Records Contributing to National Genetic Evaluations by Year, Registration Status, Herd Size, and Region

T. R. MEINERT and H. D. NORMAN
Animal Improvement Programs Laboratory
Agricultural Research Service, USDA
Beltsville, MD 20705-2350

ABSTRACT

Lactation records from official DHIA were screened for usability in computing USDA-DHIA genetic evaluations. Counts of usable lactation records by state, registration status, and year were examined. Number of cows enrolled in official record-keeping plans of DHIA was the denominator for calculation of percentage of official DHIA records usable in genetic evaluations for state-years. Percentage of official records usable for genetic evaluations had a small increase from 44% during 1968 to 49% during 1978, had a steep increase through 1988 (65%), and then showed little change during the last 2 yr. Number of usable records of registered cows for genetic evaluations increased from 604,570 during 1968 to 864,630 during 1990, which, nevertheless, represented a decline from 64% of all usable records during 1968 to only 42% during 1990. Effects of year, DHIA region, average herd size, and average percentage of registered cows were important for explaining variation in percentage of records usable for genetic evaluations for state-years. States with large average herd sizes and low percentages of dairy cows that were registered had low percentages of records usable for genetic evaluations. Increased official DHIA participation and improved sire identification increases the percentage of records usable for genetic evaluations and helps facilitate genetic improvement.

(**Key words**: genetic evaluations, registered dairy cattle, usable records)

Abbreviation key: **AIPL** = Animal Improvement Programs Laboratory, **NCDHIP** = National Cooperative DHI Program, **NDHIA** = National DHIA.

INTRODUCTION

Genetic improvement of dairy cattle for milk yield has progressed at an increasing rate in the US during the 20th century (5, 8, 10, 15, 16, 18). Accelerated rates of genetic improvement can be attributed to increased knowledge and application of genetic theory, improved statistical models and computers, increased use of AI, and successful AI progeny testing. However, one of the most important keys to the large genetic gains for milk yield, and probably the factor most taken for granted, is the large amount of production data collected and supplied by dairy producers participating in record-keeping plans of the official National Cooperative DHI Program (**NCDHIP**). Without this field data to calculate national genetic evaluations for bulls and cows and to utilize for research studies, genetic improvement of dairy cattle likely would have been much slower.

Participation by US dairy farmers in the NCDHIP plans deemed usable for computation of USDA-DHIA genetic evaluations has been far less than ideal (3, 7, 24). Lack of participation narrows the pool of dairy cows available for progeny testing of young sires. This pool is further reduced because many dairy producers do not sample young bulls because of the perceived risk associated with the use of bulls with unknown genetic merit (24). This perceived risk was quantified by Thornton et al. (20) as a disadvantage of $3.75 per unit of semen for young sires that had first-crop daughters initiating first lactations from 1975 through 1979. However, genetic improvement accelerated during the 1980s, and recent studies (9, 10) have shown little disadvantage

---

Received July 29, 1993.
Accepted December 13, 1993.

for milk yield from use of AI young sires with high pedigrees versus proven AI sires of average genetic merit. Low participation in NCDHIP and in progeny test programs limits genetic improvement.

Voelker's (23) review of the history of NCDHIP record-keeping plans in the US cited the many uses of NCDHIP records. Voelker (23) described the attempts at improving individual animal identification and its importance; identification of animals is essential for computation of genetic evaluations. Missing sire identification is the predominant reason for record removal from the master data files at the Animal Improvement Programs Laboratory (**AIPL**), which thus prevents the animal from contributing to genetic evaluations (26). Misidentification creates biased evaluations (21, 22). However, for many herds enrolled in official NCDHIP plans and participating in progeny test programs, all of the official NCDHIP records are not contributed to genetic evaluations because of missing sire identification. Proper identification of animals in progeny test herds is sometimes monitored closely by AI companies because of the large investments associated with progeny testing of each bull (28).

Kucker (7) implied that progeny test herds that are poorly managed provide little benefit because of inaccurate or missing sire identification. Ehlers et al. (4) related the percentage of sire identification in Washington during 1975 to the size of Holstein herds and the proportion of grade cows and found that percentage of sire identification decreased as herd size and proportion of grade cows increased. In the same study, Ehlers et al. (4) also stratified the 50 US states into five classes of herd size and found that states with larger average herd size had lower percentages of sire identification for the 1973 lactation records of all dairy breeds. These findings are of concern because a large proportion of grade herds contribute to progeny test programs (13), and herd size in the US has been increasing over time (6). Identification of grade daughters from progeny test programs may be accurate because of economic incentives associated with identification. However, this method does not guarantee the accurate identification of grade herdmates, which is important for accurate genetic evaluations of the progeny test daughters.

The first objective of this study was to examine historically the percentage of cows enrolled in all versus official NCDHIP plans by state and year and to compare these trends with national trends. The second objective was to examine the percentage of cows enrolled in official NCDHIP plans with official records that contributed to genetic evaluations by state and year and to relate state-year differences to average herd size, average percentage of registered cattle, year, and National DHIA (**NDHIA**) region.

MATERIALS AND METHODS

All lactation records in the AIPL master files that had been initiated from 1968 to 1990 for Ayrshire, Brown Swiss, Guernsey, Holstein, Jersey, Milking Shorthorn, and Red and White breeds were examined to determine whether they met the criteria for use in USDA-DHIA genetic evaluations. Edits of NCDHIP records are performed by USDA to ensure the accuracy and integrity of genetic evaluations (27). Records were deleted if they were marked unusable for evaluations because they failed to pass AIPL edits or if they were not deemed an official record-keeping plan by NDHIA (2). The DHI AM-PM plan (type of test code 31) had not been considered to be official by NDHIA (2). Nevertheless, USDA uses code 31 lactation records for the calculation of genetic evaluations. Code 31 records had to be excluded in this part of the study because the number of cows enrolled in each record-keeping plan by state was not available. Instead, only the number of cows enrolled in official NCDHIP plans was available by state from yearly participation reports (11, 12).

The number of usable lactations from official NCDHIP plans for all cattle and for registered cattle was recorded by state-year of calving. These numbers allow computation of the percentage of usable lactations attributed to registered cattle by state-year of calving.

The number of herds and cows enrolled in official and in all NCDHIP plans by state and year was obtained from NCDHIP participation reports from 1968 to 1991 (11, 12). From this information, average herd size was computed for each state-year for herds enrolled in official NCDHIP plans. The average number of cows in official NCDHIP plans for each state-year of calving was the mean of the number of cows enrolled in official NCDHIP plans at the beginning of the same year and the beginning of the next year. These averages were used as the denominator for computing the percentage of dairy cows in official NCDHIP plans that were usable for genetic evaluations for each state-year of calving.

The number of dairy cows on farms in the US for each state-year of calving was obtained from the Statistical Reporting Service (1). These counts were used with the number of cows in official and in all NCDHIP plans to compute the percentage of US cows in official and in all NCDHIP plans for each state for years of calving from 1968 to 1991. Tests for significance ($P \leq .10$) of the fixed effects and their interaction on the dependent variable, percentage of cows in official NCDHIP plans for state-years (Model [1]), were from ANOVA (19):

$$y_{ijk} = \mu + t_i + r_j + tr_{ij} + e_{ijk} \qquad [1]$$

where

y_{ijk} = percentage of cows in official NCDHIP plans during year i for state k within NDHIA region j,
μ = overall mean,
t_i = effect of year of calving i,
r_j = effect of NDHIA region j,
tr_{ij} = interaction of year of calving i and NDHIA region j, and
e_{ijk} = unexplained residual.

Fixed effects were calving year, NDHIA region, and their interaction. The same independent variables were examined with Model [2] for significance ($P \leq .10$) on the dependent variable, which was the percentage of cows in all NCDHIP record-keeping plans for state-years:

$$y_{ijk} = \mu + t_i + r_j + tr_{ij} + e_{ijk} \qquad [2]$$

where y_{ijk} = percentage of cows in all NCDHIP plans during year i for state k within NDHIA region j, and μ, t_i, r_j, tr_{ij}, and e_{ijk} were defined as for Model [1]. Regional differences were tested using orthogonal contrasts with both models.

Analysis of covariance (19) was used to test for significance ($P \leq .10$) of the fixed effects and of the covariants on the dependent variable, the percentage of usable records from official NCDHIP plans in USDA-DHIA genetic evaluations for state-years. Fixed effects were year of calving and NDHIA region. Covariants were average herd size and average percentage of usable records from registered cows. Interaction of covariants and region were examined to determine homogeneity of slopes of regressions with Model [3]:

$$y_{ijk} = \mu + t_i + r_j + \beta p_{ijk} + \beta s_{ijk} + r_j\beta p_{ijk} + R_j\beta s_{ijk} + e_{ijk} \qquad [3]$$

where

y_{ijk} = percentage of official NCDHIP records that were usable for USDA-DHIA genetic evaluations during year i for state k within NDHIA region j,
μ = overall mean,
t_i = effect of year of calving i,
r_j = effect of NDHIA region j,
βp_{ijk} = regression of y on percentage of usable records from registered cows,
βs_{ijk} = regression of y on average herd size,
$r_j\beta p_{ijk}$ = interaction of percentage of usable records from registered cows and NDHIA region,
$r_j\beta s_{ijk}$ = interaction of average herd size and NDHIA region, and
e_{ijk} = unexplained residual.

If interactions were significant ($P \leq .10$), covariants were examined within region with Model [4]:

$$y_{ijk} = \mu + t_i + r_j + \beta_j p_{ijk} + \beta_j s_{ijk} + e_{ijk} \qquad [4]$$

where

y_{ijk} = percentage of official NCDHIP records that were usable for USDA-DHIA genetic evaluations during year i for state k within NDHIA region j,

μ = overall mean,
t_i = effect of year of calving i,
r_j = effect of NDHIA region j,
$\beta_j p_{ijk}$ = regression of y on percentage of usable records from registered cows nested within NDHIA region j,
$\beta_j s_{ijk}$ = regression of y on average herd size nested within NDHIA region j, and
e_{ijk} = unexplained residual.

RESULTS AND DISCUSSION

Participation in Record-Keeping Plans

Least squares means of percentage of cows enrolled in NCDHIP plans for state-years (Figure 1) show that participation in both official and all NCDHIP plans nearly doubled from 1968 to 1983. However, percentage of cows enrolled in all and in official plans has remained constant for state-years since 1983. This plateau corresponds to the Dairy Diversion Program of 1983, the Dairy Termination Program of 1985 (Whole Herd Buyout), and the decline in the milk support price from \$13.10/45.4 kg of milk to \$10.10/45.4 kg (14). These government programs and economic conditions during the 1980s have stunted the linear increase in participation observed from 1968 to 1983 in all plans and in official plans. Increased use of on-farm collection of milk weights with computers and the availability of personal computer software for dairy cattle management also may have contributed to the stagnant participation in NCDHIP plans since 1983.

Decrease in percentage of cows enrolled in official plans for state-years after 1983 does not necessarily indicate a lower percentage of cows available for sire evaluations. Records from the code 31 plan have been included since July 1984 for sire evaluations (25). Cow enrollment in the code 31 plan increased from 237,765 to 368,886 from 1982 to 1991 (11, 12). Cow enrollment in the code 31 plan as a percentage of total cow enrollment in record-keeping plans used for genetic evaluations increased from 7 to 10.2 from 1984 to 1991. Growing participation in the code 31 plan accounts for some of the increased difference of percentage of cows in all plans and in official plans after 1984.

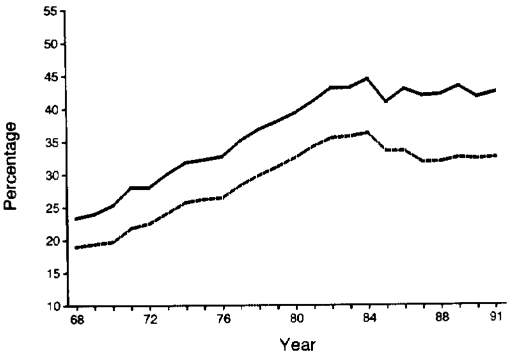

Figure 1. Least squares means of percentage of cows enrolled in official (- - -) and all (——) DHIA plans for state-years.

Tests of Type III sums of squares of the independent fixed effects indicated significance ($P \le .0001$) of year and region for explaining differences in percentage of cows enrolled in official and in all plans for state-years. Interaction of region and year was nonsignificant ($P > .10$), which indicates that year effects were consistent across regions. Interaction of state and year was then removed from the model.

Least squares means of regions for percentage of cows enrolled in official and in all plans for state-years are in Figure 2. Orthogonal contrasts were tested among NDHIA regions: 1) North Central and South versus Northeast and West, 2) North Central versus South, and

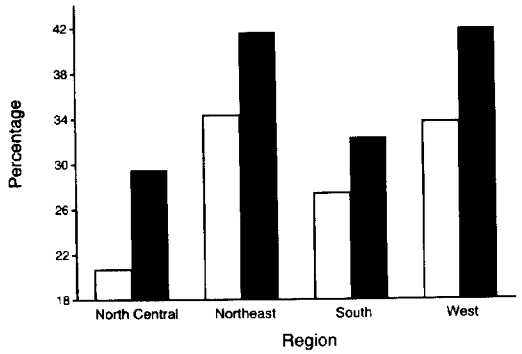

Figure 2. Least squares means of regions for percentage of cows enrolled in official (□) and all (■) DHIA plans for state-years.

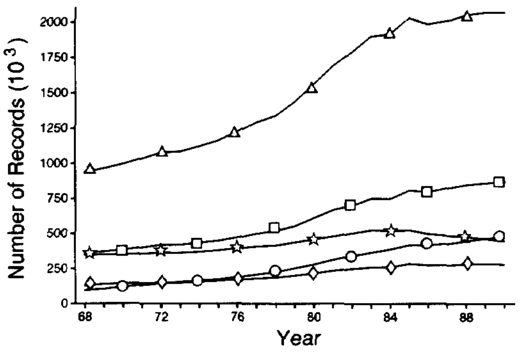

Figure 3. Number of records usable for genetic evaluations from the North Central region (□), the Northeast (★), the South (○), the West (◊), and the US (△) from 1968 to 1990.

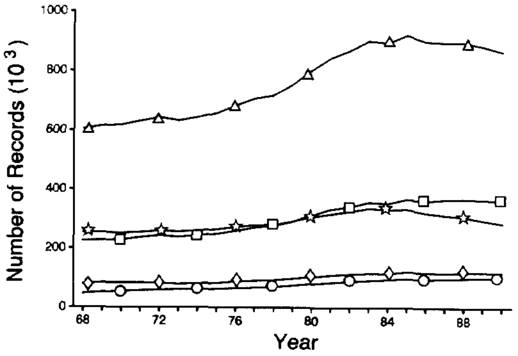

Figure 4. Number of records from registered cows usable for genetic evaluations from the North Central region (□), the Northeast (★), the South (○), the West (◊), and the US (△) from 1968 to 1990.

3) Northeast versus West. Orthogonal contrasts indicated that states in the North Central region and the South had a significantly lower ($P \leq .0001$) percentage of cows enrolled in official and in all NCDHIP plans than did states in the Northeast and the West; states in the Northeast did not differ significantly ($P \leq .0001$) from the West for percentage of cows enrolled in official and in all NCDHIP plans; and the North Central region had a significantly lower ($P \leq .0001$) percentage of cows enrolled in official and in all plans than did the South. However, differences among states and across time within regions were substantial.

Usability of Official NCDHIP Records

The numbers of official NCDHIP records that were usable for genetic evaluations by year and NDHIA region are in Figure 3. Since 1984, USDA has used code 31 records for evaluations, but they are not included in these numbers. The number of usable records in the US increased from 937,500 during 1968 to 2,068,000 during 1990. This increase is responsible for a large part of the success achieved in genetic improvement in the US. The North Central region contributed the largest number of usable records. The number of usable records from the West was considerably less than from the North Central region but followed the same general increasing pattern, with slightly less incline during the 1980s. The number of usable records from the Northeast nearly equaled that from the North Central region for 1968 but did not increase at the same rate as that from the West and the North Central region. The number of official NCDHIP records from the West surpassed that from the Northeast for 1989. The number of usable records from the South mirrored the West until the late 1970s but failed to increase at the rate of the West and the North Central region thereafter.

The numbers of usable records for genetic evaluations contributed by registered cows by year and NDHIA region are in Figure 4. From 1968 to 1990, the North Central region and the Northeast had more registered cows contributing usable records than did the South and the West. The South and the West had similar numbers and trend of numbers for usable records from registered cows from 1968 to 1990. The North Central region and the Northeast had similar numbers of usable records contributed by registered cows from 1968 to 1982; however, since 1982, the number of usable records from registered cows has declined in the Northeast compared with the North Central region. This decline reflects a dairy cattle population in the Northeast that is decreasing at a faster rate than in other regions. From 1983 to 1990, the number of all cows (registered and grade) declined 13.5% in the Northeast compared with the smaller declines of 9 and 11.5% in the South and in the North Central region, respectively, and an increase of 4.1% in the West (1).

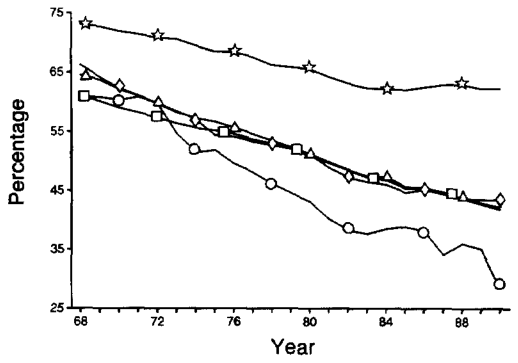

Figure 5. Percentage of all records usable for genetic evaluations for state-years from registered dairy cattle for the North Central region (□), the Northeast (★), the South (○), the West (◊), and the US (△) from 1968 to 1990.

Using the number of usable records from all cows (Figure 3) and registered cows (Figure 4), the percentage of usable records contributed by registered cows was computed and is shown in Figure 5. Even though Figure 4 indicated that the number of usable records from registered cows increased from 1968 to 1990, the percentage contributed by registered cows decreased from 64 to 42, which generally agrees with results of Powell and Norman (17). This decrease occurred because of a large increase in the number of usable records from grade cows. The increasing number of grade cows with usable records suggests that US dairy producers discovered the usefulness of official records for dairy cattle management instead of using records primarily for merchandising. These results also indicate that the efforts of DHIA staff and extension workers to improve accuracy of sire identification, especially in grade herds, have been beneficial. Increases in usable records from grade cows could also be related to requirements associated with participation in progeny test programs.

Percentages of official NCDHIP records usable for genetic evaluations and number of usable records for each state (and Puerto Rico) for 1968, 1979, and 1990 are shown in Table 1; states are grouped by NDHIA region. During 1990, the states with the highest percentage of usable records for genetic evaluations in the Northeast, the South, the West, and North Central region were Connecticut (87.9%), Virginia (74.5%), Washington (60.4%), and Minnesota (77.9%), respectively; percentages of official NCDHIP records usable during 1990 were lowest for Maryland (70.1%), Puerto Rico (10.7%), Arizona (39.8%), and Nebraska (57.9%). Regional differences were quite evident for 1990 because the lowest state in the Northeast (Maryland) had a higher percentage of official records usable than did the highest state in the West (Washington). Regional differences were evident for all years. Percentages of usable records for genetic evaluations within region for 1990 differed, which was indicated by the range between the lowest and highest states within a region. The South had the largest range (63.8%). The range between the highest and lowest states in the South would decrease to 34.3% if Puerto Rico were not included. Nevertheless, the South would still have the largest range for percentage of usable records for genetic evaluations.

Interactions of covariants and the classification variable (NDHIA region) were significant ($P \le .0001$), which invalidated the assumption of homogeneity of slopes for regressions. Therefore, covariants were nested within region.

Percentages of official records that were usable for genetic evaluations, both overall and by region, from 1968 to 1990 are shown in Figure 6. Differences for region and year were evident from these percentages. Tests of Type III sums of squares for the independent variables (year, region, percentage of usable records from registered cows within region, and average herd size within region) were significant ($P \le .001$) for explaining differences among states in their percentages of official records that were usable for genetic evaluations. Estimates of year and region effects are shown in Figures 7 and 8, respectively. Estimates of regression coefficients (percentage registered and average herd size) nested within region along with probabilities of differing from 0 are in Table 2. Figure 7 can be interpreted as the overall increase in usable records from 1968 to 1991 calculated with all states weighted equally and adjusted for regional effects and covariant effects within region. Figure 8 can be interpreted as the overall regional effect calculated with all states weighted equally and adjusted for year and covariant effects within region. Estimates of regression coefficients in Table 2 can be

TABLE 1. Percentage of records usable for genetic evaluations and number of usable records for each state within the four regions for 1968, 1979, and 1990.

Region	Usable from 1968		Usable from 1979		Usable from 1990	
	(no.)	(%)	(no.)	(%)	(no.)	(%)
Northeast						
CT	14,500	62.8	15,100	65.5	11,700	87.9
DE	2800	61.9	2200	50.0	3500	73.8
ME	13,000	70.8	16,500	74.4	11,800	83.2
MA	13,800	69.1	13,600	74.7	9500	81.6
MD	21,200	51.3	31,000	60.1	34,900	70.1
NH	8700	74.4	9300	74.8	8100	83.0
NJ	14,100	60.8	9700	62.2	8900	74.7
NY	126,500	67.6	152,600	73.4	153,200	81.7
PA	103,400	61.6	131,300	72.1	156,600	80.0
RI	1400	65.5	900	67.1	400	74.3
VT	23,000	59.5	36,800	71.2	39,300	75.8
WV	5100	57.1	7900	58.8	7400	72.2
North Central						
IL	31,900	55.2	35,800	56.1	45,600	68.3
IN	20,900	50.3	29,700	55.4	32,600	75.6
IA	32,100	52.2	38,800	50.4	54,600	74.4
KS	23,300	59.9	25,700	55.5	28,600	70.8
MI	37,200	47.2	52,900	49.6	89,000	71.3
MN	64,500	53.1	114,400	60.2	192,900	77.9
MO	13,500	48.5	22,600	46.6	30,900	58.0
NE	7300	38.1	12,700	43.7	18,700	57.9
ND	2900	48.1	3400	39.6	4900	58.6
OH	47,800	53.2	55,600	57.1	76,300	74.4
SD	3700	59.6	5900	46.3	11,400	70.8
WI	80,600	60.7	154,700	55.6	283,900	76.4
South						
AL	5700	17.8	7900	29.9	10,000	52.4
AR	2300	48.3	4000	46.4	6600	50.4
FL	5100	24.6	5000	38.5	11,400	40.2
GA	9000	28.8	11,600	31.9	20,700	47.6
KY	9300	39.2	12,400	39.8	19,600	59.9
LA	3700	39.1	10,200	31.4	12,500	50.8
MS	5800	25.9	7200	29.4	10,700	54.9
NC	20,200	40.4	29,100	44.8	36,700	59.8
OK	6600	36.2	8600	33.6	10,300	60.5
PR	0	. . .	2200	7.4	4300	10.7
SC	9700	34.9	12,900	42.7	15,700	66.7
TN	10,900	35.3	18,600	34.9	27,800	54.8
TX	9200	28.0	19,400	30.8	37,600	40.4
VA	30,400	48.0	46,900	58.8	55,100	74.5
West						
AK	100	32.2	100	78.9	0	. . .
AZ	3500	19.9	10,000	22.4	19,300	39.8
CA	35,900	9.8	145,300	35.5	302,500	47.8
CO	4400	23.1	10,000	38.2	13,000	52.9
HI	0	. . .	1600	28.7	0	. . .
ID	8300	34.5	11,900	28.2	20,100	48.4
MT	1600	34.0	1700	25.5	4300	53.8
NV	800	14.9	1500	17.8	3900	48.0
NM	5000	72.5	7500	31.9	7900	47.3
OR	10,100	39.8	17,500	42.0	29,200	55.0
UT	8400	38.5	12,300	35.8	18,800	53.9
WA	18,000	45.0	31,000	35.2	55,400	60.4
WY	200	12.9	800	24.6	0	. . .
US Total	937,500	43.9	1,437,900	49.9	2,068,300	63.8

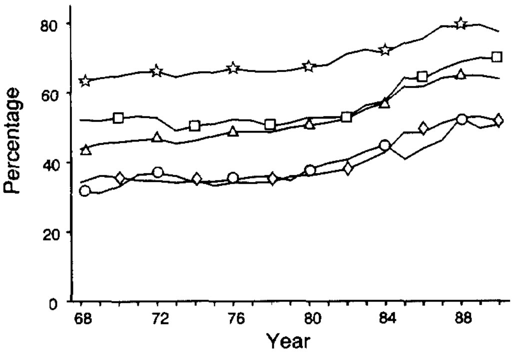

Figure 6. Percentage of records usable for genetic evaluations for state-years from the North Central region (□), the Northeast (★), the South (○), the West (◊), and the US (△) from 1968 to 1990.

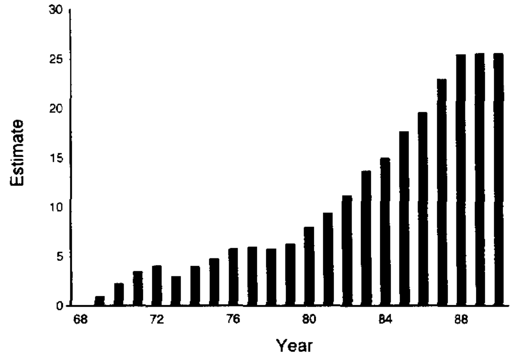

Figure 7. Estimates of effect of year on percentage of records usable for genetic evaluations for state-years.

interpreted as the overall covariant effect for that particular region calculated with all states weighted equally and adjusted for region, year, and other regional covariant effects.

Estimates of year effects suggested only a small, increasing trend in usability of official records from 1968 to 1978, but a steeper linear increase from 1979 to 1988. From 1988 to 1990, usability of official records for genetic evaluations changed little. The greater increase in usability from 1979 to 1988 may correspond to implementation of, and greater participation in, heifer identification programs (e.g., the Verified Identification Program) enacted by NDHIA or dairy records processing centers during or just prior to this period (6). Heifer identification programs encourage sire and dam identification of offspring at an early age, when this information is most current. The increase of identification could also be associated with termination of dairying by producers with poorer record-keeping and, thus, a lower percentage of official records usable for genetic evaluations.

Estimates of region effects indicated differences of regions in their usability of official records for genetic evaluations. Orthogonal contrasts were constructed that examined the following regional effects: 1) North Central and Northeast versus South and West, 2) North Central versus Northeast, and 3) South versus West. All three of these contrasts were significant ($P \leq .05$). The percentage of official records that were usable for genetic evaluations was 1) higher for states in the North Central region and the Northeast than in the South and the West, 2) higher for states in the South than in the West, and 3) higher for states in the Northeast than in the North Central region. Regional differences in usability of official records for genetic evaluations could be caused by several factors. The West and the South have larger herd sizes (Figure 9) and higher percentages of grade cows than the North Central region and the Northeast. Large herd size and a high proportion of grade cows have been associated with less complete sire

TABLE 2. Estimates of and probabilities associated with regression coefficients of the covariants, percentage registered and average herd size, nested within region.

	Percentage registered within region		Herd size within region	
Region	Estimate	*P*	Estimate	*P*
North Central	.072	.1469	–.364	.0001
Northeast	–.054	.4526	–.323	.0001
South	.111	.0099	–.067	.0001
West	.250	.0001	–.002	.7248

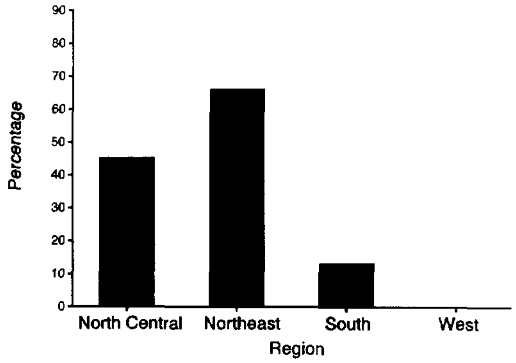

Figure 8. Estimates of effect of region on percentage of records usable for genetic evaluations for state-years.

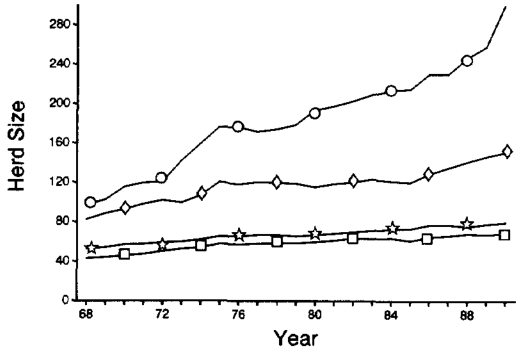

Figure 9. Average herd sizes for state-years in the North Central region (□), the Northeast (★), the South (○), and the West (◊), from 1968 to 1990.

identification for cows (4). Also, many commercial dairies in the South and the West purchase bred heifers from dairies located in the North Central region and the Northeast. These heifers may have proper identification on their original farms; however, sire and dam identification may not be provided or may not be recorded on the new farm, thus causing their official records to be unusable for genetic evaluations.

Both covariants (percentage of usable records from registered cows within region and average herd size within region) were significant ($P \leq .0001$). This significance indicates that the influence of these covariants on usability of official records for genetic evaluations differed for at least one region. Results of *t* tests to examine the hypothesis that slope of regression equaled 0 indicate that percentage of usable records from registered cows within the North Central region and the Northeast was unimportant for explaining usability of official records within these regions. However, estimates of regression coefficients for the percentage of usable records from registered cows within the South and West were significantly ($P \leq .05$) different from 0; both estimates were positive. Orthogonal contrasts were constructed that examined the following specific regression estimates from the percentage of usable official NCDHIP records from registered cows within region: 1) North Central and Northeast versus South and West, 2) South versus West, and 3) North Central versus Northeast. Only the first two contrasts were significant ($P \leq .05$).

Examination of the estimates and contrasts indicated that within the South and the West, states with a higher percentage of usable records from registered cows, had higher percentage of official records usable for genetic evaluations. Higher percentages of usable records from states with higher percentages of registered cattle are expected because sires of registered cows are generally identified at birth; therefore, rejection of official records because of missing sire identification is reduced. Missing sire identification is the major reason that official records are not used for genetic evaluations (26).

The estimate of the regression coefficient for average herd size within the West was not significantly ($P > .10$) different from 0, which indicates that average herd size within the West did not explain additional variation in percentage of official records that were usable for genetic evaluations. Estimates of the regression coefficient for average herd size within region were significantly ($P \leq .0001$) different from 0 for the North Central region, the South, and the Northeast. Estimates of these regressions were all negative, which indicated that states with larger herd sizes within region had lower percentages of official records that were usable for genetic evaluations. This result supports the results of Ehlers et al. (4). Larger herd size had a large negative impact on usability of official records within the North Central region and the Northeast, but no influence or only a small influence within the West and the South, possibly because, as dairies in the North Central region and the Northeast increased herd sizes, their management practices (e.g., identification practices) did not change to meet the new identification needs created by larger herd sizes. Average herd size in the West has been consistently larger than in the North Central region and the Northeast; therefore, an increase from 250 to 350 cows would require little change in management practices related to sire identification compared with an increase from 50 to 150 cows.

CONCLUSIONS

The percentage of US cows in all and in official plans increased from 1968 to 1983 and remained constant from 1983 to 1991. Regional differences in percentage of cows enrolled in both official and unofficial plans were evident.

The number of official records usable for genetic evaluations increased from 1968 to 1990. The number of usable registered cow records increased from 1968 to 1990. However, the percentage of usable records from registered cows declined from 64% for 1968 to 42% for 1990. The increased number of usable records from grade cows reflected the attempts to improve the accuracy of sire identification of grade cows as well as the increased use of official records for management purposes within herd rather than the traditional use of official records for the merchandising of registered cattle.

The percentage of official records usable for genetic evaluations had a small upward trend from 1968 (44%) to 1978 (49%), a steep increase to 1988 (65%), and little change from 1988 to 1990. Increased usability of official records can be attributed to improved sire identification over time. State differences in percentage of official records usable for genetic evaluations were large. For 1990, Connecticut had the highest percentage (87.9%) of official records usable for genetic evaluations, and Arizona had the lowest (39.8%) when Puerto Rico was excluded. Differences in percentage of official usable records were regional; states in the North Central region and the Northeast had higher percentages of usable records than did states in the West and the South. States with a higher percentage of registered records had larger percentage of usable records. States with larger average herd sizes had smaller percentages of usable records. These results suggest that sire identification needs to be monitored as herd size increases, particularly in the North Central region and Northeast, and on the typical commercial farm with grade cattle. Improved sire identification can be facilitated through improved record-keeping, such as early identification of heifers through enrollment in heifer management plans. Accurate sire identification results in greater accuracy of genetic evaluations for cows. Accurate genetic evaluations of cows is important for herd management practices such as monitoring within-herd genetic improvement and ranking of cows on their estimated genetic merit. Correct sire identification has economic importance on the farm because it can be used as a management tool to minimize inbreeding. For herds enrolled in AI progeny test programs, sire identification is critical because most economic incentives are related to proper sire identification and participation in official NCDHIP plans. For the dairy industry, improved sire identification will increase the percentage of official NCDHIP records that will be usable for USDA-DHIA genetic evaluations in the future and will help facilitate genetic improvements that will benefit the entire industry.

ACKNOWLEDGMENTS

Data provided through the NCDHIP are appreciated.

REFERENCES

1 Agricultural Statistics. 1968–1991. US Government Printing Office, Washington, DC.

2 Benson, R. H. 1985. The NCDHIP record plans. Natl. Coop. DHI Prog. Handbook, Fact Sheet A-4. Washington, DC.

3 Dickinson, F. N. 1978. Future dairy record systems. Page 780 *in* Large Dairy Herd Management. C. J. Wilcox, H. H. Van Horn, B. Harris, Jr., H. H. Head, S. P. Marshall, W. W. Thatcher, D. W. Webb, and J. M. Wing, ed. Assoc. Headquarters, 309 W. Clark St., Champaign, IL.

4 Ehlers, M. H., B. F. Kelso, and R. W. Anderson. 1975. Sire identification as related to size of Holstein herds and proportion of grade cows. J. Dairy Sci. 58(Suppl. 1):754.(Abstr.)

5 Hintz, R. L., R. W. Everett, and L. D. Van Vleck. 1978. Estimation of genetic trends from cow and sire evaluations. J. Dairy Sci. 61:607.

6 Hooven, N. W., Jr. 1978. Cow identification and recording systems. J. Dairy Sci. 61:1167.

7 Kucker, W. L. 1975. Sampling bulls from planned matings in artificial insemination. J. Dairy Sci. 58: 1083.

8 Lee, K. L., A. E. Freeman, and L. P. Johnson. 1985. Estimation of genetic change in the registered Holstein cattle population. J. Dairy Sci. 68:2629.

9 McDaniel, B. T., and W. E. Bell. 1989. Genetic gain in milk yield from three systems of sire selection. J. Dairy Sci. 72(Suppl. 1):68.(Abstr.)

10 Meinert, T. R., R. E. Pearson, and R. S. Hoyt. 1992. Estimates of genetic trend in an artificial insemination progeny test program and their association with herd characteristics. J. Dairy Sci. 75:2254.

11 National Cooperative Dairy Herd Improvement Program Participation Reports. 1968–1984. Agriculture Research Service, Dairy Herd Improvement Letters. Agric. Res. Serv., USDA, Beltsville, MD.

12 National Cooperative Dairy Herd Improvement Program Participation Reports. 1985–1991. Natl. Coop. DHI Prog. Handbook, Fact Sheet K1. Washington, DC.

13 Norman, H. D., and R. L. Powell. 1983. Use of grade animals in United States Department of Agriculture programs. J. Dairy Sci. 66:1567.

14 Olson, K. E. 1993. Economic, political, and global demands on the United States dairy industry. J. Dairy Sci. 76:3133.

15 Powell, R. L. 1992. Breeding for Profitable Holsteins in the USA. Holstein Sci. Rep. 1. Holstein-Fresian Assoc. Am. Brattleboro, VT.

16 Powell, R. L., and A. E. Freeman. 1974. Genetic trend estimates. J. Dairy Sci. 57:1067.

17 Powell, R. L., and H. D. Norman. 1986. Genetic and environmental differences between registered and grade Holstein cows. J. Dairy Sci. 69:2897.

18 Powell, R. L., H. D. Norman, and F. N. Dickinson. 1977. Trends in breeding value and production. J. Dairy Sci. 60:1316.

19 SAS® User's Guide: Statistics, Version 6, Edition 4, Vol. 1. 1989. SAS Inst., Inc., Cary, NC.

20 Thornton, R. B., G. L. Hargrove, and L. W. Specht. 1982. Differences in semen values between summarized and sampling sires. J. Dairy Sci. 65:1588.

21 Van Vleck, L. D. 1970. Misidentification and sire evaluation. J. Dairy Sci. 53:1697.

22 Van Vleck, L. D. 1970. Misidentification in estimating the paternal sib correlation. J. Dairy Sci. 53:1469.

23 Voelker, P. E. 1981. Dairy Herd Improvement Associations. J. Dairy Sci. 64:1269.

24 White, J. M. 1975. Choosing and sampling dairy sires: future needs for better sampling methods. J. Dairy Sci. 58:1086.

25 Wiggans, G. R., and S. M. Hubbard. 1986. Changes in USDA-DHIA genetic evaluation procedures since January 1984. Natl. Coop. DHI Prog. Handbook, Fact Sheet H-13. Washington, DC.

26 Wiggans, G. R., and D. R. Ostrander. 1985. Counts of 305-day lactation records eliminated from genetic evaluations for 1984. Natl. Coop. DHI Prog. Handbook, Fact Sheet H-10. Washington, DC.

27 Wiggans, G. R., and L. G. Waite. 1985. Editing lactation records for USDA-DHIA genetic evaluations. Natl. Coop. DHI Prog. Handbook, Fact Sheet H-9. Washington, DC.

28 Wilson, R. D. 1984. Realistic goals and field problems inhibiting progress. Page 139 *in* Proc. Natl. Inv. Workshop on Genetic Improvement of Dairy Cattle. Cornell Univ., Ithaca, NY.