Genotype × Environment Interaction for Grazing Versus Confinement. I. Production Traits*

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ABSTRACT

The objective of this study was to investigate the possible existence of a genotype × environment interaction (G×E) for production traits of US Holsteins in grazing versus confinement herds. Grazing herds were defined as those that utilized grazing for at least 6 mo and were enrolled in dairy herd improvement (DHI). Control herds were confinement DHI herds of comparable size in similar regions. The performance of daughters in grazing herds and control herds was examined using linear regression of mature equivalent milk, fat, and protein yield on the November 2000 USDA-DHI predicted transmitting abilities (PTA) of their sires for those traits. Heritabilities and genetic correlations were estimated using restricted maximum likelihood in a bivariate animal model that considered the same trait in different environments as different traits. Product-moment and rank correlations were calculated between sires' estimated breeding values, estimated separately in both environments. For grazing herds, the coefficient of regression of milk, fat and protein on PTA were 0.78, 0.76, and 0.78, respectively. Corresponding coefficients in the control herds were 0.99, 0.96, and 0.98. Estimates of heritability for the traits ranged from 0.2 to 0.25, and differences between grazing and control environments were small. Estimates of the genetic correlations for the traits in both environments were 0.89, 0.88, and 0.91 for milk, fat, and protein, respectively. Within-quartile analyses revealed a lower correlation for milk and protein between the upper and lower grazing quartiles, while the same quartiles for the control herds did not differ from unity. Rank correlation coefficients

between sire estimated breeding values from the 2 environments were 0.59, 0.63, and 0.66 for milk, fat, and protein, respectively. The mean rank change for the top 100 sires between the two environments was 27. The regression coefficients indicate that expected daughter differences may be overstated by current sire PTA in grazing herds. Genetic correlations less than unity suggests that there is, at least, some reranking among sires in both environments, while the rank correlations indicate the possibility of sire reranking when evaluations were performed within management system. However, differences are not so large as to justify separate genetic evaluations for each system.

(Key words: grazing, production, genotype × environment interaction)

Abbreviation key: G×E = genotype × environment interaction, MEM = mature equivalent milk, MEF = mature equivalent fat, MEP = mature equivalent protein.

INTRODUCTION

Grazing as a form of low input dairy production to maximize profit is increasing in popularity in the United States, and is the mainstay of dairy production in several countries such as Ireland and New Zealand. Herds where cows consume mostly grass forage produce, on average, less milk than their confinement counterparts (Parker et al., 1993; Rust et al., 1995; Kolver and Muller, 1998). However, it has also been documented that the lower costs of production associated with grazing are more than enough to offset this decrease, and maintain or improve farm profitability (Parker et al., 1992; Kriegel, 2000). Reasons for lower costs of production may include less overhead, capital, and feeding costs.

A major concern for graziers is the choice of genetics for optimal performance in pasture-based systems. The primary question is whether a genotype by environment interaction (G×E) exists between the 2 distinct

Received October 11, 2001.

Accepted August 22, 2003.

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*Contribution #16652 of Purdue University Agricultural Research Program.

environments, confinement and grazing. In other words, does one expect those sires whose daughters are producing in both environments to rank the same genetically in both environments? Three possibilities exist. First, there may be no interaction present. Second, there may be a scaling effect, that is, the rankings of sires are the same but the advantage of the highest ranking sires is less in the less favorable environment. Third, a reranking of the sires between the 2 environments may exist. The third possibility suggests that different genes may regulate the production of milk in the 2 environments, or the expression of genes for milk production is dependent on the environment.

Investigation of possible G×E has included both across- and within-country analysis. Some across-country analyses may be biased in that G×E may be confounded by strain or genotype differences. Cienfuegos-Rivas et al. (1999) reported significant G×E for milk yield of Holstein cows in Mexico and the United States while, Carabano et al. (1989) found significant reranking for fat production between United States and Spain. Peterson (1988) found evidence for G×E interaction between Holsteins in Canada and New Zealand for milk production. In Ireland, Buckley et al. (2000) found no interaction for milk, fat, and protein production between high merit imported animals and medium genetic merit animals for 3 intensive grazing systems. However, in New Zealand, Kolver et al. (2000) found that while there was no interaction between heifers of New Zealand and overseas origin for production, heifers of overseas origin lost more liveweight on pastures than the New Zealand heifers, raising questions regarding the suitability of such heifers on an all-pasture based system.

Several studies have investigated the existence of G×E by comparing daughters of similar genotype producing under different management levels by testing for a sire × ration interaction. Wiggans and Van Vleck (1978) considered the evaluations of sires based on daughter performance in groups representing increasing proportions of concentrates in the ration on a herd basis and concluded there was no G×E for sires. These results are in agreement with Cromie et al. (1998) and Weigel et al. (1999). Weigel et al. (1999) noted a much lower heritability for fat production in the grazing versus confinement herds, but a genetic correlation of 0.88 between the 2 groups suggested limited evidence of reranking. Boettcher et al. (2003) found a scaling effect across environments for yield traits when studying grazing versus conventional dairies in Canada. They concluded that effects of G×E on yield traits were small, based on estimates of genetic correlation greater than 0.90 for yields across the 2 environments.

Table 1. Number of states, herds, records, cows, and sires for grazing and control.

Variable	Group	
	Grazing	Control
States	12	13
Herds	393	432
Records	82479	142924
Cows	34566	60667
Sires	3815	7091

The objective of this study was to investigate the existence of a G×E for production traits of US Holsteins in confinement and grazing dairies in the Eastern United States.

MATERIALS AND METHODS

Grazing herds were defined as those in which cows consumed the majority of their forage from pasture for at least 6 mo of the year. These herds were identified with the help of DHIA personnel, dairy specialists, and grazing consultants who verified that herds met these requirements. Herds had to be enrolled in a DHI recording program. Data were provided by Dairy Records Management Services, (Raleigh, NC) and AgSource, Inc. (Verona, WI). In addition, DHI herds of similar size from the same states but not known to be utilizing grazing were selected as control herds. In some states, few control herds were available. Therefore more control herds from other states were requested to balance the data set.

The grazing data consisted of 82,479 records of 34,566 cows in 12 eastern US states, while the control data consisted of 142,924 records of 60,667 cows in 13 eastern US states (Table 1). Further description of udder health and reproductive characteristics of the herds and cows are in a companion paper (Kearney et al., 2004). Common edits to the data set were: 1) only records after 1990 were included; 2) cows were required to have a first lactation; 3) cows were required to have pedigree information; 4) parities greater than 5 were deleted; 5) cows with records $\pm$ 4 phenotypic standard deviations of mean mature equivalent milk (**MEM**), fat (**MEF**), and protein (**MEP**) yield were deleted; and 6) cows with <60 DIM for each group were deleted.

The performance of daughters in grazing and confinement was examined using linear regression of MEM, MEF, and MEP on the November 2000 USDA-DHIA PTA of their sires for those traits using the following model:

$$Y_{ijkl} = h_i + y_{sj} + a_k + \beta PTA_{ijkl} + e_{ijkl}$$

where:

- Y_{ijkl} = MEM, MEF, or MEP for the first lactation record of cow l , in herd i , calving in year-season j , in age class k ;
 h_i = fixed effect of herd i ;
 ys_j = fixed effect of the year-season of calving j ;
 a_k = fixed effect of age class k ;
 β = coefficient of regression of daughter MEM, MEF, or MEP yield on sire PTA;
 PTA_{ijkl} = November 2000 USDA-DHIA PTA for milk, fat, and protein of the sire of cow l ; and
 e_{ijkl} = random residual.

Separate regression analyses using PROC GLM (SAS, 2000) were performed for first-lactation records of each yield trait. For milk, fat, and protein analyses, regression coefficients were estimated for all records, for 4 random subsets, and for 4 subsets based on quartiles of herd average MEM. The univariate regression models were fit separately to grazing and control data. Quartile analysis was performed to observe the adequacy of prediction of the sires' PTA at different levels of production. A requirement of regression analysis was that cows have an AI sire with USDA-DHIA PTA for each trait. Seasons 1 to 4 were defined as January to March, April to June, July to September, and October to December. Within each herd, seasons with only a single record were merged with the nearest season with at least one record. Herd and year season effects were considered separately in the model for computational feasibility and to match previous results (Weigel et al., 1999).

Restricted maximum likelihood using the (co)-variance component estimation program, VCE4 (Neumaier and Groeneveld, 1998), was used to estimate heritabilities and genetic correlations between the 2 environments for each trait. The REML algorithm chosen for this study used analytical gradients (Neumaier and Groeneveld, 1998). A bivariate animal model that considered traits in different environments as separate traits was used to estimate the variance components. Due to the large computational demands, heritabilities and genetic correlations were estimated for 4 random subsets of the overall data set. Overall estimates presented in this paper are the mean of estimates for each of the 4 subsets weighted by the number of observations in each subset. Overall standard errors were estimated as the empirical standard errors of the subset estimates of heritabilities and genetic correlations.

Previous studies have indicated a decline in the genetic correlation between environments as the difference in environments becomes more pronounced (Cunningham and O'Byrne, 1997; Cromie et al., 1998). To

determine if there was reranking between the upper- and lower-producing herds a similar analysis was conducted for milk, fat, and protein, between the upper and lower quartiles and between the middle quartiles defined by herd average MEM, within each environment.

To assess the level of reranking among sires within each environment, product-moment and rank correlations between EBV were calculated using PROC CORR (SAS, 2000). Correlations were calculated for sires that had at least five daughters producing in both grazing and confinement herds. Predictions of breeding values were obtained for all sires separately in both the grazing and control groups using PEST (Groeneveld and Kovac, 1990). Correlations were also calculated between the sires' EBV in either grazing or control herds with their November 2000, USDA-DHIA PTA.

The following model was used for the estimation of the genetic parameters and estimation of the breeding values:

$$Y_{ijkl} = hys_i + ap_j + a_k + pe_k + e_{ijkl}$$

where:

- Y_{ijkl} = MEM, MEF, or MEP for the l th record of animal k , calving in herd-year-season i , in age-parity class j ;
 hys_i = fixed effect of herd-year-season of calving i ;
 ap_j = fixed effect of age-parity class j ;
 a_k = random additive genetic effect of animal k ;
 pe_k = random effect of permanent environment for cow k ; and
 e_{ijkl} = random residual.

The USDA Animal Improvement Programs Laboratory provided complete pedigree information going back 3 generations. Unknown parent groups were used when parents were not identified.

RESULTS AND DISCUSSION

Means and standard deviations of MEM, MEF, and MEP for control and grazing herds are in Table 2. As expected, the mean MEM, MEF, and MEP were higher in the control versus the grazing herds and similar to those obtained by Weigel et al. (1999) for herds in Wisconsin. The standard deviations for milk, fat, and protein were 117, 3, and 1 kg higher for the control herds. In Canada, Boettcher et al. (2003) found similar means for control herds, but much greater means under grazing conditions, although typical grazing seasons were presumably much shorter than in this study.

Table 2. Means and standard deviations (in parenthesis) of first lactation mature-equivalent milk (MEM), fat (MEF), and protein (MEP) production for regression analysis for overall and random subsets.

	Overall	RS ¹ 1	RS 2	RS 3	RS 4
Grazing					
Mean MEM, kg	8588 (1917)	8715 (1930)	8430 (1849)	8529 (1813)	8635 (2020)
Mean MEF, kg	294 (74)	298 (77)	287 (70)	291 (70)	297 (77)
Mean MEP, kg	252 (56)	255 (56)	246 (55)	252 (53)	253 (59)
Control					
Mean MEM, kg	9948 (2034)	9947 (2151)	9934 (2110)	9960 (1921)	9947 (1972)
Mean MEF, kg	355 (77)	354 (83)	356 (82)	355 (71)	355 (73)
Mean MEP, kg	291 (58)	311 (65)	310 (66)	311 (58)	309 (29)

¹RS – random subset.

A summary of the production data for the regression analyses is in Table 2 for random subsets and in Table 3 for quartiles based on herd mean for MEM. For the random subsets for the regression analysis, mean first-lactation production and standard deviations were similar to the complete data set. For the quartile analysis the difference between the highest and lowest quartiles was over 3200 kg of MEM for both grazing and control herds.

Coefficients of regression of daughter performance in first lactation on the USDA-DHIA sire PTA for grazing and control herds are in Table 4. The expectation of the coefficients is 1. For the overall grazing data the coefficients for milk, fat, and protein were significantly less than 1. These results differ from those reported by Weigel et al. (1999) who found only fat for the grazing herds to be significantly different from 1. A possible

Table 3. Means and standard deviations (in parenthesis) of mature-equivalent milk (MEM), fat (MEF), and protein (MEP) production for regression analysis for quartiles based on herd mean MEM.

	0–25% ¹	26–50%	51–75%	76–100%
Grazing				
Mean MEM, kg	6435 (1355)	7577 (1477)	8337 (1468)	9656 (1735)
Mean MEF, kg	216 (50)	252 (55)	285 (55)	335 (70)
Mean MEP, kg	187 (40)	222 (44)	244 (43)	284 (50)
Control				
Mean MEM, kg	7925 (1620)	9192 (1657)	9952 (1609)	11254 (1875)
Mean MEF, kg	284 (60)	325 (61)	357 (62)	402 (74)
Mean MEP, kg	231 (52)	271 (52)	292 (51)	329 (54)

¹Quartiles based on herd mean MEM.**Table 4.** Coefficients of regression of first lactation mature equivalent yield on November 2000 USDA-DHIA sire PTA for grazing and control herds for all records, and 4 random subsets. Standard errors are in parentheses.

	Grazing			Control		
	Milk	Fat	Protein	Milk	Fat	Protein
All records	0.78** (0.030)	0.76** (0.020)	0.78** (0.020)	0.99 (0.026)	0.96 (0.024)	0.98 (0.027)
Random subset						
A	0.75** (0.060)	0.82** (0.050)	0.68** (0.060)	1.06* (0.050)	0.98 (0.050)	0.98 (0.050)
B	0.76** (0.050)	0.88* (0.060)	0.85** (0.060)	0.99 (0.050)	0.96 (0.050)	1.03 (0.056)
C	0.79** (0.066)	0.70** (0.062)	0.83* (0.070)	0.94 (0.050)	0.98 (0.040)	0.95 (0.050)
D	0.70** (0.053)	0.70** (0.057)	0.79** (0.058)	1.01 (0.053)	0.91 (0.05)	0.95 (0.053)

*Significantly different from 1 ($P < 0.05$).**Significantly different from 1 ($P < 0.01$).

explanation is that only 5621 records were used in that study, limiting the likelihood of detecting modest differences. Boettcher et al. (2003) reported regression coefficients that were considerably greater for yield traits in both management systems and considerably larger than unity for control herds.

The coefficients of regression for the overall data sets are in agreement with the random subsets, in that the coefficients generally do not differ from expectation for the controls, while those for the grazing herds are significantly different from expected values. For the overall data sets the coefficients of regression indicate that actual sire PTA may overstate the true differences between bulls' daughters in grazing herds. The estimated differences between environments should be conservative for 2 reasons. First, these records may have contributed to the USDA-DHIA genetic evaluations from which the PTA are derived. Thus a part-whole relationship may have existed and the larger number of control herds could partly account for a higher correlation with the USDA-DHIA PTA. Second, control herds were of similar size to grazing herds (133 cows for controls, 95 cows for grazing), therefore differences could be greater for larger herds that are perhaps more intensively managed.

Coefficients of regression and standard errors for the analyses within quartiles are in Table 5. For the quartile analysis it appears that milk, fat, and protein yield are adequately predicted by sire PTA for the middle 2 quartiles for control herds, but are over-predicted for grazing herds, and most severely for the lowest quartile. When depicted graphically, there appears to be little difference in regression coefficients in the middle quartiles for milk, fat, or protein (Figure 1). Differences between daughters may be over-predicted in the

Table 5. Coefficients of regression of mature equivalent yield on November 2000 USDA-DHIA sire PTA for grazing and control herds for quartiles based on herd mean mature equivalent milk. Standard errors are in parentheses.

Quartile	Grazing			Control		
	Milk	Fat	Protein	Milk	Fat	Protein
0-25%	0.58** (0.064)	0.64** (0.056)	0.64** (0.068)	1.05* (0.050)	0.86 (0.047)	0.98 (0.050)
26-50%	0.81** (0.058)	0.85** (0.052)	0.78** (0.059)	0.95 (0.046)	0.97 (0.044)	0.93 (0.047)
51-75%	0.81** (0.050)	0.85** (0.050)	0.77** (0.060)	0.95 (0.046)	0.93 (0.046)	0.97 (0.046)
76-100%	0.91 (0.049)	0.90* (0.046)	0.92 (0.050)	1.11** (0.049)	1.18** (0.045)	1.13** (0.048)

*Significantly different from 1 ($P < 0.05$).

**Significantly different from 1 ($P < 0.01$).

lowest producing control herds for fat and under-predicted in the highest producing control herds for milk, fat, and protein. When regression coefficients of the quartiles are taken together without consideration of the environment, there appears to be a consistent relationship between the regression coefficients and ME milk yield, suggesting at least a moderate scaling effect with increasing milk production. This may partly account for smaller changes in regression coefficients between the inner quartiles, since differences and within-quartile variation might be expected to be less if distribution of records approaches normality. That is, the standard deviation of MEM, MEF, and MEP is very similar for the inner quartiles, but differs considerably for outer ones.

Estimates of heritabilities and genetic correlations for the 4 subsets and the weighted average estimates

Figure 1. Coefficients of regression for milk (□), fat (○), and protein (◇) in grazing, and control herds (■, ●, ◆) for quartiles based on herd average MEM.

Table 6. Estimates of heritability (diagonal) and genetic correlations (above each diagonal) for 4 random subsets, and weighted average estimates of milk, fat and protein. Standard errors are in parentheses.

Subset	Milk		Fat		Protein	
	Control	Grazing	Control	Grazing	Control	Grazing
A	0.23 (0.010)	0.94 (0.029)	0.22 (0.01)	0.94 (0.04)	0.23 (0.011)	0.98 (0.026)
B	0.16 (0.011)	0.81 (0.053)	0.23 (0.012)	0.94 (0.032)	0.17 (0.011)	0.86 (0.042)
C	0.20 (0.010)	0.94 (0.028)	0.22 (0.011)	0.93 (0.029)	0.18 (0.01)	0.94 (0.031)
D	0.21 (0.011)	0.87 (0.043)	0.23 (0.006)	0.70 (0.05)	0.20 (0.01)	0.86 (0.05)
Overall	0.20 (0.015)	0.89 (0.031)	0.23 (0.002)	0.88 (0.059)	0.20 (0.013)	0.91 (0.030)

are in Table 6. Estimates of the ratio of permanent environment to phenotypic variance ranged from 0.20 to 0.22 for traits in the control herds and 0.18 to 0.21 for traits in the grazing herds. The estimates for control herds were about 2% greater than those for grazing herds for each trait. Estimates of phenotypic variance for the 4 random subsets are in Table 7.

Estimates for the same parameters but for the quartile analyses are in Tables 8 and 9. Estimates of phenotypic variance for the milk yield quartiles also are in Table 7. The overall estimates of heritability for milk, fat, and protein were slightly higher for the control herds than for the grazing herds, and also were highest for the upper quartiles for both management systems. This is in agreement with previous studies, which have shown less genetic variation in lower producing herds (Cromie et al., 1998; Cienfuegos-Rivas et al., 1999). The heritabilities for all traits for both grazing and controls were similar for the middle quartiles. Across subsets, there was variation among the estimates for each trait, which can probably be attributed to sampling error. Heritability estimates were more stable across subsets for fat than either milk or protein. Overall estimates of the genetic correlation between traits in different environments were significantly different from unity. The estimates obtained were similar to those of Weigel et al. (1999), but due to larger standard errors in that study (approximately 0.1), the estimates were not found to be significantly different from unity.

Table 7. Estimates of phenotypic variances (kg^2) of milk, fat, and protein yields for quartiles based on milk yield and random subsets of grazing and control herds.

	Milk		Fat		Protein	
	Control	Grazing	Control	Grazing	Control	Grazing
Quartile						
0–25%	4,943,763	3,197,416	6490	3940	4380	2929
26–50%	5,917,040	4,382,503	7590	5169	5166	3949
51–75%	6,970,056	4,753,261	8126	5851	4972	4240
76–100%	12,103,834	6,001,013	9629	7830	5834	5227
Random subset						
A	6,055,960	5,283,302	8143	6527	5231	4569
B	6,088,055	5,179,949	8726	6674	5386	4553
C	5,829,701	5,043,616	7736	6458	5001	4514
D	6,237,623	5,074,447	8322	6560	5352	4452

The correlations obtained in this study indicate that there is at least a scaling effect among sires in both environments, i.e., the advantage of sires in the control herds is less when their daughters are producing under grazing conditions. However, the correlations are still higher than the value of 0.8 that Robertson (1959) proposed as a value indicative of a biologically important $G \times E$. For the quartile analysis, a correlation of unity existed between the upper and lower quartiles for the control herds. However, the correlations for the grazing quartiles did differ significantly from unity for milk (0.82) and protein (0.85) but not for fat. This indicates that genes for milk and protein production may be expressed differently in lower producing grazing herds. Cromie et al. (1988) also found a similar decline in the genetic correlation for milk and protein as the differences in environments became more pronounced. Genetic correlations for the middle quartiles for both grazing and control for all traits were not different from unity. The high correlations between these quartiles might be expected as the level of management should be similar.

The results may not be surprising as cows producing in the lowest quartile of grazing herds are probably

producing under very extensive conditions. For instance, in the lowest quartile, 86 of the 99 herds were from Louisiana, while there were only 30 of 99 herds in the upper quartile. Due to the very warm summer climate it is likely that pasture shortages occur frequently resulting in less intensive grazing practices. These results are in agreement with the quartile regression analysis, which had relatively low coefficients of regression for milk, fat, and protein in the lowest quartile.

Product-moment and rank correlation coefficients for sires based on their EBV calculated separately for both grazing and control are in Table 10. The table also includes the rank correlation between the sire's EBV in both systems and his official November 2000 USDA-DHIA PTA for the same traits. The correlations are based on 792 sires with greater than 5 daughters producing in both environments. Product-moment correlations were similar to the rank correlations for all traits. Product-moment correlations between sires' EBV in both groups were 0.62, 0.64, and 0.66 for milk, fat, and protein, respectively. These agree strongly with Cromie et al. (1998), who found similar results for sires in high and low input herds in Ireland. The correlations for

Table 8. Estimates of heritability (diagonal) and genetic correlations (above diagonal) for upper and lower milk yield quartiles for milk, fat, and protein for grazing and control herds. Standard errors are in parentheses.

	Milk		Fat		Protein	
	0–25%	76–100%	0–25%	76–100%	0–25%	76–100%
Control	0.17 (0.015)	0.98 (0.036) 0.22 (0.010)	0.17 (0.014)	0.99 (0.017) 0.26 (0.008)	0.13 (0.015)	1.00 (0.0) 0.22 (0.009)
Grazing	0.16 (0.020)	0.82 (0.071) 0.19 (0.010)	0.17 (0.022)	0.89 (0.07) 0.19 (0.010)	0.16 (0.021)	0.85 (0.069) 0.18 (0.010)

Table 9. Estimates of heritability (diagonal) and genetic correlations (above diagonal) for middle milk yield quartiles for milk, fat, and protein for grazing and control herds. Standard errors are in parentheses.

	Milk		Fat		Protein	
	25–50%	51–75%	25–50%	51–75%	25–50%	51–75%
Control	0.21 (0.010)	1.00 (0.00) 0.20 (0.010)	0.23 (0.010)	0.97 (0.030) 0.28 (0.008)	0.186 (0.010)	0.98 (0.001) 0.195 (0.009)
Grazing	0.18 (0.020)	1.00 (0.000) 0.19 (0.020)	0.22 (0.020)	0.96 (0.031) 0.2 (0.013)	0.18 (0.020)	0.94 (0.044) 0.17 (0.013)

Table 10. Correlations for EBV for milk, fat, or protein for sires from grazing herd data (grazing) and confinement herd data (control) and with USDA-DHIA PTA (November, 2000; USDA).

	Rank correlation			Product-moment correlation		
	$r_{\text{grazing,control}}$	$r_{\text{grazing,USDA}}$	$r_{\text{control,USDA}}$	$r_{\text{grazing,control}}$	$r_{\text{grazing,USDA}}$	$r_{\text{control,USDA}}$
Milk	0.59	0.65	0.74	0.62	0.66	0.76
Fat	0.63	0.70	0.76	0.64	0.71	0.79
Protein	0.66	0.71	0.78	0.66	0.71	0.78

both grazing and control herds with the USDA-DHIA PTA are higher than the correlations between grazing and control herds. This may be partly because the USDA-DHIA PTA include the information from both grazing and control herds and partly because the USDA-DHIA PTA are calculated more accurately (e.g., higher reliability) from more records.

For all traits, the rank correlation of the sire's EBV in control herds and their USDA-DHIA evaluation were approximately 6 to 10% higher than the correlation between the grazing EBV and the USDA-DHIA evaluation. To quantify the change in rank between sire EBV in both systems, an average rank change for milk was calculated. For all 895 sires, the average rank change between grazing and confinement was 156. For the top 100 sires (based on milk EBV in control herds), the average rank change was 27, and 16% of bulls had absolute rank changes of more than 50 (Table 11). For bulls with at least 25 daughters in both environments, Figure 2 has the rank of the bull's EBV for milk in control herds plotted against the same bull's EBV in grazing herds. The rank correlation for these bulls was 0.62. When evaluations were performed within systems, a fair amount of reranking occurred. A limitation of this approach is that only the information from within each environment is taken into account when calculating the EBV, leading to differences in accuracy of the EBV, as some sires may have many more daughters in confinement herds than grazing and vice versa. For example, a sire with many daughters in confinement herds may have a high accuracy EBV reflecting his true breeding worth in control environments, but if he has few daughters in grazing, his EBV will be

regressed more toward the parent average, which may not accurately reflect his true genetic value as well and, thereby, reduce correlations. Also, these were 2-trait evaluations, considering only MEM, MEF, or MEP in the same analysis. Evaluations considering all traits simultaneously may be more accurate but were not computationally feasible in this study.

Some of the observed differences between grazing and control herds and among quartiles within each management system may be explained by a relationship between the means and variance within each of these described systems or quartiles. Such heterogeneous variance could explain the increasing heritability that accompanied increasing yields (Table 8). Pearson et al. (1989) found that response to selection is affected only by herd variance and that the effect of herd mean on response to selection arises through the relationship between the mean and variance. Thus effects of increasing heritability or regression coefficients observed within grazing or confinement quartiles may largely result from heterogeneous variance, and this will be determined in ongoing work.

CONCLUSIONS

Genetic correlations less than unity suggest that there is some G $\times$ E for production traits between confinement and grazing in the US. The magnitude of the difference from unity provides an indication as to whether the G $\times$ E exists or if reranking of sires will occur. The genetic correlations obtained in this study were less than unity, indicating that there is at least some reranking. However, based on a genetic correlation of 0.9 between control and grazing herds, Weigel et al. (1999) estimated that graziers would have to sample 500 to 700 young sires each year to achieve the same level of genetic gain available from selecting among the current AI sires sampled annually. Estimates calculated in this study are close to 0.9, and therefore a young sire sampling scheme solely to identify sires that excel under grazing does not appear to be economically feasible, given that a high level of genetic gain will be achieved by selecting sires based on current evaluations.

Table 11. Frequency distribution of the absolute change in rank of EBV of the top 100 bulls for milk in grazing herds when compared to EBV for milk from control herds.

Change in rank	Frequency	Change in rank	Frequency
0–10	28	51–60	10
11–20	17	61–70	1
21–30	11	71–80	3
31–40	15	81–90	4
41–50	10	91–100	5

Figure 2. Rank of 274 sires with at least 25 daughters in grazing and control herds. Bull's rank EBV for milk in control herds (x-axis) and grazing herds (y-axis). Actual ranks for individual bulls (●) and expected ranks if a perfect rank correlation existed (◆) are shown.

However, some graziers may need to be concerned that that reranking can occur. This is especially true for those graziers with low-producing herds. Differences in daughter performance predicted by USDA-DHI sire PTA values may be reduced by as much as half in these herds. Also, a lower correlation for the traits between the upper and lower quartiles for grazing indicates the possibility for reranking. As indicated by the differences in coefficients of regression of yields on sire PTA, it is questionable whether grazing herds, especially in very extensive conditions, can afford to pay as much for semen of bulls transmitting the highest yields. Indeed, Cienfuegos-Rivas et al. (1999) suggests that daughter performance in Mexico would be better predicted based upon paternal half-sister performance in low producing US environment. However, the authors failed to recognize the lower cow numbers in low production herds and thus lower reliability, which suggests reduced accuracy if selection were based only on these records.

ACKNOWLEDGMENTS

This study was funded in part by the USDA's Sustainable Agriculture Research and Education (SARE) program, Lincoln, NE and the National Association of Animal Breeders, Columbia, MO. The authors wish to

thank the numerous individuals who contributed data to the study, especially John Clay and Crystal Vierhout of DRMS, Raleigh, NC, for supplying the records and appreciate the helpful comments of two anonymous reviewers.

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