Genetic Evaluation of Holstein Bulls for Somatic Cells in Milk of Daughters[1]

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ABSTRACT

Lactational means of somatic cell score from sample days of primiparous DHI cows were analyzed to compare dairy records processing centers for data properties, to examine effects of age at calving and month of calving on somatic cell score, and to calculate preliminary PTA of sires for somatic cell scores. Five processing centers contributed data but differed substantially with respect to availability of records in progress, DIM on last sample day, and length of time that data were submitted. Highest lactational means of somatic cell score tended to be in short lactations for young cows but in long lactations for older cows. Regions of the country differed substantially for effect of month of calving on lactational means of somatic cell score, but lactational means of somatic cell scores increased with age at calving for all dairy records processing centers. Standardized yields of milk, fat, and protein were included as multiple traits with somatic cell score for analysis. Heritability of somatic cell score was .08 to .16 for individual processing centers and .10 across processing centers. Phenotypic correlations of somatic cell score with yield traits were negative, but genetic correlations were positive. Selection for decreased somatic cell score on a national basis should be possible and would seem advisable to decrease mastitis infections. Response may be slow, however, because of antagonistic genetic relationships with the yield traits, which have great economic importance.

(**Key words**: somatic cells, mastitis, genetic evaluation)

Abbreviation key: DIMLS = DIM at last sample day, DRPC = Dairy Records Processing Center; LSCS = lactational average SCS; $LSCS_A$ = LSCS preadjusted for DIMLS, month of calving, and age at calving; RIP = records in progress; SCS = somatic cell score.

INTRODUCTION

Mastitis is the most costly disease for commercial dairy production, causing yearly losses exceeding $2 billion, mostly because of decreased milk yield from infected cows (14). Much of the variation for mastitis is associated with environment, but genetic variation also exists (26). Heritabilities for measures of clinical mastitis are low (7, 26). Inexpensive and easy means of routinely recording infections are needed.

As an indicator trait for mastitis, SCC of milk has several desirable attributes as a trait for selection. Heritability of SCC is higher than direct measures of mastitis (7), SCC reflects subclinical infections, and genetic correlations between SCC and mastitis are moderately high (4, 7). Furthermore, SCC is routinely recorded on a monthly basis for more than 3 million DHI cows in 39,000 US herds (6). Estimates of heritability for SCC have

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TABLE 1. Data from dairy records processing centers (DRPC).

DRPC	Records in progress	Lactation length	Months of calving	
			First	Last
		(d)	(mo–yr)	
Agri-Tech	Yes	≤305	1–87	9–89
Cornell	No	≤305	1–87	11–88
Pennsylvania	Yes	Unlimited	9–87	10–89
Raleigh	Yes	≤305	1–87	10–89
Wisconsin	Yes	Unlimited	2–87	9–89

been from .05 to .29 (2, 3, 7, 10, 15, 16, 20), and SCC is unfavorably correlated with milk yield, especially for first parity (2, 7, 10, 15, 20).

Despite low heritability and unfavorable genetic relationships with yield, Strandberg and Shook (21) determined that selection to lessen the increase of mastitis accompanying selection for yield is economically justified. From simulation, increase of mastitis as a correlated response was reduced by 20%, whereas only 1 to 2% of genetic gain for milk yield was sacrificed.

Concern remains regarding the wisdom of selection for lower SCC. Phenotypically high SCC suggests poor udder health, but it has not been demonstrated that genetically lowered SCC will necessarily result in decreased frequency of mastitis infections. Grootenhuis (9) reported, however, that heifers with low SCC had older half sisters with lower SCC and lower rates of infection than half sisters of heifers with high SCC.

Genetic evaluations of sires for SCC have been calculated from data of individual states or regions of the US, but a national analysis has yet to be attempted. Preliminary results of research with SCC on a national basis is needed before experiments can be designed to determine actual responses to selection and before formal genetic evaluations are produced.

Objectives of this study were 1) to compare properties of SCC data contributed by individual dairy records processing centers (DRPC), 2) to examine differences among DRPC for effects of age at calving and month of calving, and 3) to obtain preliminary PTA of sires for SCC from national DHI data.

MATERIALS AND METHODS

Lactational DHI records of milk, fat, and protein were obtained from the Animal Improvement Programs Laboratory, USDA, for all lactations with SCC data. Yields were standardized (305-d lactation, twice daily milking, mature equivalent), and SCC from sample days had been transformed to the $\log_2$ scale recommended by National Cooperative DHI (1, 18). Somatic cell scores (SCS) range from 0 to 9. Data received from DRPC were simple means of sample day SCS and were considered to be lactational SCS (LSCS). Previous studies (16, 25) compared arithmetic means of SCS from sample days to other measures such as geometric mean, harmonic mean, median, and various weighted means; however, differences among these measures were small, and correlations with LSCS were greater than .95. Tentative plans are to use LSCS for national genetic evaluations.

Five DRPC, representing a broad geographic area of the US, contributed LSCS: Agri-Tech (Tulare, CA), Cornell (Ithaca, NY), Pennsylvania (University Park), Raleigh (NC), and Wisconsin (Madison). Data included calvings from January 1, 1987 to October 31,

TABLE 2. Number of records and herd-years for model estimating effects of month of calving and age at calving.

DRPC[1]	Records	Herd-years
	(n)	
Agri-Tech	91,151	885
Cornell	60,883	4050
Pennsylvania	144,567	6592
Raleigh	154,137	4750
Wisconsin	198,225	9228

[1] Dairy Records Processing Center.

TABLE 3. Description of groups and classes (nested within groups) for age at calving.

Age group	Number of classes	Months per class	Age
	(n)	(n)	(mo)
1	1	4	18–21
	7	1	22–28
2	6	1	29–34
3	3	1	35–37
4	5	1	38–42
5	6	2	43–54
	4	3	55–66
6	1	5	67–71
	4	6	72–95
	1	25	96–120

1989. Pennsylvania began submitting data slightly later with September 1987 calvings. Records in progress (RIP) were included for all DRPC except Cornell, for which 1989 LSCS were not available. Table 1 summarizes the data supplied by DRPC.

Initially, data included 1,115,643 Holstein records. Preliminary edits required sires to have US registration numbers between 1,500,000 and 2,100,000. Lactations were required to have at least 15 DIM and to have protein recorded. Standardized yields were required to be from 2273 to 22,727 kg of milk, 114 to 909 kg of fat, and 91 to 795 kg of protein. The lower bounds for yields eliminated cows with profound anomalies that were unlikely to be due to mastitis only. Furthermore, cows were required to have from 1 to 20 sample d. Other researchers have required at least 4 sample d (2, 3, 10, 15, 16), but this requirement could introduce bias by removing records from cows culled for mastitis (high SCS) in early lactation. Following initial edits, 987,801 records remained.

Additionally, records were discarded (83,460 or 8.4%) from Vermont, Indiana, and West Virginia. These states are geographically remote from their respective DRPC, and fixed effects in models may arise from climatic factors specific to regions of the US. Also, cows were required to have DIM at last sample day (DIMLS) from 15 to 365 d and age at calving from 18 to 120 mo, and cows with RIP were required to have at least 40 DIM. These requirements resemble those used by the Animal Improvement Programs Laboratory for yield traits. Another edit ensured that sample days were reflective of lactations by requiring no more than 60 DIMLS for records with 1 sample d and ≤100 d for 2, ≤140 d for 3, ≤180 d for 4, ≤220 d for 5, and ≤260 d for 6 (DIMLS and sample days, respectively). These edits reduced the data to 721,101 records.

Previous studies have demonstrated that SCC is affected by DIM, month of calving, and age at calving (8, 11). When estimating the effect of only DIMLS, cows culled for mastitis should be excluded so that genetic differences are not attributed to DIMLS. Therefore, only RIP and records exceeding 305 DIMLS were used to determine the influence of DIMLS on LSCS. Records from three DRPC (Agri-Tech, Pennsylvania, and Wisconsin) were used, but resulting adjustment factors for DIMLS were applied to all five DRPC. Cornell data did not include RIP. Raleigh RIP were lost because of accidental rounding of LSCS to one significant digit for RIP, which has since been corrected.

Effects of stage of lactation from sample days on SCC have been reported (19, 25) and were similar across geographic regions of the US. Six classes for DIMLS in this study were <45 d, 45 to 109 d, 110 to 174 d, 175 to 239 d, 240 to 304 d, and 305 to 365 d. Because

TABLE 4. Number of cows, sires, and herd-year-seasons for genetic analyses.

Analyses	Cows	Sires		Herd-year-seasons
		With progeny	Ancestor	
	(n)	(n)	(n)	(n)
Agri-Tech	31,904	339	44	1572
Cornell	28,364	164	34	4212
Pennsylvania	40,043	293	42	7005
Raleigh	64,557	338	41	7007
Wisconsin	67,109	376	44	11,355
All	241,786	778	66	32,094

TABLE 5. Numbers of cows and herd-year-seasons for analysis that included all dairy records processing centers (DRPC).

DRPC	Cows	Herd-year-seasons
	(n)	
Agri-Tech	33,661	1636
Cornell	30,009	4405
Pennsylvania	42,826	7380
Raleigh	66,386	7123
Wisconsin	68,904	11,550

lactation curves for SCS differ with age at calving (19, 25), DIMLS was nested within six age groups at calving. These groups were similar to those of Miller (13) for estimating effect of age at calving on yield. Age groups at calving were 18 to 28 mo, 29 to 34 mo, 35 to 37 mo, 38 to 42 mo, 43 to 66 mo, and 67 to 120 mo. Comparisons of means suggested that DIMLS classes did not differ for DRPC. Five records were required per herd-year, and 266,382 records were analyzed by ordinary least squares with the following model:

$$Y_{ijkl} = \mu + hy_i + a_j + d_k(a_j) + e_{ijkl}$$

where

Y_{ijkl} is the LSCS of record l in DIMLS class k nested within age group at calving j in herd-year i,
μ is the overall mean,
hy_i is the effect of herd-year i (absorbed),
a_j is the effect of age group at calving j,
$d_k(a_j)$ is the effect of DIMLS class k nested within age group at calving j, and
e_{ijkl} is the random residual.

Additive factors were used to adjust LSCS for DIMLS because variance of LSCS was unrelated to mean of DIMLS. Wiggans and Shook (25) likewise adjusted SCS from sample days for stage of lactation with additive factors.

Effects of month of calving and age at calving on LSCS preadjusted for DIMLS were estimated separately for DRPC with ordinary least squares. As previously discussed, RIP were not included from Cornell or Raleigh. Records from Agri-Tech, Pennsylvania, and Wisconsin included RIP as well as complete records (ended with dry period) and terminal records (cow left herd). Five records were again required per herd-year, and Table 2 has records by DRPC and herd-year. The model was

$$Y_{ijklm} = \mu + hy_i + t_j + a_k + c_l(a_k) + e_{ijklm}$$

where

Y_{ijklm} is the LSCS preadjusted for DIMLS of record m in age class at calving l nested within age group at calving k in month of calving j in herd-year i,
μ is the overall mean,
hy_i is the effect of herd-year i (absorbed),
t_j is the effect of month of calving j,
a_k is the effect of age group at calving k,
$c_l(a_k)$ is the effect of age class at calving l nested within age group at calving k, and
e_{ijklm} is the random residual.

TABLE 6. Unadjusted means of lactational somatic cell score for age groups at calving.

Age group	Dairy records processing center[1]					
	AT	CO	PA	RA	WI	All
18–28	2.47	2.89	2.51	2.40	2.55	2.54
29–34	2.63	3.03	2.64	2.54	2.66	2.67
35–37	2.64	3.14	2.66	2.56	2.70	2.69
38–42	2.71	3.29	2.75	2.52	2.70	2.71
43–66	2.91	3.64	3.09	2.77	2.95	2.98
67–120	3.47	4.27	3.73	3.59	3.67	3.70
All	2.69	3.10	2.77	2.56	2.74	2.73

[1] AT = Agri-Tech, CO = Cornell, PA = Pennsylvania, RA = Raleigh, and WI = Wisconsin.

TABLE 7. Standard deviations of lactational somatic cell score for age groups at calving.

Age group	Dairy records processing center[1]					
	AT	CO	PA	RA	WI	All
18–28	1.01	1.25	1.23	1.42	1.35	1.29
29–34	1.08	1.25	1.27	1.41	1.37	1.34
35–37	1.07	1.32	1.31	1.43	1.44	1.36
38–42	1.12	1.42	1.36	1.48	1.45	1.39
43–66	1.27	1.50	1.51	1.54	1.56	1.51
67–120	1.42	1.68	1.61	1.75	1.71	1.67
All	1.14	1.35	1.38	1.48	1.46	1.40

[1] AT = Agri-Tech, CO = Cornell, PA = Pennsylvania, RA = Raleigh, and WI = Wisconsin.

Table 3 has a description of age groups and age classes at calving, which were based on those of Miller (13). Nesting age class within age group is an equivalent model to fitting the individual ages shown in Table 11. The nested model simplified specification of tests of significance of interest. Adjustment factors for month of calving were calculated from least squares solutions and were additive because mean and variance were independent. Schutz et al. (20) also used additive factors to adjust LSCS for month of calving. Least squares solutions for age at calving were smoothed by Tukey's (22) medians of 7 and hanning (consecutive, successive means of 2). Because variance increased with mean of LSCS, multiplicative adjustment factors were used for age at calving and were calculated simply by adding the least squares solutions to the overall mean for LSCS of that DRPC and dividing by the same overall mean. For the remainder of the study, LSCS was adjusted for DIMLS, month of calving, and age at calving (LSCS_A).

Each DRPC was analyzed separately for genetic effects because of the numerous differences of data that have been discussed. Only first lactations were analyzed genetically to avoid bias from culling for mastitis (12). First lactations for cows that were more than 34 mo for age at calving were discarded.

Components of (co)variance and PTA of sires were from the multiple-trait REML program of VanRaden (23). Four dependent variables were LSCS_A and milk, fat, and protein yields. Independent variables were fixed effect of herd-year-season (absorbed) and random effect of sire. Seasons were January to April, May to August, and September to December, and three cows were required per herd-year-season. Sires were required to have at least 25 daughters, and relationships among ancestors (sires and maternal grandsires) were included. Convergence was declared when all genetic variances changed no more than .001 times current value and when genetic correlations changed no more than .001 (23).

TABLE 8. Least squares solutions[1] for effect of DIM at last sample day (DIMLS) nested within age group at calving on lactational somatic cell score.

DIMLS	Age group at calving					
	18–28 mo	29–34 mo	35–37 mo	38–42 mo	43–66 mo	67–120 mo
(d)						
40–44	.12	.07	–.14	–.06	–.12	–.22
45–109	–.01	–.01	–.08	–.07	–.07	–.05
110–174	.03	.00	.03	–.04	.00	–.06
175–239	.01	.02	.03	.00	.03	.06
240–304	–.04	.01	.12	.10	.12	.19
305–365	–.11	–.09	.05	.06	.03	.06

[1] Solutions sum to zero within column.

TABLE 9. Tests of significance for effects of month of calving, age group at calving, and age class at calving nested within age group on lactational somatic cell score.

Effect	df	Dairy records processing center[1] AT	CO	PA	RA	WI
Month of calving	11	**	**	**	**	**
Age group at calving	5	**	**	**	**	**
Age class						
18–28 mo	7	**	**		**	
29–34 mo	5	**	*	†	*	*
35–37 mo	2			**		*
38–42 mo	4	**		**	**	**
43–66 mo	9	**	**	**	**	**
67–120 mo	5	**	**	**	**	**

[1] AT = Agri-Tech, CO = Cornell, PA = Pennsylvania, RA = Raleigh, and WI = Wisconsin.

†$P \leq .10$.

*$P \leq .05$.

**$P \leq .01$.

In addition to separate genetic analyses for DRPC, a "national" analysis was performed that included records from all five DRPC. Sires were required to have 25 daughters from at least one DRPC. Table 4 has number of cows, sires, and herd-year seasons for all genetic analyses, and Table 5 has the contribution of individual DRPC to the analysis that included all DRPC.

RESULTS AND DISCUSSION

Table 6 has unadjusted means of LSCS for age groups at calving by DRPC, and Table 7 has their respective standard deviations. Data were those remaining (671,314 records) after all preliminary edits and removal of RIP from Raleigh. Obviously, LSCS tended to increase with age at calving. Within DRPC, standard deviations also increased with age at calving and with mean LSCS (Table 7). Raleigh had lowest but most variable LSCS, whereas Cornell had highest LSCS. Agri-Tech had least variance of LSCS, which may suggest less mastitis among cows from that DRPC. Yield traits were highest for records from Agri-Tech and lowest from Raleigh (Table 12), but variation of yield traits was similar across DRPC.

TABLE 10. Least squares solutions[1] for effect of month of calving on lactational somatic cell score.

Month of calving	Dairy records processing center[2] AT	CO	PA	RA	WI
January	.04	–.39	–.09	–.04	.07
February	.02	–.20	–.10	–.05	.05
March	.03	.00	–.06	–.04	.03
April	.04	.04	–.08	.05	–.01
May	.06	.06	–.01	.10	–.03
June	.08	.09	.04	.15	–.02
July	.08	.12	.07	.22	.02
August	–.02	.08	.01	.13	–.03
September	–.05	–.01	–.06	–.03	–.09
October	–.09	–.01	.00	–.14	–.05
November	–.10	.07	.07	–.18	.04
December	–.08	.16	.21	–.18	.02

[1] Solutions sum to zero within column.

[2] AT = Agri-Tech, CO = Cornell, PA = Pennsylvania, RA = Raleigh, and WI = Wisconsin.

TABLE 11. Smoothed solutions[1] for effect of age at calving[2] on lactational somatic cell score.

Age at calving	Dairy records processing center[3]				
	AT	CO	PA	RA	WI
(mo)					
18–21	–.18	–.28	–.27	–.36	–.28
22	–.28	–.34	–.31	–.38	–.27
23	–.31	–.35	–.31	–.36	–.26
24	–.30	–.31	–.28	–.34	–.25
25	–.29	–.28	–.27	–.30	–.24
26	–.28	–.27	–.27	–.26	–.24
27	–.27	–.26	–.26	–.24	–.24
28	–.26	–.26	–.26	–.22	–.23
29	–.25	–.26	–.25	–.22	–.22
30	–.24	–.26	–.23	–.21	–.20
31	–.23	–.26	–.22	–.20	–.19
32	–.22	–.26	–.22	–.19	–.19
33	–.20	–.26	–.22	–.19	–.19
34	–.19	–.26	–.22	–.19	–.19
35	–.18	–.26	–.21	–.19	–.19
36	–.17	–.25	–.19	–.18	–.19
37	–.15	–.25	–.18	–.17	–.19
38	–.13	–.19	–.17	–.16	–.19
39	–.12	–.17	–.17	–.14	–.18
40	–.11	–.15	–.15	–.13	–.16
41	–.09	–.13	–.11	–.11	–.14
42	–.07	–.12	–.09	–.10	–.13
43–44	–.05	–.07	–.07	–.09	–.12
45–46	–.03	.01	–.03	–.08	–.10
47–48	.00	.05	.03	–.06	–.05
49–50	.04	.09	.08	.00	.01
51–52	.09	.16	.10	.07	.06
53–54	.12	.24	.12	.14	.08
55–57	.17	.30	.16	.19	.12
58–60	.23	.37	.26	.24	.21
61–63	.30	.45	.35	.32	.30
64–66	.39	.50	.40	.40	.38
67–71	.48	.53	.46	.48	.48
72–77	.54	.58	.58	.57	.59
78–83	.59	.66	.68	.66	.68
84–89	.64	.72	.73	.77	.77
90–95	.74	.85	.84	.88	.88
96–120	.97	1.20	1.03	.95	1.06

[1] Solutions summed to zero within column before smoothing.

[2] Combines effects of age group and age class nested within age group at calving.

[3] AT = Agri-Tech, CO = Cornell, PA = Pennsylvania, RA = Raleigh, and WI = Wisconsin.

Preadjustment for Fixed Effects

Age group at calving and DIMLS nested within age group were significant ($P < .01$) for explaining variation of LSCS. Least squares estimates for the effect of DIMLS nested within age groups at calving on LSCS are in Table 8. Lactation curves for LSCS apparently differed with age at calving, and results are similar to those of previous reports (8, 11, 19, 25). Young cows tended to have highest LSCS in short lactations, whereas older cows had highest LSCS in long lactations. For cows with last sample day between 110 d (age class 3) and 239 d (age class 4), LSCS differed very little.

Table 9 has tests of significance for effects of month of calving, age group at calving, and age class at calving nested within age group on LSCS for each DRPC. Once again, effect of age group at calving was significant ($P < .01$)

TABLE 12. Means of data included in genetic analyses.

Dairy records processing center	Dependent variable[1]			
	Milk	Fat	Protein	$LSCS_A$
	(kg)			
Agri-Tech	9897	353	304	2.77
Cornell	8932	323	281	3.20
Pennsylvania	9037	331	279	2.82
Raleigh	8479	293	260	2.69
Wisconsin	8832	327	274	2.81
All	8932	322	276	2.82

[1] Milk, fat, and protein are 305-d lactation, twice daily milking, mature equivalent, and $LSCS_A$ is lactational somatic cell score preadjusted for DIM on last sample day, month of calving, and age at calving.

in all cases. Month of calving also affected LSCS ($P < .01$) for each DRPC. Specific age classes at calving nested within age groups were usually significant ($P < .05$); those not significant were for the younger age groups (less than 37 mo) with one exception.

Least squares solutions for effect of month of calving are in Table 10. Estimates for Cornell and Pennsylvania were similar; LSCS was lowest for cows calving in January and February, rising until midsummer, decreasing for September and October calvings, and then increasing to highest LSCS in December. For Raleigh, LSCS was lowest for cows calving in early winter and highest for cows calving in early summer. Apparently, SCS was highest during the hot and humid months of July and August. Cows calving during winter had highest LSCS for Wisconsin, but LSCS were highest for Agri-Tech when cows calved in spring and early summer. Climatic factors may explain most monthly fluctuations.

Smoothed estimates for age at calving (combined effects of age group and age class nested within age group at calving) are in Table 11, and LSCS increased with age at calving for all DRPC in agreement with previous research (8, 11, 19). The only exception to this was for heifers calving at very young ages (18 to 21 mo), and they often had higher LSCS than heifers calving at 22, 23, or 24 mo.

Genetic Analysis

Means of standardized yields and $LSCS_A$ for records used for genetic analyses are in Table 12. Means for $LSCS_A$ are higher than for LSCS in Table 6 for first lactations (age groups 1 and 2) because of preadjustment for age at calving. Yield traits were again highest for Agri-Tech and lowest for Raleigh.

Table 13 has estimates of error and sire variances, heritability, and approximate standard errors of heritability for $LSCS_A$. Error and sire variances and heritability were lower for Agri-Tech than for other DRPC. Perhaps mastitis was more rigorously controlled for herds with records processed at Agri-Tech than for others. Wade and Van Vleck (24) also found a smaller heritability for fat percentage

TABLE 13. Estimates of error variance, sire variance, heritability, and approximate standard errors of heritability for preadjusted lactational somatic cell score.

Dairy records processing center	Error variance	Sire variance	h^2	Approximate SE
Agri-Tech	.965	.0195	.08	.013
Cornell	1.434	.0355	.10	.022
Pennsylvania	1.485	.0599	.16	.022
Raleigh	1.753	.0472	.10	.015
Wisconsin	1.808	.0537	.12	.015
All	1.573	.0390	.10	.009

TABLE 14. Estimates[1] of heritability for yield traits.

Dairy records processing center	Milk	Fat	Protein
Agri-Tech	.20	.21	.20
Cornell	.32	.24	.28
Pennsylvania	.29	.25	.23
Raleigh	.28	.24	.25
Wisconsin	.26	.23	.23
All	.27	.23	.24

[1] Approximate standard errors were .02 for Agri-Tech, .04 or .05 for Cornell, .03 for Pennsylvania, .03 for Raleigh, .02 for Wisconsin, and .02 for the analysis across processing centers.

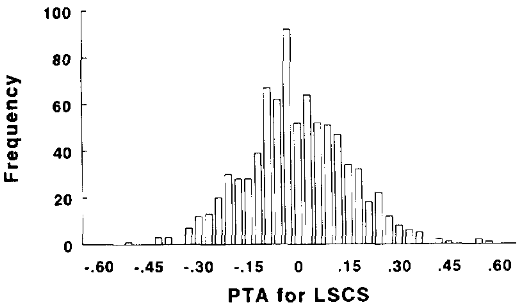

Figure 1. Distribution of PTA for preadjusted lactational somatic cell score (LSCS) of 844 sires from the analysis across dairy records processing centers.

of cows in California than in New York or Wisconsin, but heritabilities for milk and fat yields were similar for all three states.

Heritabilities of $LSCS_A$ ranged from .08 (Agri-Tech) to .16 (Pennsylvania) and averaged .11. Differences may reflect more than chance alone; approximate standard errors averaged .017. As expected, the estimate of .10 for the analysis with records from all DRPC was intermediate to those from individual DRPC. All estimates of heritability were within the range of previous estimates for cows in first lactation (2, 3, 7, 10, 15, 16, 20).

Moderately low heritability for $LSCS_A$ suggests that selection for decreased LSCS should be possible, but genetic response may be slow. Heritabilities for yield traits from the multiple-trait analyses are in Table 14. Estimates were from .20 to .32 for milk, .21 to .25 for fat, and .20 to .28 for protein, in agreement with estimates from the literature (2, 15, 20).

Phenotypic and Genetic Correlations

Correlations between $LSCS_A$ and yield traits are in Table 15. Phenotypic correlations were consistently negative for all analyses (except 0 for protein at Pennsylvania). Estimates are only for first lactations and agree with previous estimates (2, 7, 10, 15, 20). Cows with mastitis, and therefore high LSCS, were likely to have depressed yields.

All genetic correlations (Table 15) between $LSCS_A$ and yield traits were positive. Genetic correlations of $LSCS_A$ and fat (.01 to .17) were lower than respective genetic correlations of $LSCS_A$ with milk (.05 to .26) and protein (.10 to .26). Genetic correlations were in general agreement with the few estimates that are in the literature (4, 7). Schutz et al. (20) hypothesized that higher genetic correlations of SCC with protein than fat may be an artifact of methods used for estimating protein content of milk. Lactose is reduced in mastitic milk (high SCC) to maintain osmotic balance within the udder for milk secretion. Protein content of milk may be overestimated if lactose content is not taken into consideration (20).

The positive genetic correlations between $LSCS_A$ and yield traits definitely present a

TABLE 15. Phenotypic and genetic correlations of preadjusted lactational somatic cell score with yield traits.

Dairy records processing center	Phenotypic correlations			Genetic correlations		
	Milk	Fat	Protein	Milk	Fat	Protein
Agri-Tech	–.12	–.09	–.10	.20	.17	.20
Cornell	–.13	–.13	–.11	.20	.08	.17
Pennsylvania	–.03	–.04	.00	.26	.02	.26
Raleigh	–.11	–.11	–.09	.17	.05	.17
Wisconsin	–.14	–.11	–.10	.05	.01	.10
All	–.11	–.10	–.08	.16	.11	.18

TABLE 16. Mean, standard deviations, maximum and minimum PTA, and effective numbers of daughters for preadjusted lactational somatic cell score.

Dairy records processing center	PTA For sires				Mean effective daughters	Median effective daughters
	Mean	SD	Maximum	Minimum		
					(n)	
Agri-Tech	.04	.14	.33	−.69	81.7	47.6
Cornell	.00	.13	.38	−.30	130.1	52.1
Pennsylvania	−.02	.19	.73	−.52	101.6	40.4
Raleigh	−.03	.16	.42	−.52	151.6	62.8
Wisconsin	−.01	.18	.69	−.51	135.6	59.7
All	−.01	.15	.56	−.50	244.6	68.5

drawback to selection against SCS. Genetic correlations of SCS and yield from previous studies (2, 15, 20) tended to be positive for first lactations but declined for later lactations. Culling bias could be from culling of low yielding cows with genetically low LSCS or culling of cows with high LSCS and high genetic potential for yield.

PTA for Sires

Mean, standard deviations, and maximum and minimum for PTA of $LSCS_A$ for sires are in Table 16. Largest range of PTA for a single DRPC was 1.25 (−.52 to .73) for Pennsylvania, which also had the highest estimate of heritability for $LSCS_A$. For the analysis with cows from all DRPC, the range of PTA was 1.06 (−.50 to .56). The 100 sires with highest PTA for $LSCS_A$ were all above .17, and the 100 sires with lowest PTA for $LSCS_A$ were all below −.18. Figure 1 shows that the distribution of PTA for $LSCS_A$ from the analysis with cows from all DRPC was approximately normal. Because $LSCS_A$ was on a $\log_2$ scale, each unit of $LSCS_A$ represented a doubling of SCC.

To interpret these results, let D be the positive difference between PTA of two bulls. Then 2^D is the expected ratio of geometric mean of SCC for daughters of the high bull to geometric mean for the low bull in the same environment. For example, if PTA of two bulls are .3 and −.25, then D is .55. The geometric mean SCC for the high bull is 1.46 ($2^{.55}$) times the geometric mean SCC for the low bull in any given environment.

CONCLUSIONS

Heritability of $LSCS_A$ was moderately low (.10) and ranged from .08 to .16 for data from individual DRPC. Genetic correlations of $LSCS_A$ and yield traits were small, yet positive; therefore, some selection intensity for yield traits must be sacrificed to accommodate SCS in selection programs. Genetic correlation with $LSCS_A$ was higher for protein than fat yield, and protein yield is currently gaining popularity for selection. Some degree of selection to limit the correlated increase of SCS anticipated to accompany selection for yield may be economically justifiable, but research is needed to quantify correlated responses in clinical mastitis.

Several recommendations can be made regarding future genetic evaluations of SCS for public distribution. Data with uniform properties should be available from DHI cows across the nation, but data for this study varied markedly for DRPC with respect to RIP, DIMLS, and recording period. Surprisingly, differences of data seemed to have modest effect on PTA when predictions from individual DRPC were compared with those from the evaluation across DRPC. Recommended standards for submission of SCS for genetic evaluation should be similar to those for yield (5). A simple mean of sample day SCS (LSCS) up to 305 d seems sufficient, but RIP also should be provided, and weighting factors should be developed for number of contributing sample days. Variance of LSCS decreases as number of sample days increases, and methods similar to those used for yield traits (17) need to be developed to accommodate RIP. Later lactations for cows were not used for these preliminary evaluations, but they could further reduce sampling variation. The PTA for SCS could take various forms, such as categories (high, medium, or low), continuous, or specification of only extreme individuals. Incorporation in selection indices, however, should optimize economic gain, and this would necessitate continuous PTA. If eventually produced and released for public use, genetic evaluations for SCS may be combined with evaluations for yield, udder, and other traits in a selection index to create healthier, higher yielding cows.

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