0115	0.0106	0.0102	0.0102	0.0093	0.0090

¹Index abbreviations are: PD\$ = Predicted Difference Dollars, MFPS = Milk-Fat-Protein Dollars, CY\$ = Cheese Yield Dollars, NM\$₁₉₉₄ = 1994 Lifetime Net Merit, NM\$₂₀₀₀ = 2000 Lifetime Net Merit, NM\$₂₀₀₆ = 2006 Lifetime Net Merit, NM\$₂₀₁₀ = 2010 Lifetime Net Merit, NM\$₂₀₁₄ = 2014 Lifetime Net Merit, NM\$₂₀₁₇ = 2017 Lifetime Net Merit, NM\$₂₀₁₈ = 2018 Lifetime Net Merit, NM\$₂₀₂₁ = 2021 Lifetime Net Merit, and NM\$₂₀₂₅ = 2025 Lifetime Net Merit.

²Trait abbreviations are: PL = productive life, SCS = somatic cell score, UC = udder composite, FLC = foot and leg composite, BSC = body size composite, BWC = body weight composite, DPR = daughter pregnancy rate, CAS = calving ability dollars, HCR = heifer conception rate, CCR = cow conception rate, LIV = cow livability, HTHS = health dollars, RFI = residual feed intake, EFC = early first calving, and HLIV = heifer livability.

³BSC was replaced with BWC in April 2017.

Table 7. Value of expected selection response as a proportion of total index response for traits and composites included in USDA selection indices, 1971–2025¹

Trait ²	PD\$ (1971)	MFPS (1976)	CY\$ (1984)	NM\$ ₁₉₉₄	NM\$ ₂₀₀₀	NM\$ ₂₀₀₆	NM\$ ₂₀₁₀	NM\$ ₂₀₁₄	NM\$ ₂₀₁₇	NM\$ ₂₀₁₈	NM\$ ₂₀₂₁	NM\$ ₂₀₂₅
Milk	0.0519	0.0378	0.0298	0.0313	0.0317	0.0205	0.0179	0.0225	0.0202	0.0194	0.0218	0.0214
Fat	0.5472	0.5838	0.6141	0.5230	0.5066	0.4887	0.4691	0.5136	0.5105	0.5223	0.4806	0.4851
Protein	0.2243	0.2170	0.1986	0.1911	0.1944	0.1604	0.1487	0.1686	0.1593	0.1579	0.1565	0.1502
PL	0.0460	0.0552	0.0568	0.1158	0.1233	0.1474	0.1581	0.1312	0.1323	0.1282	0.1320	0.1269
SCS	0.0038	0.0009	0.0006	0.0102	0.0124	0.0164	0.0183	0.0132	0.0129	0.0118	0.0113	0.0103
BSC/BWC ³	0.0518	0.0414	0.0405	0.0505	0.0514	0.0545	0.0614	0.0555	0.0612	0.0589	0.0782	0.0863
UC	0.0027	0.0030	0.0030	0.0034	0.0065	0.0059	0.0059	0.0057	0.0048	0.0047	0.0028	0.0017
FLC	0.0009	0.0005	0.0004	0.0006	0.0002	0.0001	0.0001	0.0000	0.0002	0.0001	0.0007	0.0009
DPR	0.0188	0.0154	0.0141	0.0072	0.0069	0.0019	0.0044	0.0018	0.0012	0.0015	0.0014	0.0023
CAS	0.0121	0.0138	0.0144	0.0183	0.0180	0.0240	0.0247	0.0224	0.0228	0.0233	0.0233	0.0231
HCR	0.0001	0.0002	0.0004	0.0013	0.0014	0.0024	0.0027	0.0022	0.0021	0.0021	0.0022	0.0021
CCR	0.0087	0.0062	0.0054	0.0009	0.0012	0.0081	0.0101	0.0052	0.0052	0.0052	0.0054	0.0047
LIV	0.0204	0.0120	0.0077	0.0171	0.0150	0.0326	0.0389	0.0249	0.0331	0.0320	0.0348	0.0359
HTHS	0.0015	0.0047	0.0058	0.0125	0.0132	0.0171	0.0183	0.0149	0.0151	0.0153	0.0150	0.0141
RFI	0.0012	0.0003	0.0011	0.0075	0.0083	0.0098	0.0110	0.0086	0.0090	0.0083	0.0240	0.0250
EFC	0.0079	0.0076	0.0072	0.0079	0.0077	0.0080	0.0079	0.0079	0.0077	0.0077	0.0082	0.0080
HLIV	0.0005	0.0001	0.0000	0.0015	0.0018	0.0021	0.0023	0.0018	0.0018	0.0017	0.0020	0.0020

¹PD\$ = Predicted Difference Dollars, MFPS = Milk-Fat-Protein Dollars, CY\$ = Cheese Yield Dollars, NM\$₁₉₉₄ = 1994 Lifetime Net Merit, NM\$₂₀₀₀ = 2000 Lifetime Net Merit, NM\$₂₀₀₆ = 2006 Lifetime Net Merit, NM\$₂₀₁₀ = 2010 Lifetime Net Merit, NM\$₂₀₁₄ = 2014 Lifetime Net Merit, NM\$₂₀₁₇ = 2017 Lifetime Net Merit, NM\$₂₀₁₈ = 2018 Lifetime Net Merit, NM\$₂₀₂₁ = 2021 Lifetime Net Merit, and NM\$₂₀₂₅ = 2025 Lifetime Net Merit.

²PL = productive life, SCS = somatic cell score, UC = udder composite, FLC = foot and leg composite, BSC = body size composite, BWC = body weight composite, DPR = daughter pregnancy rate, CAS = calving ability dollars, HCR = heifer conception rate, CCR = cow conception rate, LIV = cow livability, HTHS = health dollars, RFI = residual feed intake, EFC = early first calving, and HLIV = heifer livability.

³BSC was replaced with BWC in April 2017.

traits because the selection pressure applied gets “diluted,” and there is ultimately little improvement in any of them. However, in that derivation all traits were assumed to have the same economic weight, heritability, and phenotypic variance, which is never true. Results were also based on the use of mass selection, rather than within-family selection. Traits were assumed to be uncorrelated, which is untrue (e.g., Oliveira Junior et al., 2021, and many others), and it is challenging to estimate correlations among the growing number of traits included in selection indices. There is no simple, closed-form expression for computing the relative efficiency of arbitrary indices in which the traits have different properties, but Young (1961) did show that the superiority of the index increases as the number of traits increases. Zhang and Amer (2021) also noted that traits with high economic values may be over-weighted if their heritabilities are low, limiting the amount of selection emphasis which can be placed on them. It is difficult to make more general statements because the relative efficiency of an index is influenced by the phenotypic and genetic correlations among the traits in the index, the economic value of each trait, and the signs and magnitudes of the correlations, which affect the index in complex ways.

A more important point, which often is lost when translating index selection from the genetic evaluation center to the field, is that the goal of the index is to increase the population value of an aggregate genotype. This means that the rate of selection response for individual traits is the wrong thing on which to focus. In fact, when Smith formally presented the idea of discriminant functions for plant selection, the genetic value of a line was clearly rooted in the idea of improving the overall value of plants, not individual characteristics of those plants (Smith, 1936, p. 240). Hazel and Lush (1943, p. 393) expressed this to animal breeders as the concept of “relative economic value,” and they convincingly showed that the total score method (index selection) is more efficient than other methods of selection studied. In a later paper, Hazel (1943) emphasized the importance of economic values by listing them first among the parameters needed to construct an index. The challenge is that there is a long time between when a breeding decision is made and when its consequences are seen in the barn, and people tend to focus on what they can easily see, such as a cow’s protein yield, rather than aggregate properties that are not easy to see, such as the profitability of an individual animal. Martin-Collado et al. (2018) noted that farmers are more likely to adopt heuristics for decision making when animal breeding decisions are complex, and that ineffective heuristics are associated with poor selection decisions and a loss of genetic progress. Those findings are consistent with anecdotal reports from the field that

indices are often not being used in a manner consistent with their intended function.

A complicating factor is the practice in the field of imposing additional thresholds (minimum culling levels) when selecting mating sires using an index. This is often done to prevent the loss of progress in a trait that is difficult to improve or to ensure strong performance in a trait that is closely tied to farm income. An example is the value of SCC to organic farmers that are more heavily penalized for using antibiotics to treat mastitis. However, if the index is properly constructed and the economic values are correct for a farm’s market, then there is no need to make ad hoc modifications to the index. It has also been suggested that economic values should be adjusted to reflect the reliabilities of the traits to which they are applied to provide accurate predictions of genetic response (Togashi et al., 2018). Due consideration is also often not paid to genetic trend or base changes when imposing such criteria. For example, a bull born in 2020 with a PTA of -1 for DPR has better fertility than a bull with a PTA of $+1$ born in 2010. Simianer et al. (2023) recently studied several aspects of realized genetic response to index selection and noted that this behavior can produce “realized economic weights,” which differ substantially from the weights used to construct the index. In an example based on a German Holstein index, RZG, introduced in 2021, Simianer et al. (2023) found that the realized weights applied to each trait were substantially different than the weights used to construct the index because of the thresholds applied to individual traits by farmers, and in one case there was even a change in sign.

Number of Traits Included in the Index

The number of traits included in a typical selection index has grown over time, from a few yield traits, to include many additional phenotypes, such as fertility, health, and fitness traits. This allows farmers to make use of more information than in the past and takes advantage of relationships among traits, which rarely have correlations of zero. Many traits may also have direct economic value; for example, milk processors often pay premiums for low SCS in addition to payments for high protein and fat content. Traits also can have indirect value; for example, SCS can predict losses from IMI if clinical mastitis is not recorded directly. Substantial losses can occur when indirect values are ignored; for example, the well-documented negative correlation of fertility with milk yield (Lucy, 2001). Balanced selection improves traits according to their economic values, and selection indices should be periodically revised to include new traits and reflect changing economic conditions, as well as to update genetic parameters between and among

traits. However, as traits are added to an index it becomes increasingly difficult to predict a priori if the new index will have greater or reduced response compared with an index with fewer traits (Sivanadian and Smith, 1997). Selection indices are generally robust to changes in economic values as long as they have the correct sign (e.g., Vandepitte and Hazel, 1977; Legarra et al., 2007; Cole and VanRaden, 2018).

The title of this paper poses a question: “Are there too many traits in our selection indices?” It has been addressed in the literature in only very general terms. For example, Lush (1945, p. 161) felt very strongly about the matter, writing, “The fact that several things must be considered lowers the intensity of selection possible for each of them, but there is no escape from that so long as all those things have something to do with the net desirability of the animal to the breeder or to his customers.” In his generally comprehensive survey of selection index methodology, Van Vleck (1993) avoids the issue entirely, as does Cameron (1997). The simplest explanation for this may be that the number of traits included in a selection index is of no particular scientific interest unless it leads to interesting problems, such as challenges in estimation. It is, however, a question that is important to users of the selection indices, including dairy producers, genetics consultants, and sire analysts.

In the absence of a closed-form expression relating trait properties to index efficiency, indirect measures were used to study this question. Correlated responses to selection for 12 different selection indices were calculated for 24 traits and composites included in US national genetic evaluations. The initial index, PD\$, was introduced in 1971 and had only 2 traits, milk and far yields. The current NM\$ index, released in 2025, includes 17 traits and composites. Correlated responses to selection show that the addition over time of new traits to the index sometimes reduces the rate of gain for other traits, such as milk production, rates of gain usually remain favorable. This implies that adding new traits does not eliminate progress for existing traits. Correlations of index values for Holstein bulls over time were lowest for animals born before 2000, when selection focused primarily on yield, and highest for bulls born after 2000, reflecting more complex selection goals. This suggests that selection using total merit indices was successful at achieving gains for many traits. Reliabilities did change somewhat as new traits were added to the index, but the introduction of genomic selection resulted in higher reliabilities even though lower-heritability traits were added to the index. This tells us that the use of more traits did not affect our ability to correctly evaluate animals. These results suggest that the continuous growth in the number of traits included in selection indices has not reduced realized genetic progress or accuracy of selection.

CONCLUSIONS

Properly constructed selection indices produce desirable rates and directions of gain for many traits at once. The imposition of minimum culling levels on existing indices will produce suboptimal rates of gain. Changes in response to index revisions are generally modest except in cases where traits of substantial importance that were not previously included in the selection objective are added.

NOTES

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Nonstandard abbreviations used: BSC = body size composite; BWC = BW composite; CA\$ = calving ability; CCR = cow conception rate; CT\$ = calving trait dollars; CY\$ = cheese yield dollars; DPR = daughter pregnancy rate; DSAB = displaced abomasum; EFC = early first calving; FLC = foot and leg composite; FSAV = feed saved; GL = gestation length; HCR = heifer conception rate; HLIV = heifer livability; HTH\$ = health dollars; KETO = ketosis; LIV = cow livability; MAST = mastitis; METR = metritis; MFEV = milk fever; MFP\$ = milk-fat-protein dollars; NM\$ = Lifetime Net Merit; NM\$₁₉₉₄ = 1994 NM\$; NM\$₂₀₀₀ = 2000 NM\$; NM\$₂₀₀₆ =

2006 NM\$, $NM\$_{2014} = 2014$ NM\$, $NM\$_{2017} = 2017$ NM\$, $NM\$_{2018} = 2018$ NM\$, $NM\$_{2021} = 2021$ NM\$, $NM\$_{2025} = 2025$ NM\$, PD\$ = predicted difference dollars; PL = productive life; PTA = predicted transmitting abilities; REL = reliabilities; REPL = retained placenta; REPL = retained placenta; RFI = residual feed intake; TTA = true transmitting abilities; UDC = udder composite.

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