

## Genotype by environment interaction for Holstein Friesian reproductive performance between Saudi Arabia and the United States

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**Abstract:** Co-variance components and genetic parameters of some reproductive performance for Holstein Friesian cows were estimated by multiple-trait animal model using Method R procedures. The objective of this study were to determine if genotype by environment interactions for some reproductive traits exist between Saudi Arabia and the United States. The Saudi data included 46,777 records of 20,815 cows as daughters of 255 sires and the US data included 38,293 records of 19,456 cows as daughters of 176 sires. There were 151 sires common to both countries with average number of daughters 260 in the Saudi data and 246 in the USA data. Heritability estimates for gestation length: 0.22 vs. 0.08, calving interval: 0.11 vs. 0.08, and age at first calving: 0.62 vs 0.14 in KSA and USA, respectively. Genetic correlations between the two environments were 0.81, 0.83 and 0.08, for gestation length, calving interval and age at first calving, respectively. The low estimate of genetic correlation for age at first calving between countries is an indicator of the existence of genotype by environment interaction. Therefore, selection within the Saudi Holstein population may be the best tool for improving reproductive performance for these animals under Saudi environmental conditions.

**Keywords:** genetic, environment, interaction, heritability, age at first calving, gestation length, calving interval

### INTRODUCTION

Relationships between performances of dairy cattle breeds in different climatic conditions must be studied to determine the impact of the different environments on reproductive performance. It is widely established that if a genotype is developed under particular environmental conditions but reared under different environmental conditions, then investigation of genotype – environment interaction becomes important. Thus how much of the genetic superiority of the best bulls in the better environment will be manifested in the poorer environment. If the investigation reveals a violation of any of the two following assumptions, then there is interaction. The 1<sup>st</sup> assumption is that different environmental conditions have the same effect on different genotypes, and the second is that phenotypic and genetic variances are homogeneous across environment (Croime *et al.*, 1998 and Stanton, 1990).

The objective of the present study were to determine whether interactions between genotype and environment for some reproductive traits in daughters of sires used in the United States and Saudi Arabia exist by estimating and comparing genetic, residual, and phenotypic co-variances across environments from a multi trait animal model.

### MATERIALS AND METHODS

Approximately 66,000 records of Holstein cows were available from six large farms located in the central region of the Kingdom of Saudi Arabia. The records available were those of cows calved between 1990 and 1998, allowing for some cows to have more than eight normal parities. All records of a cow were discarded if she had a missing or an invalid sire identification number (i.e. sire name was not considered unique), and or if breed of sire was not Holstein. Sires

of cows were identified and then sent to Dairy Records Management System, Raleigh, North Carolina to obtain performance records of daughters of the same sires in the United States. Approximately 916,000 records of Holstein cows that calved in the United States between 1990 and 1998 were provided. Cows were required to have a sequential data pattern to be included in the analysis (i.e. if the 3<sup>rd</sup> record is to be used, 1<sup>st</sup> and 2<sup>nd</sup> records should be available). If any of a cow's previous records were missing, then all her records were eliminated. This helped to overcome the problem of selection or culling of heifers based on their 1<sup>st</sup> lactation. All production records were restricted to at least 240 days of milking regardless of milk yield, and herds chosen from the overall data contained 230 dairy cows or more. Those last edits decreased USA data to  $\approx$  540,000 records but did not significantly reduce the Saudi data. Structures of the data in both countries are presented in Table 1.

### Statistical Analysis of Variance

The Saudi data were first analyzed using a multitrait; random components animal model to investigate whether the effect of sire by herd interaction was large enough to be included in the multi-trait model. The model included age at first calving, gestation length and calving interval as the dependent variable, herd-year-season as fixed effects, and sire by herd interaction, animal, permanent environment, and residual as random effects. Multi trait animal model was used to obtain co-variances for all investigated reproductive traits of both countries. Reproductive traits in the Saudi Arabia and the United States were treated as separate traits in joint analysis. Genetic co-variances and residual variance components were estimated simultaneously.

**Table (1):** Summary of the data structure for mature equivalent milk yield by parity and month of calving groups in Saudi Arabia and the United States

		Lactations					Total <sup>1</sup>	Total <sup>2</sup>
		1st	2nd	3rd	4th	5th		
Saudi Arabia	Sires	255	242	198	160	107	255	
	Cows	20,815	12,862	7,636	3,769	1,695	20,815	46,777
	HYS <sup>3</sup>	193	183	179	161	128	376	
United States	Sires	176	176	155	152	127	87	176
	Cows	19,456	10,215	5,698	2,247	677	19,456	38,293
	HYS <sup>3</sup>	1,525	1,525	1,100	990	639	283	2,640

  

		Months of calving						
		Jan- Feb	Mar - Apr.	May - Jun	July -Aug	Sep - Oct	Nov - Dec	Total
Cows	First Calving	4,226	4,705	2,895	4,251	3,278	1,460	20,815
	Multiple Calving	4,626	4,597	3,696	4,647	4,597	3,799	25,962

<sup>1</sup>Total number of unique sire, cow (records) or HYS, <sup>2</sup>Total number of records, <sup>3</sup>Herd-Year-Season

The first model used single trait animal model from method R procedure (Reverter *et al.*, 1994) to analysis within country for gestation length and calving interval using all lactation data set. Method R produces estimates of variances from which genetic, environment, and phenotypic parameters can be derived. The mathematical model was:

$$Y_{ijk} = \mu + HYS_i + A_k + Pe_k + \varepsilon_{ikl} \dots (1^{st} \text{ model})$$

Where:  $Y_{ikl}$  is the  $l^{th}$  record for  $k^{th}$  cow of calving interval and gestation length,  $HYS_i$  is the fixed effects due to  $i^{th}$  herd-year-season of freshening,  $A_k$  is the random additive genetic effect due to  $k^{th}$  animal,  $Pe_k$  is the permanent environment due to  $k^{th}$  cow and  $\varepsilon_{ikl}$  is the random residual effect for the  $l^{th}$  record of  $k^{th}$  animal in  $i^{th}$  herd-year-season. In matrix notation the model can be described as

$$Y = Xb + Za + Wpe + e$$

Where:  $Y$  is a vector of observations for reproductive variables,  $b$  is a vector of fixed effects for herd-year-season,  $a$  is a vector of additive genetic values of individual animals for the trait or traits considered,  $pe$  is a vector of random permanent effect,  $e$  is a vector of residual effects and  $X$ ,  $Z$ , and  $W$  are known incidence matrices that assign fixed, additive random, and permanent effects to records in  $Y$ . The mixed model equations (MME) were

$$\begin{bmatrix} X'X & X'Z & X'W \\ Z'X & Z'Z + A^{-1}\phi & Z'W \\ W'X & W'Z & W'W + I_{1r} \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{a} \\ pe \end{bmatrix} = \begin{bmatrix} X'Y \\ Z'Y \\ W'Y \end{bmatrix}$$

$$E \begin{bmatrix} a \\ pe \\ e \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \end{bmatrix}, \text{ var} \begin{bmatrix} a \\ pe \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & 0 & 0 \\ 0 & I_1\sigma_{pe}^2 & 0 \\ 0 & 0 & I_2\sigma_e^2 \end{bmatrix}$$

Where :  $A$  is the numerator relationship matrix,  $\sigma_a^2$  is the additive variance,  $\sigma_{pe}^2$  is the permanent environmental variance,  $\sigma_e^2$  is the residual variance  $I_1$ ,  $I_2$  are the identity matrix 1 for cows with records, 2 for all animals in  $A$ ,  $\phi = \frac{\sigma_e^2}{\sigma_a^2}$  and  $\gamma = \frac{\sigma_e^2}{\sigma_{pe}^2}$

The second model was used to analyze age at first calving in different two data sets using joint analysis of multi-trait animal model of Method R.

The mathematical model was

$$Y_{ikl} = \mu + HYS_i + A_k + \varepsilon_{ikl} \dots (2^{nd} \text{ model})$$

Where:  $Y_{ikl}$  is the  $l^{th}$  record for  $k^{th}$  cow of age at first calving,  $HYS_i$  is the fixed effect due to  $i^{th}$  herd-year-season of freshening,  $A_k$  is the random additive genetic effect due to  $k^{th}$  animal, and  $\varepsilon_{ikl}$  is the random residual effect for the  $l^{th}$  record of  $k^{th}$  animal in  $i^{th}$  herd-year-season. In matrix notation the 2<sup>nd</sup> model can be described as shown for the 1<sup>st</sup> model.

## RESULTS AND DISCUSSION

Phenotypic means and standard deviations for studied reproductive traits in first four parities are illustrated in Table 2.

Averages for gestation length were identical in both countries, but calving intervals in the United States were 15 days on average longer than those in Saudi Arabia in all four lactations. Although means for measures of fertility were similar across parities in both countries, means for calving interval tended to decrease and means for gestation length tended to increase as lactations advance. The average of NOS was 1.86 is similar to 1.68 that reported by Mansour (1992) for HF in KSA. While the means of DO:106 days, CI: 386 days, and AFC:25.5 months were shorter than the 120 days, 398 days, and 29.7 months, respectively that reported by Mansour (1992). The overall mean of gestation length (279 days) was similar for that reported by Mansour (1992) and Rayan and Biland (1991) for HF-KSA.

### Joint analysis for gestation length between the United States and Saudi Arabia

Parameters for variance components, heritability, and genetic correlation estimates from 20 subsamples of Method R for gestation length using all lactation are shown in Table 3.

The range of the phenotypic variance in the United States was also greater than that in KSA, which can be attributed to the greater environmental variance available under the United States' environmental conditions. Because the records are from small number

of well managed farms, more environmental uniformity can be seen in KSA data. The range of the coefficient of genetic variance is slightly smaller in KSA than in USA. It appears that under relatively good management conditions, less genetic variance can be seen for some traits such as fertility. Heritability estimate for gestation length of HF-KSA was (0.22) greatly higher than the corresponding estimate for HF-USA (0.08). The median estimates of heritability for gestation length in Saudi Arabia (0.22) is similar to estimates of 0.22 and 0.24 reported by Silva *et al.* (1992) and Simerl *et al.* (1991), respectively. However it is larger than the majority of results in the literature, may be in part due to using a different statistical procedure or different statistical model components (Dong and Van Vleck, 1989).

Estimates of repeatabilities for gestation length and calving interval in both countries are listed in Table 3, 4. Median and Mean repeatabilities of gestation length in Saudi data were higher (0.24 and 0.24) than those estimates (0.12 and 0.13) in the United States data.

Though genetic variances were similar in both countries, phenotypic and permanent environmental variance in the Saudi data set were substantially smaller than those of United States resulting in larger estimates of repeatability. Because permanent environmental variance for Saudi data was small, median and mean repeatabilities and corresponding heritabilities were almost equal, but repeatabilities for the United States data were close to two times the corresponding heritability estimates. Repeatability estimates for gestation length in the Saudi data set were almost twice the estimate reported by El Amin *et al.* (1986) of 0.14 for crosses of Holstein, Shorthorn, Ayrshire and Guernsey with Butana cattle in Sudan.

#### Joint analysis for calving interval between the United States and Saudi Arabia:

Parameters for variance components, heritability, and genetic correlation estimates from 20 subsamples of Method R for calving interval using all lactation are shown in Table 4.

**Table (2):** Means and standard deviations for studied reproductive traits in Saudi Arabia and the United States in the first four parities.

Locations	Saudi Arabia									
	DO		GL		CI		AC		NOS	
1 <sup>st</sup>	108	53	278	4.6	387	53	25.5	1.8	1.42	0.9
2 <sup>nd</sup>	105	52	279	5.0	385	52	38.1	2.7	2.27	1.7
3 <sup>rd</sup>	102	50	280	5.1	383	50	50.3	3.3	2.25	1.6
4 <sup>th</sup>	104	51	280	5.0	384	51			2.27	1.6
<b>Overall</b>	106	52	279	4.8	386	52			1.86	1.4
United States										
1 <sup>st</sup>			278	5.0	402	63	25.5	3.1		
2 <sup>nd</sup>			279	5.3	400	60	38.6	4.3		
3 <sup>rd</sup>			280	5.1	399	59	51.4	5.2		
4 <sup>th</sup>			280	5.3	399	59				
<b>Overall</b>			278	7.2	402	61				

DO: Days open, GL: Gestation length, CI: calving interval, AC: Age at calving, NOS: Number of services per conception. Shaded traits were introduced only for genetic analysis

**Table (3):** Estimates of variance components, heritability ( $h^2$ ), additive coefficient of variation (ACV%), repeatability ( $r$ ), genetic correlation ( $r_{aUSA,KSA}$ ) and standard errors (SE) for gestation length joint analysis between Saudi Arabia and United States using all lactations.

		Variance components				Parameters			
		$\sigma_a^2$	$\sigma_{pe}^2$	$\sigma_e^2$	$\sigma_p^2$	$h^2$	$r$	$r_{aUSA,KSA}$	ACV%
Saudi Arabia	Minimum	3.6	0.07	13	17	.20	.23	.14	.80
	Maximum	9.0	1.00	29.6	39	.24	.26	.99	1.10
	Median	5.7	0.30	20	27	.22	.24	.96	.90
	Mean	6.0	0.45	20	26	.22	.24	.81	.90
	SE	0.11	0.02	0.40	0.54	.00	.00	.03	.00
United States	Minimum	1.0	.80	15.2	172	.03	.10		.40
	Maximum	14.7	5.0	95.4	112.8	.13	.16		1.30
	Median	5.3	3.4	64	74.6	.07	.12		.80
	Mean	5.88	3.2	60	69	.08	.13		.90
	SE	0.31	0.1	1.6	2	.00	.00		.00

$\sigma_a^2$ : Additive genetic variance,  $\sigma_{pe}^2$ : permanent environment variance,  $\sigma_e^2$ : Environmental variance,  $\sigma_p^2$ : phenotypic variance

**Table (4):** Estimates of variance components, heritability ( $h^2$ ), repeatability ( $r$ ), additive coefficient of variation (ACV%), genetic correlation ( $r_{aUSA,KSA}$ ) and standard errors (SE) for calving interval from joint analysis between Saudi Arabia and United States in all lactations.

		Variance components				Parameters			
		$\sigma_a^2$	$\sigma_{pe}^2$	$\sigma_e^2$	$\sigma_p^2$	$h^2$	$r$	$r_{aUSA,KSA}$	ACV%
Saudi Arabia	Minimum	14	57	2,214	2,477	.01	.07	.03	.90
	Maximum	8,159	255	2,816	10,513	.78	.80	.99	.23
	Median	142	137	2,555	2,835	.05	.10	.99	3.10
	Mean	571	129	2,527	3,228	.11	.15	.83	4.40
	SE	61	2	6.5	59.6	.01	.01	.01	.00
United States	Minimum	11	76.5	3,057	3,288	.00	.05		.80
	Maximum	15,187	362	3,923	18,827	.80	.81		30
	Median	109	229	3,438	3,824	.08	.09		2.60
	Mean	782	235	3,441	4,459	.08	.14		4.10
	SE	113	2.7	7.6	113	.01	.00		00

$\sigma_a^2$ : Additive genetic variance,  $\sigma_e^2$ : Environmental variance,  $\sigma_p^2$ : phenotypic variance,  $\sigma_{pe}^2$ : permanent environmental variance

Everett *et al.* (1966), using Henderson's method I, reported heritabilities of calving interval for HF of 0.08, remarkably in agreement with the median heritability estimates of calving interval of 0.05 and 0.08 for KSA and USA in the present study, respectively. Other estimates were also reported in this range (from 0.021 to 0.098) by Silva *et al.* (1992), and Campos *et al.* (1994). However, present estimates are smaller than those of 0.17 and 0.14 reported by Dong and Van Vleck (1989).

Median and mean repeatability estimates for calving interval were similar in both countries. Median estimates in Saudi Arabia and the United States were 0.10 and 0.9, respectively. Comparative results from the literature for calving interval in temperate areas were consistent with the present study. Majjlala (1976) reported a weighted average repeatability of 0.131 from six studies for calving interval. The repeatability estimate of 0.10 reported by Silva *et al.* (1992) is similar to the median estimates of both countries in the present study. It seems that under good management, especially in reducing heat stress and keeping good reproductive

records, Holstein cow' reproductive performance in Saudi Arabia is similar to that in temperate areas.

#### Joint analysis for age at first calving between the United States and Saudi Arabia

Parameters for variance components, heritability, and genetic correlation estimates from 20 subsamples of Method R for age at first calving using all lactations are shown in Table 5.

The median heritability estimate of 0.62 for age at first calving in KSA undoubtedly represents genetic differences among animals in rate of maturity or it reflects the intention of the Saudi dairyman to herd daughters of some sires whom known to have potential in milk yield earlier than daughters of other sires. Though not as large, high heritability estimate for age at first calving were also reported by Allaire and Lin (1980), Lee (1976), and Simerl *et al.* (1991). However, the estimates in the present study substantially different from the smaller heritability estimates of 0.04 and 0.05 reported by Moore *et al.* (1992) and Seykora and McDaniel (1983), respectively.

**Table (5):** Estimates of variance components, heritability ( $h^2$ ), additive coefficient of variation (ACV%), genetic correlation ( $r_{aUSA,KSA}$ ) and standard errors (SE) for age at first calving from joint analysis between Saudi Arabia and the United States in all lactations.

		Variance components			Parameters		
		$\sigma_a^2$	$\sigma_e^2$	$\sigma_p^2$	$h^2$	$r_{aUSA,KSA}$	ACV%
Saudi Arabia	Minimum	1.02	0.62	1.65	0.60	-.01	4.0
	Maximum	2.18	1.4	3.60	0.66	0.18	5.7
	Median	1.9	1.13	3.01	0.62	0.10	5.4
	Mean	1.9	1.14	3.00	0.62	0.08	5.3
	SE	0.03	0.02	0.05	0.00	0.01	.00
United States	Minimum	0.44	2.80	3.40	0.04		2.6
	Maximum	1.18	12.1	12.53	0.28		4.3
	Median	0.60	4.5	5.37	0.14		3.0
	Mean	0.70	6.03	6.7	0.14		3.3
	SE	0.02	0.32	0.31	0.01		0.00

$\sigma_a^2$ : Additive genetic variance,  $\sigma_e^2$ : Environmental variance,  $\sigma_p^2$ : phenotypic variance

Estimates of genetic correlations between countries for gestation length, calving interval and age at first calving are presented in Tables (3, 4, 5). Median genetic correlations for gestation length and calving interval across the two environments were virtually unity (0.96 and 0.99, respectively). Means of estimates were also large (above 0.80) and the estimates of standard error of the mean were small. This is a strong indicator of the absence of the first type of genetic by environment interaction in these two traits.

Median and mean genetic correlations between countries for age at first calving were considerably lower (0.1 and 0.08, respectively) than correlations for gestation length and calving interval. The low estimate of genetic correlation is an indicator of the existence of genotype by environment interaction. There were 125 sires common to both countries with age at first calving observation available.

### CONCLUSION

Reproductive performance of Holstein Friesian cows performing under Saudi environmental conditions showed a variability as greater as in temperate areas and in some case greater. The current results showed that high genetic variation and small to moderate heritability for investigated reproductive traits. Although most estimates of heritability and repeatability for reproductive traits for Holsteins from Saudi Arabia were small, improvement by selection for reproductive traits is possible. In other point of view, though heritability is small, defining the most economically important reproductive trait is necessary so it can be incorporated in sire indexes to help prevent the deterioration of reproductive traits that could accompany sire selection for milk production. Because it is influenced by other reproductive traits (i.e., days open, number of services, and gestation length), calving interval may be the best measure to represent reproductive efficiency.

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