

## GENOTYPE BY ENVIRONMENT INTERACTION FOR US HOLSTEINS IN TWO PRODUCTION SYSTEMS

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### INTRODUCTION

Grazing as a form of low input production is increasing in the US. Concern regarding the suitability of conventional AI sires for grazing herds, has resulted in some grazing herds switching to alternative breeding schemes such as crossbreeding, use of sires from established grazing countries, notably New Zealand, and natural service sires. Recent studies by Weigel *et al.* (1999), and Cromie *et al.* (1998) have supported the results of numerous other studies, which provide little evidence for significant genotype by environment interaction (GE) for milk production traits. Few studies have reported on GE for somatic cell count and reproductive traits. These traits may attain added importance in grazing herds especially where seasonal calving is practiced. Also, it is possible that GE plays a greater role in traits under less additive genetic control compared to traits with large additive genetic effects for which the accuracy of sire predicted transmitting abilities (PTA) is greater.

The objective of this study was to investigate the existence of GE for production, health and reproduction traits of US Holsteins in confinement and grazing dairies in the eastern US.

### MATERIALS AND METHODS

**Data.** Grazing herds were defined as those in which cows consumed the majority of their forage from grass for at least 6 months of the year. Herds must have been enrolled in a milk-recording program. In addition, herds of similar size from the same states but not utilizing grazing were selected as control herds.

The grazing data included records from 393 herds in 12 states, while the control data included records from 432 herds in 13 states. Due to the voluntary nature of the recording system, fewer records were available for somatic cell score (SCS) and the reproductive traits. 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 ignored, 5) cows with records  $\pm 4$  standard deviations of mean mature equivalent milk, fat, and protein were deleted, and 6) cows with <60 days in milk for each group were deleted. The traits analysed were milk, fat, and protein production, somatic cell score (SCS), days open (DO), days to first service (DFS), and the number of services per conception (SPC).

**Statistical Analysis.** The performance of cows in grazing and confinement was examined using linear regression of mature equivalent milk (MEM), fat (MEF), and protein (MEP) yield and lactation average SCS (LSCS), on the November 2000 USDA PTA of their sires for those traits. A univariate regression model was fit separately to grazing and control data.

The REML (co)variance component estimation program, VCE4 (Neumaier and Groeneveld, 1998), was used to estimate heritabilities and genetic correlations between the two environments for each trait. A bivariate animal model that considered traits in different environments as separate traits was used to estimate the variance components.

To assess the level of re-ranking among sires within each environment, product-moment and rank correlations between sires' estimated breeding values (EBV) were calculated. Correlations were calculated for sires with at least five daughters producing in both grazing and confinement herds. The Best Linear Unbiased Prediction (BLUP) breeding values were obtained for all sires separately in both the grazing and confinement groups using PEST (Groeneveld, 1990). The models included the fixed effect of herd-year-season, and age at parity and the random effects of animal, and permanent environment.

## RESULTS AND DISCUSSION

Means and standard deviations for the phenotypic performance of herds for each of the traits analysed are in Table 1. As expected, mean production performance for grazing herds was less than in control herds. Mean somatic cell scores were higher in grazing herds, while reproductive performance was similar for both groups.

**Table 1. Mean phenotypic performance (and standard deviations) of grazing and control herds in Eastern US**

Trait	Grazing	Control
MEM, kg	8588 (1917)	9948 (2034)
MEF, kg	294 (74)	355 (77)
MEP, kg	252 (56)	291 (58)
LSCS	3.19 (1.5)	2.92 (1.52)
Days open	154 (88)	148 (83)
Days to first service	106 (69)	104 (57)
Services per conception	2.87 (2.05)	2.50 (1.76)

Coefficients of regression of daughter performance in first lactation for MEM, MEF, and MEP and LSCS, USDA sire PTA for these traits is in Table 2. The expectation of the coefficients was near 1.

**Table 2. Coefficients of regression (and standard errors) of daughter performance on November 2000 USDA sire PTA for grazing and control herds**

Trait	Grazing	Control
Milk	0.78* (0.030)	0.99 (0.026)
Fat	0.76* (0.020)	0.96 (0.024)
Protein	0.78* (0.020)	0.98 (0.027)
SCS	0.88 (0.085)	0.96 (0.030)

\* significantly different from 1 ( $P < 0.01$ )

The coefficients of regression were significantly different from 1 for milk, fat, and protein for the grazing herds but not the control herds. These coefficients indicate that the actual sire PTA may overstate the true difference between sires' daughters in grazing herds. For somatic cell score, the coefficients of regression were 0.88 and 0.96 respectively for grazing and control groups, but were not significantly different from 1. Further regression analysis was carried out for quartiles based on herd average MEM. Results (not shown) indicate that sire PTA for milk, fat, and protein yield would be most severely over-predicted for those grazing herds in the lowest quartile.

Estimates of heritabilities and genetic correlations for each of the traits analysed are in Table 3. The heritabilities for all traits are in general agreement to those found in the literature. Estimates of heritabilities for the control herds were slightly higher for all traits but the differences were small. The low estimates of heritability for the reproductive traits indicate that improvements for these traits through selection would be slow. However, traits with moderate heritabilities such as body condition score (Dechow *et al.*, 2001, Pryce *et al.*, 2001) and energy balance and live weight (Veerkamp *et al.*, 2000) may be useful to improve reproductive performance.

**Table 3. Estimates of heritabilities and genetic correlation**

Trait	$h^2$	$r_g$	Trait	$h^2$	$r_g$
<b>Milk</b>			<b>DO</b>		
Grazing	.19 (0.013)	.89 (0.039)	Grazing	.028 (0.050)	.86 (0.080)
Control	.20 (0.010)		Control	.034 (0.050)	
<b>Fat</b>			<b>DFS</b>		
Grazing	.19 (0.013)	.88 (0.037)	Grazing	.020 (0.010)	1.0 (0.0)
Control	.23 (0.010)		Control	.047 (0.009)	
<b>Protein</b>			<b>SPC</b>		
Grazing	.17 (0.012)	.91 (0.036)	Grazing	.007 (0.006)	1.0 (0.0)
Control	.20 (0.010)		Control	.030 (0.007)	
<b>SCS</b>					
Grazing	.12 (0.014)	.89 (0.060)			
Control	.13 (0.010)				

The same traits in grazing and control herds were treated as separate traits, therefore the estimates of genetic correlation indicates the extent to which the two traits are influenced by the same genes, and whether any re-ranking would be expected among sires between the two environments. For all traits, the estimated genetic correlations were greater than the value of 0.8, which has been proposed as indicative of a biologically important GE.

To determine whether the genetic correlation between the same traits measured in two different environments changes as the difference between the environments become more pronounced, the genetic correlation between the upper and lower quartiles for production within grazing and control herds was calculated for milk, fat, and protein. A correlation of unity was obtained for the upper and lower quartiles for all traits in the control herds and for fat in the grazing herds. However, the correlation between the upper and lower quartiles in the grazing herds for milk (0.82), and protein (0.85) approached the level where GE may cause significant re-ranking.

Product-moment and rank correlation coefficients for sires based on their estimated breeding values (EBV) were calculated separately for grazing and control herds for milk, fat, protein, and SCS. The correlations were based on a total of 792 sires with >5 daughters in both environments. For all traits the product-moment correlations were similar to the rank correlations. The product-moment correlations for milk (0.62), fat (0.64), and protein (0.66) are in good agreement with those found by Cromie *et al.* (1998) in Ireland. The product-moment correlation for SCS was 0.5. For the top 100 sires based on EBV for milk in control herds, the average rank change was 27, and 16% of sires had an absolute rank change of more than 50. When evaluations were performed within systems, a considerable amount of re-ranking occurred.

### CONCLUSIONS

Based on a genetic correlation between grazing and control herds of 0.9, Weigel *et al.* (1999), estimated that grazing herds would need to progeny test between 500 to 700 young sires annually to achieve the same level of genetic gain by selecting among current AI sires. Similar correlations in this study suggest this would not appear to be economically feasible. Also, inclusion of health, longevity, and soon fertility traits in the US selection indices should identify sires that produce daughters better able to fulfill the breeding goals of grazing herds, namely, daughters that can reproduce efficiently while also maintaining satisfactory production levels.

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