

Holstein white coat color and performance: Phenotypic, genetic and environmental correlations*

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ABSTRACT

Correlations of measures of percentages of white coat color, five measures of production and two measures of reproduction were obtained from 4293 first lactation Holsteins from eight Florida dairy farms. Percentages of white coat color were analyzed as recorded and transformed by an extension of Box-Cox procedures. Statistical analyses were by derivative-free restricted maximum likelihood (DFREML) with an animal model. Phenotypic and genetic correlations of white percentage (not transformed) were with milk yield, 0.047 and 0.097; fat yield, 0.002 and 0.004; fat percentage, -0.047 and -0.090; protein yield, 0.024 and 0.048; protein percentage, -0.070 and -0.116; days open, -0.012 and -0.065; and calving interval, -0.007 and -0.029. Changes in magnitude of correlations were very small for all variables except days open. Genetic and phenotypic correlations of transformed values with days open were -0.027 and -0.140. Modest positive correlated responses would be expected for white coat color percentage following direct selection for milk, fat, and protein yields, but selection for fat and protein percentages, days open, or calving interval would lead to small decreases.

INTRODUCTION

Coat color affects productive and reproductive traits of cattle under adverse climatic conditions of high temperature and solar radiation (Finch, 1983, 1986; King *et al.*, 1988; Hansen, 1990a,b; Becerril *et al.*, 1994b); therefore determination of the genetic component of coat color and of the genetic and phenotypic interrelationships between coat color and other economically important traits is important to animal geneticists. Evidence on this topic is scarce and mainly related to estimation of heritability of coat color (Dunn, *et al.*, 1923;

Briquet and Lush, 1947; Koger and Mankin, 1952; King, *et al.*, 1988; Becerril *et al.*, 1994b).

Heritability of percentage of white coat color (WP) in Holsteins seems to be high and > 0.70 (Briquet and Lush, 1947; Becerril *et al.*, 1994b), which suggests the possibility of rapid change in coat color following selection and a relatively small influence of environmental and nonadditive genetic variance on this trait, although these have not been estimated. However, genetic correlations of WP with economically important traits have not been reported in the literature, except for Becerril *et al.* (1994b), which perhaps is an indication that little attention has been given to this trait as a possible factor contributing to Holstein performance. Coat color essentially has been considered only as a breed trademark, and standards for color of registered animals of many breeds have existed for many years.

Becerril *et al.* (1994b), using first lactation Holstein heifers in a single herd, estimated (by ordinary

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least squares analysis of variance) genetic correlations of WP with milk yield (MY), and fat yield (FY), fat percentage (FP) of -0.12 ± 0.39 , -0.41 ± 0.24 , and -0.38 ± 0.22 . Although the correlation for MY had a standard error larger than the estimate, such was not the case for FY and FP; all correlations were negative.

Most estimates of heritability of WP and its genetic correlations with production traits have been obtained from small data fields (<1000 records). Yet, because of the high heritability of WP, even moderate genetic correlations could cause correlated responses in other traits.

Consideration of improved management practices for many Florida herds, including implementation of new technologies (e.g., use of sprinklers, fans, ponds, shade areas) to reduce climatic stress (Bray and Shearer, 1988), indicates the need for the study of the (co)variance structure among WP and production and reproduction. Availability of necessary computing power and programs, as well as recent mixed model statistical methodology, provide the proper tools for better estimation of genetic correlations. No genetic or phenotypic studies of correlations between WP and other traits have been attempted previously using an animal model and restricted maximum likelihood (REML). As Meyer (1991a) pointed out, multivariate animal models are of added value for traits with low heritability but high variability (such as reproduction), especially if those traits are correlated with highly heritable marker traits. The WP can be thought of as a marker. Since a measurement of coat color can be obtained shortly after birth, as well as other times during the life of an animal, knowledge of its relationship with economically important traits of dairy cattle is extremely important.

However, because WP measured on the upper body is not normally distributed and because heritability was slightly higher when transformed WP was studied (Becerril *et al.*, 1994a), WP was also transformed in the present study using the Guerrero and Johnson (1984) transformation.

Objectives of research reported here were to estimate genetic correlations between WP (untransformed and transformed) and MY and reproductive traits, using the relationship matrix and the animal model with a larger data set in several herds.

MATERIAL AND METHODS

Records of production and reproduction and registry certificates of 4293 first lactation heifers were used. Descriptions of registry certificate data are given

by Becerril and Wilcox (1992) and Becerril *et al.* (1993). Productive and reproductive data for each animal included MY, FY, and protein yield (PY), fat (FP) and protein (PP) percentages, days open (DO), and calving interval (CI).

Model and Analysis

To estimate (co)variances between WP and TWP (transformed WP) and productive and reproductive traits, the bivariate additive animal model used was:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} 1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} \mu \\ \beta_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

where y_1 is an $N \times 1$ vector of WP or TWP observations, y_2 is an $N \times 1$ vector of a productive or reproductive trait, N is the total number of cows with records, μ is the underlying mean, β_2 is a t vector of herd-year-season effects and covariables, a_1 and a_2 are $N \times 1$ vectors of additive genetic effects, e_1 and e_2 are $N \times 1$ vectors of random errors, 1 is the $N \times 1$ vector in which entries are all ones, X_2 is the $N \times t$ incidence matrix of fixed effects, and Z_1 and Z_2 are $N \times N$ incidence matrices of additive effects for each trait. First and second moments are defined as:

$$E \begin{bmatrix} y_1 \\ y_2 \\ a_1 \\ a_2 \\ e_1 \\ e_2 \end{bmatrix} = \begin{bmatrix} 1\mu \\ X_2\beta_2 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}$$

and

$$\text{Var} \begin{bmatrix} y_1 \\ y_2 \\ a_1 \\ a_2 \\ e_1 \\ e_2 \end{bmatrix} = \begin{bmatrix} Z_1 G_{11} Z_1 + R_{11} & & & & & \\ & Z_1 G_{12} Z_2 & & & & \\ & & Z_2 G_{22} Z_2 + R_{22} & & & \\ & & & & G_{11} & G_{12} & 0 & 0 \\ & & & & G_{22} & 0 & 0 & \\ & & & & & R_{11} & 0 & \\ & & & & & & & R_{22} \end{bmatrix}$$

symmetric

where $G_{11} = A \sigma_{a1}^2$, $G_{22} = A \sigma_{a2}^2$ and $G_{12} = A \sigma_{a12}$, for A , the additive relationship matrix, and σ_{a1}^2 , σ_{a2}^2 and σ_{a12} are the additive variances and covariance for the traits considered in each model; $R_{11} = I \sigma_{e1}^2$ and $R_{22} = I \sigma_{e2}^2$ where σ_{e1}^2 and σ_{e2}^2 are the residual variances. With traits measured at different times and assuming only additive genetic effects, the error covariance σ_{e12} could be assumed to be null. Normality assumptions are required to hold only for WP and TWP.

The REML estimates of (co)variance components and genetic parameters were obtained by a

derivative-free method (Meyer, 1991b) using Powell's method of conjugate gradients. Estimates of genetic correlation were assumed to be represented by the correlations of estimated breed values; hence, they may overestimate the genetic correlations.

RESULTS AND DISCUSSION

Genetic and phenotypic correlations between WP and other traits are presented in Table I. These correlations were estimated under the assumption that $R_{12} = |\sigma_{e12}| = 0$. Environmental covariances between WP and TWP and any other trait were assumed to be zero because WP was measured at a different time than the remaining traits. Moreover, if it is assumed that WP is constant throughout the animal's life (Briquet and Lush (1947) found very high repeatabilities between different ages), environmental factors affecting other traits would not affect WP. Heritabilities of all traits were very close to their univariate estimates (Becerril *et al.*, 1993). As shown in Table I, all genetic correlations were small, and most were close to zero. These results suggested that common additive genetic effects were small for WP and the other traits. These estimates disagreed with our previous results, in which genetic correlations were higher for FY and FP (-0.39 and -0.38) although a small data set, a single herd, and ordinary least squares analyses of variance were used (Becerril *et al.*, 1994b). As expected, phenotypic correlations were low, doubtless because of the same assumption; these correlations were lower but with same sign as the genetic correlations. All phenotypic correlations were close to zero.

Analyses of TWP then were performed; the results are in Table II. For both genetic and phenotypic correlations, changes were small, but still the correlations tended to be low; only DO showed an

appreciable increase to more than twice its first estimate. Correlations for FY, very close to 0 and although similar in size, changed sign; the rest kept the same sign.

Possible nonadditive genetic effects were suggested to be present by Becerril *et al.* (1994b), after estimating heritability of WP, although none were expected to be present. If these kinds of effects were important, not only for WP, but for other traits, an assumption of $\sigma_{e12} = 0$ would not account for that part of the environmental correlation explained by nonadditive genetic deviations. This assumption (restriction) was removed, in additional analyses, and estimates of correlations for WP were obtained using previous estimates of (co)variance components as initial values for REML iterations. Results are in Table III. Changes in genetic correlations did not follow a clear pattern. Correlations for MY, PY, PP, and DO decreased, but those for FY, FP, and CI increased. However, most estimates were close to zero. Phenotypic correlations followed the same pattern as genetic correlations, again with values that were close to zero.

The environmental correlations are noteworthy, and were larger for MY than any other correlation

Table II - Genetic and phenotypic correlations of transformed white coat percentages with production and reproduction traits.

Trait	Genetic correlation	Change ¹ (%)	Phenotypic correlation	Change ¹ (%)
Milk yield	0.100	3.0	0.051	8.5
Fat yield	-0.004	0	-0.002	0
Fat percentage	-0.097	7.8	-0.053	12.8
Protein yield	0.052	8.3	0.028	16.7
Protein percentage	-0.126	8.6	-0.080	14.3
Days open	-0.140	115.4	-0.027	125.0
Calving interval	-0.031	6.9	-0.008	14.3

¹Compared with untransformed white percentage (Table I).

Table I - Genetic and phenotypic correlations of untransformed white coat percentages with production and reproduction traits.

Trait	Correlations	
	Genetic	Phenotypic
Milk yield	0.097	0.047
Fat yield	0.004	0.002
Fat percentage	-0.090	-0.047
Protein yield	0.048	0.024
Protein percentage	-0.116	-0.070
Days open	-0.065	-0.012
Calving interval	-0.029	-0.007

Table III - Genetic, environmental, and phenotypic correlations of transformed white percentage with production and reproduction traits assuming that the environmental covariances are not zero.

Trait	Correlations		
	Genetic ¹	Phenotypic	Environmental
Milk yield	-0.068	0.034	0.181
Fat yield	-0.178	-0.016	0.169
Fat percentage	-0.136	-0.058	0.046
Protein yield	-0.042	0.017	0.107
Protein percentage	-0.031	-0.066	-0.140
Days open	0.006	-0.025	-0.056
Calving interval	-0.066	-0.009	0.018

¹Representing correlations of estimated breeding values.

estimated in this study. For other yield traits they also were positive (0.10), which was still low but not as close to zero. If it is assumed that the pure environmental part of the environmental correlation is zero (no heuristic evidence indicates otherwise), these environmental correlations could be due mostly to nonadditive genetic effects. For reproductive traits, DO and CI correlations were close to zero, although negative. These apparent discrepancies doubtless should be examined further.

CONCLUSIONS

Genetic and phenotypic correlations of WP with production and reproduction generally were low and close to zero. Transformation of WP to approach normality tended to increase the magnitude of estimates slightly, but correlations still were low. These results suggest that WP would not be an important trait to be considered if correlated responses for improving productive traits were expected from selection for WP (despite its high heritability) under current Florida dairy management conditions. Environmental correlations were expected to be 0, but when this assumption was dropped, changes in both genetic and phenotypic correlations occurred. However, most of them were still very close to zero. For fat traits, the genetic correlations were negative and higher. Since there is no apparent reason for environmental correlations to differ from zero, nonadditive genetic effects could be playing an important role in the relationships of WP with other traits.

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RESUMO

Correlações das medidas de porcentagem de cor branca do pêlo com cinco medidas de produção e duas

medidas de reprodução foram obtidas em 4293 Holsteins de primeira lactação em oito fazendas de gado da Flórida. As porcentagens de cor branca do pêlo foram analisadas tal como registradas e também após transformação por uma extensão dos procedimentos Box-Cox. As análises estatísticas foram feitas por REML sem derivativo, com um modelo animal. As correlações fenotípica e genética de porcentagem de branco (não transformada) foram: com produção de leite, 0,047 e 0,097; com produção de gordura, 0,002 e 0,004; com porcentagem de gordura, -0,047 e -0,090; com produção de proteína, 0,024 e 0,048; com porcentagem de proteína, -0,070 e -0,116; com período de serviço, -0,012 e -0,065 e com intervalo entre partos, -0,007 e -0,029. As alterações na magnitude de correlações foram muito pequenas para todas as variáveis, exceto período de serviço. As correlações genética e fenotípica de valores transformados com período de serviço foram -0,027 e -0,140. Respostas correlacionadas levemente positivas seriam esperadas para porcentagem de cor branca de pêlo após seleção direta para produção de leite, gordura e proteína, mas a seleção para porcentagens de gordura e proteína, para período de serviço ou para intervalo de procriação levaria a pequenas reduções.

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