Usability for Genetic Evaluations of Records from Herds Participating in Progeny Test Programs of Artificial Insemination Organizations

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ABSTRACT

Thirteen AI organizations provided identification of herds that participated in their progeny test programs in 1989 and 1990; 15% of those herds participated in programs of more than one AI organization, but only 2.6% participated in programs of more than two AI organizations. Of the 19,589 participating herds, 82 and 76% were enrolled in DHI test plans that were considered to be usable for genetic evaluations during 1991 and 1992. For herds that had participated in AI progeny test programs, mean percentages of usable records were 77% in 1991 and 78% in 1992; the mean percentages of usable records for nonparticipating herds were 62% in 1991 and 60% in 1992. Participating herds had larger mean herd sizes, higher means and standard deviations of milk yields, younger cows, and a lower percentage of registered cows than did nonparticipating herds. Analysis of variance was used to explain the variation in the percentage of records that were usable for genetic evaluations. Herds that participated in AI progeny test programs or that had smaller herd sizes, higher mean milk yields, younger cows, or larger percentages of registered cows had higher percentages of records that were usable for genetic evaluations. Improved usability of records for genetic evaluations would increase the efficiency of AI progeny testing, and consideration of herd characteristics associated with higher percentages of usable records should aid AI organizations in evaluating prospective herds for progeny test programs.

(**Key words**: genetic evaluation, usable records, progeny test, Dairy Herd Improvement)

INTRODUCTION

Rapid improvement in the genetic merit of US dairy cattle for milk yield (6) is being attained partly because AI organizations progeny test a large number of bulls per year (e.g., 1753 bulls in 1995). The US AI organizations have increased the number of Holstein bulls that are enrolled with the National Association of Animal Breeders for sampling each year from 857 in 1980, to 1257 in 1985, and to 1526 in 1995 (C. G. Sattler and H. D. Norman, 1997, unpublished data). Growth in sampling programs has provided an opportunity for more intense selection, thus enabling AI organizations to market bulls that have outstanding genetic merit.

Unfortunately, little information has been published on the scope and effectiveness of progeny testing in the US except for the number of bulls sampled (4). Effective progeny test programs depend on herd owners and employees to use semen from young sires promptly, to identify the progeny born, to keep the daughters until they are in first lactation, and to maintain herd enrollment in an acceptable DHI test plan. Records from herds enrolled in test plans traditionally used in genetic evaluations (coded 0 through 31) [(1); P. Dukas, 1994, personal communication) were designated as qualifying for use in calculation of USDA-DHIA genetic evaluations. In addition, AI organizations rely on industry organizations, such as DHI cooperatives and breed associations, to integrate herd data properly into the national database.

Many individual records from herds enrolled in DHI plans that are designated as usable for genetic evaluations are not in fact used in genetic evaluations (5, 8). Missing sire identification is a common reason that records do not pass USDA edits (5, 7); slightly over 25% of records from usable plans do not include sire identification. Of records with sire identification, 4.9% were excluded from July 1993 evaluations because of one or more other errors in the information

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provided (5). Unfortunately, many herds that are enrolled in DHI testing when semen from young sires is used discontinue testing before the daughters start lactation.

Meinert and Norman (3) found that the percentage of records in official test plans that was usable for genetic evaluations increased from 44% during 1968 to 64% during 1990. States differed markedly in their percentage of usable records, which ranged from 40 to 88% in 1990 (3); states with small mean herd size or a high percentage of cows registered in breed association herdbooks were more likely to have a high percentage of usable records for evaluations. Ehlers et al. (2) also had found that the percentage of records with sire identification was inversely associated with herd management characteristics, such as herd size and percentage of grade cows.

Some extremely large herds have ≥50 cows in a 2-mo contemporary group. Large herds with accurate sire identification and uniform management are valuable to AI organizations because those herds often use semen from many young sires, which reduces the cost of progeny testing. Specific knowledge about the accuracy of sire identification of participating and prospective cooperating herds would be valuable. Using herd management characteristics such as herd size or registry status would be useful as an indirect screening criterion to identify potential herds for cooperation in progeny testing. An individual direct herd measure of usability of records would be even more useful in predicting future usability.

An increase in the percentage of usable records from participating herds could 1) support the progeny testing of more bulls; 2) result in more progeny test daughters per bull and, therefore, higher accuracy for first-crop genetic evaluations; or 3) result in a reduction in the units of semen needed to obtain a sufficient number of daughters for the first-crop evaluation. More progeny test bulls or daughters per bull would increase the rate of genetic improvement by identifying more young bulls of superior merit or improving the accuracy of first-crop evaluations; however, some additional expense would be incurred by AI organizations. A reduction in the amount of semen that was needed to obtain a sufficient number of first-crop daughters would reduce the cost of progeny testing for AI organizations while maintaining the rate of genetic gain.

The objectives of this research were 1) to determine the percentage of records that were usable for genetic evaluations for herds that participate in AI progeny testing compared with that for nonparticipating herds and 2) to determine herd management characteristics that might be helpful in predicting the percentage of usable records.

MATERIALS AND METHODS

In the early 1990s, 13 AI organizations that were members of the National Association of Animal Breeders identified the 19,593 herds that participated in their Holstein progeny test programs in 1989 and 1990 to provide research data for studies on the effectiveness of progeny testing. Some cooperating herds were formally organized with a contract and predetermined guidelines; in other cases, AI organizations achieved progeny test results through innovative programs for semen distribution with economic incentives. For a few AI organizations, this distribution program was primarily through AI technicians.

The herd identification numbers that were supplied by the AI organizations were matched with 1991 and 1992 USDA summary data for Holstein herds with ≥10 cow-years. A herd-year is the number of days that the cows of a given herd were enrolled in a DHI record-keeping program, divided by 365. Because many individual herds participated in one or more AI progeny test programs, the number of programs in which each herd participated was determined, and the herd information for AI participation was merged with other herd-year characteristics. Herds that were enrolled in more than one AI progeny test program were only counted once for analyses of status of AI progeny test participation. Herds that participated in a progeny test program but were not enrolled in a test plan that was usable for genetic evaluations were identified to calculate the percentage of progeny test herds on DHI test for each year; however, those herds were not included in the analyses to predict the percentage of usable records for genetic evaluations. Although records from owner-sampler and other test plans also are included in genetic evaluations as of February 1997, those records were not considered to be usable for genetic evaluations in this study.

For each herd and year (1991 and 1992), the percentage of usable records was calculated as the number of records used for USDA-DHIA genetic evaluations times 100 and then divided by herd size from USDA herd summary data. The percentage of usable records is likely to be biased for a number of reasons. Because herd size is the annual mean and does not consider turnover rate of cows, the percentage of usable records is overestimated; high cow turnover because of voluntary or involuntary culling increases the number of usable records when herd size is kept constant. In contrast, the percentage of usable records is underestimated for herd-years with cows that have long calving intervals because only one potentially usable record is available per lactation. The percentage of records that were calculated by this method as being usable could be >100% for herd-years with complete pedigree identification, moderate to high culling rates, and short to moderate calving intervals. Similarly, other herd-years could produce <100% usable records solely because of long calving intervals.

The means of the percentage of records that were usable for genetic evaluations and other characteristics of herd management were examined for each AI organization by calving year as well as by status of AI progeny test participation (participation vs. nonparticipation). Other herd-year characteristics included mean standardized milk yield (m), standard deviation of mean standardized milk yield (s), mean cow age in months (a), and mean percentage of registered cows (r).

The model to predict usability of records from herd-year characteristics for all herds enrolled in test plans that are used in genetic evaluations was

$$y_{ijk} = \alpha + b_1 m_{ijk} + b_2 s_{ijk} + b_3 a_{ijk} + b_4 r_{ijk} + p_i + c_j + e_{ijk}, \qquad [1]$$

where y_{ijk} = percentage of usable records for herd k within status i for AI progeny test participation in calving year j, α = a constant, b = regression coefficients, p = fixed effect that indicates whether herd participated in AI progeny testing, c = fixed effect of calving year 1991 or 1992, and e = unexplained residual.

A model also was fitted that included the interactions between fixed effects and covariates. If the interactions were significant ($P < 0.10$), then a model similar to [1] was fitted, except that the covariates were fitted as nested within fixed effects. If the interactions were not significant, then Model [1] was used. Estimates of the regression coefficients were examined; if the estimates were similar for each covariate, indicating that the interactions were small, then Model [1] was used.

For those herds that participated in AI progeny test programs, the model to predict usability of records from herd-year characteristics was

$$y_{ijk} = \alpha + b_1 m_{ijk} + b_2 s_{ijk} + b_3 a_{ijk} + b_4 r_{ijk} + o_i + c_j + e_{ijk}, \qquad [2]$$

where y_{ijk} = percentage of usable records for herd k within AI organization i in calving year j, o_i = fixed effect of AI organization i, and the other variables are as defined for Model [1].

TABLE 1. Numbers of Holstein herds that participated in AI progeny test programs in 1989 and 1990 by AI organization and numbers and percentages of those herds during 1991 and 1992 that were enrolled in DHI test plans designated as being acceptable for use in genetic evaluations.

		1991		1992	
AI Organization	Herds participating in progeny testing	Progeny test herds in acceptable test plans	Percentage of all herds in acceptable test plans that participated in progeny testing	Progeny test herds in acceptable test plans	Percentage of all herds in acceptable test plans that participated in progeny testing
	(no.)		(%)	(no.)	(%)
A	4264	3596	84	3371	79
B	2035	1698	83	1612	79
C	254	217	85	205	81
D	539	398	74	374	69
E	3220	2867	89	2738	85
F	2425	2060	85	1937	80
G	100	79	79	75	75
H	319	237	74	222	70
I	3046	2360	77	2135	70
J	302	83	27	77	25
K	2864	2417	84	2264	79
L	2030	1746	86	1644	81
M	1797	1470	82	1381	77
All participating herds[1]	19,593	15,972	82	14,940	76
Nonparticipating herds[2]	. . .	17,209	. . .	17,389	. . .

[1] Herds enrolled in more than one AI progeny test program were only counted once.

[2] Herds enrolled in DHI test plans acceptable for use in genetic evaluations but not participating in an AI progeny test program.

TABLE 2. Frequency of herds enrolled in one or more AI progeny test programs in 1989 and 1990.

Progeny test programs	Herds	Frequency
(no.)		(%)
1	16,630	84.9
2	2445	12.5
3	413	2.1
4	88	0.4
5	15	0.1
6	1	<0.1
7	1	<0.1

For herds that participated in AI progeny test programs, a model also was fitted that included the interactions between fixed effects and covariates. If the interactions were significant ($P < 0.10$), then a model similar to [2] was fitted, except that the covariates were fitted as nested within fixed effects. If the interactions were not significant, then Model [2] was used. Estimates of the regression coefficients were examined; if the estimates were similar for each covariate, indicating the interactions were small, then Model [2] was used.

RESULTS AND DISCUSSION

The numbers of Holstein herds that participated in AI progeny test programs in 1989 and 1990 are shown in Table 1 by AI organization along with the numbers of those herds that were enrolled in DHI test plans 0 through 31 (designated acceptable for use in genetic evaluations) during 1991 and 1992. Of all herds participating in AI progeny test programs in 1989 and

TABLE 3. Herd characteristics for 1991 and 1992 calvings by status of participation in AI progeny test programs in 1989 and 1990 and by AI organization.

Calving year and AI organization	Herd size		Percentage of records usable for genetic evaluations		Herd standardized milk yield		Standard deviation of herd standardized milk yield		Cow age		Percentage of cows registered	
	$\overline{X}$	SD	$\overline{X}$	SD	$\overline{X}$	SD	$\overline{X}$	SD	$\overline{X}$	SD	$\overline{X}$	SD
	(cow-years)		(%)		(kg)				(mo)		(%)	
1991												
A	73	76	77	32	8839	1173	1432	292	48	9	23	33
B	167	279	78	30	9194	1202	1539	289	49	8	38	38
C	742	579	51	32	9844	939	1725	273	47	8	23	33
D	202	392	75	31	8750	1058	1548	277	49	9	39	39
E	163	254	84	28	9307	1091	1566	261	48	7	34	37
F	70	47	76	30	9176	1250	1515	312	51	9	50	40
G	1026	551	40	24	9705	815	1823	208	45	10	9	19
H	153	119	61	32	8178	1190	1415	279	52	13	30	35
I	82	75	76	32	9071	1220	1501	341	51	10	37	39
J	73	34	75	33	8543	1192	1452	295	48	9	19	29
K	165	296	74	32	8993	1177	1535	305	48	8	25	34
L	73	65	78	29	9073	1212	1499	315	51	9	50	39
M	130	222	79	31	9151	994	1485	284	48	7	35	37
All participating herds[1]	110	181	77	31	9051	1192	1499	307	49	9	34	38
Nonparticipating herds[2]	86	126	62	40	8743	1328	1459	376	51	13	42	42
1992												
A	75	77	78	29	9113	1209	1481	304	48	9	23	34
B	175	299	78	28	9425	1226	1581	298	48	9	38	38
C	766	585	59	78	10,007	902	1722	244	43	12	23	32
D	212	433	73	29	8935	1068	1591	286	49	9	39	38
E	168	268	83	31	9561	1109	1606	274	47	7	34	37
F	71	48	78	27	9366	1239	1559	329	50	9	48	40
G	1073	543	44	23	9601	723	1693	150	41	11	9	19
H	150	118	59	31	8416	1267	1450	321	52	10	28	34
I	85	78	79	28	9255	1212	1558	340	50	9	36	39
J	81	33	70	29	8535	1141	1453	301	47	6	17	27
K	171	310	75	30	9225	1183	1579	313	48	9	25	34
L	75	64	80	26	9224	1235	1532	318	50	9	50	39
M	134	233	81	39	9423	1036	1533	320	47	8	35	38
All participating herds	114	189	78	30	9277	1207	1544	315	48	9	34	38
Nonparticipating herds	89	134	60	39	8963	1345	1493	381	50	13	42	42

[1] Herds enrolled in more than one AI progeny test program were only counted once.

[2] Herds enrolled in DHI test plans acceptable for use in genetic evaluations but not participating in an AI progeny test program.

1990, 82% were participating in test plans used in genetic evaluations in 1991, and 76% were still enrolled in test plans used in genetic evaluations in 1992. Enrollment of <100% in test plans used in genetic evaluations by herds that participated in AI progeny tests programs could be caused by 1) herd dispersal, 2) discontinuation of participation in DHI, or 3) participation in a plan other than an acceptable DHI test plan. Continued participation in acceptable DHI test plans by a high percentage of progeny test herds is necessary to achieve high reliability for genetic evaluations of young bulls. The AI organizations that had smaller progeny test programs usually also had a lower percentage of their herds that remained on test and were more variable as well.

Over half of the herds that were enrolled in acceptable DHI test plans in 1991 and 1992 did not participate in the progeny testing of AI bulls in 1989 and 1990. Even modest success in enrolling more of these herds in progeny test programs would allow more young bulls to be sampled per year or would result in more progeny test daughters per bull, thereby giving dairy producers access to sires chosen from greater selection pressure or higher accuracy of genetic information for bulls with only first-crop daughters.

Table 2 shows the numbers and percentages of herds that participated in one or more AI progeny test programs during 1989 and 1990. Of those 19,593 herds, 85% participated in a progeny test program of only one AI organization. Surprisingly, only 15% of the herds participated in more than one progeny test program. Although this study did not investigate the use of semen for herds that participated in more than one program, those herds would be expected to have used semen from more young sires than did herds that participated in only one program, thereby increasing the number of young sires sampled per year, the number of daughters per young sire, and the accuracy of evaluations because of more direct ties between young bulls. Only 2.6% (518) of the herds participated in the progeny test programs of more than two AI organizations.

TABLE 4. Coefficients of determination, mean squares, and *F* values from a model[1] that included effect of status of herd participation in an AI progeny test program to predict herd-year percentage of records usable for genetic evaluations.[2]

Model effect or covariate	MS	*F*
Status of participation in AI progeny testing	1,815,886	2285****
Calving year	89,270	112****
Herd size	1,963,738	2471****
Herd standardized milk yield		
$\overline{X}$, kg	3,430,395	4316****
SD, kg	516	1
Cow age, mo	617,675	777****
Cows registered, %	3,389,178	4264****

[1] Model [1].

[2] $R^2 = 0.24$.

****$P < 0.0001$.

TABLE 5. Estimates of fixed effects and covariates from a model[1] that included effect of status of herd participation in an AI progeny test program to predict herd-year percentage of records usable for genetic evaluations.

Model effect or covariate	Estimate	SE
Participation status in AI progeny test program		
Participant[2]	0.000	0.00000
Nonparticipant[3]	–11.107	0.23238
Calving year		
1991	2.435	0.22977
1992	0.000	0.00000
Herd size	–0.037	0.00074
Herd standardized milk yield, kg	0.003	0.00005
Cow age, mo	–0.333	0.01196
Cows registered, %	0.196	0.00301

[1] Model [1] with standard deviation of herd standardized milk yield excluded.

[2] Herds enrolled in more than one AI progeny test program were only counted once.

[3] Herds enrolled in DHI test plans that were acceptable for use in genetic evaluations but not participating in an AI progeny test program.

Means for the percentage of records that were usable for genetic evaluations and other herd management characteristics for calving years 1991 and 1992 are shown in Table 3 by AI organization and by status of AI progeny test participation in 1989 and 1990. For all DHI herd-years from acceptable test plans, the mean percentage of usable records was 69% for both 1991 and 1992. The mean percentage of records that were usable for herds participating in AI progeny test programs was 77% in 1991 and 78% in 1992; the mean percentage of usable records for nonparticipating herds was 62% in 1991 and 60% in 1992. Participating herds had larger mean herd sizes, larger mean standardized milk yields and standard deviations of milk yields, younger cows, and a lower percentage of registered cows than did nonparticipating herds. The lower percentage of registered cows and higher mean yield for participating herds indicated that commercial herds are increasingly important in US progeny test programs. The greater usability of records and larger standardized milk yields indicated that herds that participated in AI progeny test programs generally had better herd management than did nonparticipating herds. Examination of herd management information could benefit AI organizations when they solicit new DHI herds for participation in AI progeny test programs.

Coefficients of determination, mean squares, and *F* values from the analysis of variance used to analyze all herd-years based on status of participation in AI progeny test programs (Model [1]) are shown in Table 4. Interactions (not shown) of covariates and fixed effects were significant ($P < 0.1$) for all variables except mean standardized milk yield with calving year and status of AI progeny test participation, herd size with calving year, and mean age with status of AI progeny test participation. However, because signs of the estimates from Model [1] with covariates nested within fixed effects were identical for each covariate, covariates were examined across fixed effects (i.e., Model [1] without inclusion of interactions between covariates and fixed effects). Both fixed effects (calving year and status of AI progeny test participation) were significant ($P < 0.0001$) as were all covariates except standard deviation of milk yield. Of the significant variables, mean standardized milk yield and percentage of registered cows had the largest *F* values, and calving year had the smallest. The coefficient of determination was 0.24, which indicates that the model was only moderately reliable in predicting the percentage of usable records within a given herd-year.

Parameter estimates of the fixed variables for the model that included herd status for AI progeny test participation (Table 5) indicated that, during 1991, herds had a higher percentage of records that were usable for genetic evaluations than during 1992, and herds participating in AI progeny test programs had a higher percentage of usable records than did nonparticipating herds. Estimates for covariates indicated that herds with smaller herd sizes, higher mean standardized milk yields, younger cows, or larger percentages of registered cows had higher percentages of records that were usable for genetic evaluations.

TABLE 6. Coefficients of determination, mean squares, and *F* values from a model[1] that included effect of AI progeny test program to predict herd-year percentage of records usable for genetic evaluations.[2]

Model effect or covariate	MS	*F*
AI Organization	25,668	38****
Calving year	11,551	17****
Herd size	945,630	1387****
Herd standardized milk yield		
$\bar{X}$, kg	1,686,216	2474****
SD, kg	32,562	48****
Cow age, mo	187,783	275****
Cows registered, %	1,379,211	2023****

[1] Model [2].

[2] $R^2 = 0.20$.

****$P < 0.0001$.

TABLE 7. Estimates of fixed effects and covariates from a model[1] that included effect of AI organization to predict herd-year percentage of records usable for genetic evaluations.

Model effect and covariate	Estimate	SE
AI Organization		
A	11.461	1.2847
B	8.164	1.3263
C	–1.818	1.8391
D	8.806	1.5622
E	12.803	1.2951
F	4.894	1.3151
G	–5.222	2.5127
H	0.000	0.0000
I	9.184	1.3059
J	8.534	2.4210
K	8.536	1.3020
L	7.007	1.3257
M	10.215	1.3395
Calving year		
1991	1.132	0.2750
1992	0.000	0.0000
Herd size	–0.025	0.0007
Herd standardized milk yield		
$\bar{X}$, kg	0.003	0.0001
SD, kg	–0.002	0.0002
Cow age, mo	–0.297	0.0179
Cows registered, %	0.174	0.0004

[1] Model [2].

Table 6 presents the coefficients of determination, mean squares, and *F* values from the analysis of variance used to analyze herds participating in AI progeny test programs (Model [2]). Interactions (not shown) were not significant ($P > 0.1$) for calving year with covariates but were significant ($P < 0.001$) for AI organization with covariates. However, because signs of the estimates from Model [2] with covariates nested within fixed effects were identical for each covariate, covariates were examined across fixed effects (i.e., Model [2] without inclusion of interactions between covariates and fixed effects). All fixed effects and covariates were significant ($P < 0.0001$). Mean standardized milk yield had the largest *F* value, and calving year had the smallest *F* value. The coefficient of determination was 0.20, which indicates that the model did not explain most differences in the percentages of usable records within a herd-year.

Parameter estimates of the fixed variables for the model that included AI organization (Table 7) indicated that herds had a higher percentage of usable records for genetic evaluations during 1991 than 1992 and that AI organizations varied in the percentage of usable records that their cooperating herds contributed. Estimates of covariates indicated higher percentages of usable records for genetic evaluations from herds with smaller herd sizes, higher mean standardized milk yields, smaller standard deviations for milk yield, younger cows, and larger percentages of registered cows.

CONCLUSIONS

Some attempts have been made to examine the effectiveness of progeny test programs by individual AI organizations, but the results have been used for internal planning and, therefore, have not been made public because of concern that information would be revealed to competitors within the AI industry. Provision of this information across AI organizations should aid in evaluation of the national breeding strategy.

Herds participating in progeny test programs of AI organizations produced a higher percentage of records that were usable for USDA-DHIA genetic evaluations than did nonparticipating herds. Whether participation in progeny testing resulted in an increased percentage of usable records or whether that percentage was higher because herds with better herd management information were given opportunities to participate could not be determined. Targeting a herd owner for more education if that herd had characteristics that were associated with lower percentages of usable records could be beneficial in increasing the number of usable records. Further study of the relationships between record usability and herd characteristics, such as number of progeny-test daughters, semen usage, and genetic merit of sires, would provide additional information for identifying herds with characteristics associated with a lower percentage of usable records. A different approach would be needed to compile those characteristics, but the results could improve the understanding of the US genetic program and reveal areas where improvements could be made.

A variable for record standards (or herd profile), the percentage of cows with valid sire and dam identification, became available for all DHI herds in January 1997 (J. H. McGregor, 1996, personal communication). This herd variable has a high relationship with record usability for USDA-DHIA genetic evaluations and should be of considerable value when AI organizations evaluate prospective herds for progeny test programs.

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