J. Dairy Sci. 88:3886–3893

Effects of Week of Lactation and Genetic Selection for Milk Yield on Milk Fatty Acid Composition in Holstein Cows*

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ABSTRACT

Control (CL) and select line (SL) dairy cows (n = 22) managed identically but differing in milk yield (>4100 kg/305 d) were used to determine differences in milk fatty acid profile as lactation progressed. Milk yield was recorded daily and milk samples were collected during wk 1, 4, 8, 12, and 16 postpartum for milk composition analysis. Milk samples from wk 1, 8, and 16 were also analyzed for fatty acid composition. Select-line cows produced more milk (44.4 vs. 31.2 kg/d) and milk components than CL cows during the 16-wk period. There was no difference in rate of milk yield increase, but peak milk yield for SL cows was greater and occurred later in lactation. There were no differences in milk SCC or milk fat, protein, or lactose content. Selection for milk yield did not affect the content of most individual milk fatty acids; however, compared with CL, SL cows had a reduced Δ^9-desaturase system and tended to produce milk with lower monounsaturated fatty acid content. Selection for milk yield did not affect milk fatty acid origin but the percentage of de novo fatty acids increased and preformed fatty acids decreased as lactation progressed. Milk fat *trans*-11 18:1 and *cis*-9,*trans*-11 conjugated linoleic acid increased with progressing lactation (10.7 vs. 14.1 and 3.1 vs. 5.4 mg/g, or 31 and 76%, respectively) and were correlated strongly among wk 1, 8, and 16 of lactation. Temporal changes in the Δ^9-desaturase system occurred during lactation but these changes were not correlated with milk fat *cis*-9,*trans*-11 conjugated linoleic acid content. Results indicate prolonged genetic selection for milk yield had little effect on milk fatty acid composition, but milk fatty acid profiles varied markedly by week of lactation.

(**Key words:** conjugated linoleic acid, milk fat, genetic selection, dairy cow)

Abbreviation key: CL = low-merit control line, **CLA** = conjugated linoleic acid, **SL** = high-merit select line, **VA** = vaccenic acid (*trans*-11 18:1), **WOL** = week of lactation.

INTRODUCTION

Genetic selection of dairy cattle during the last half century has primarily focused on yield traits. The impact of this intense selection for milk yield is expected to decrease component content (Kelm et al., 2000); and our previous studies suggest selection for milk yield has slightly decreased milk fat content (B. A. Crooker, personal communication, 2005), but effects on milk fatty acid profiles have not been reported.

Milk fatty acid content is known to be governed by unique rumen-derived fatty acids (Bauman et al., 2000, 2001) and to vary with stage of lactation and among individual cows (Palmquist et al., 1993). Cows that produce more milk consume more feed, which increases digestive tract passage rates and alters rumen microbial populations (Van Soest, 1982). In addition, homeorhetic mechanisms responsible for the coordinated alterations in tissue metabolism that occur with the onset of lactation may also partition a greater proportion of dietary and tissue-derived nutrients toward milk synthesis. These alterations (rumen and metabolic) could affect the relative contribution of preformed and de novo fatty acids in milk fat from low- and high-merit cows. Selection for increased milk yield therefore has potential to affect milk fatty acid content by altering rumen dynamics and by increasing the magnitude and duration of postpartum tissue mobilization.

Milk fatty acid composition is important for both milk processing and human health. Increased fatty acid unsaturation can lead to oxidization problems for milk product manufacturers, and fatty acids such as conjugated linoleic acid (**CLA**) and *trans*-11 18:1 (vaccenic acid; **VA**) have been linked with health benefits in animal models including reduced incidence of diabetes,

Received March 3, 2005.
Accepted July 8, 2005.
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*This work partially supported by the University of Arizona Experiment Station #ARZT-136339-H-24-130 and the University of Minnesota Experiment Station (project number 16-46 and Regional Project NE-148).

atherosclerosis, obesity, and cancer (Belury, 2002; Corl et al., 2003).

Recent research focused on enhancing milk fat CLA concentrations has demonstrated that dietary manipulations can alter CLA content at least 5-fold (Bauman et al., 2001; Chilliard et al., 2001). However, large individual animal variation in milk fat CLA content exists (Kelly et al., 1998; Bauman et al., 2001) and the effects of stage of lactation on CLA content are not clear, as some report an increase in CLA content as lactation progresses (MacGibbon et al., 2001; Auldist et al., 2002) and others do not (Kelsey et al., 2003).

The *cis*-9,*trans*-11 CLA isomer is produced primarily from endogenous conversion of VA, a biohydrogenation intermediate of linoleic and linolenic acid, via the enzyme Δ^9-desaturase (Corl et al., 2001; Kay et al., 2004). Although a small amount of milk fat *cis*-9,*trans*-11 CLA originates from the rumen, the 2 main factors believed to influence milk fat *cis*-9,*trans*-11 CLA concentration are substrate (VA) availability and mammary Δ^9-desaturase activity and/or expression (Bauman et al., 2001).

Because the most dramatic changes in milk fatty acid content occur during early lactation, study objectives were to determine effects of week of lactation (**WOL**) and selection for increased milk yield on production measures and milk fatty acid composition during the first 16 wk of lactation.

MATERIALS AND METHODS

Animal Management and Feeding

Multiparous cows from 2 genetic lines of Holsteins were maintained under identical environment and management practices in free-stall facilities at the University of Minnesota Southeast Experiment Station (Waseca, MN). Development of the static, low-merit control line (**CL**) and the contemporary, high-merit select line (**SL**) was initiated in 1964 by Charles Young as a component of a multistate, North Central regional project (NC-2; Hansen, 2000). The original foundation cows were paired by genetic merit and assigned to either low- or high-merit line. The high-merit cows and their female descendants have been inseminated with semen from the highest PTA for milk (PTA-milk) sires (n = 4) available each year. From 1964 to 1991, the low-merit cows and their female descendants were bred with semen from 20 sires (4 sires/yr in a 5-yr rotation) that were breed-average for PTA-milk in 1964. Since 1991, breeding the low-merit cows and their female descendants has continued according to the original design except that semen has been from sons of the original 20 low-merit bulls. Genetic merit for milk yield by low-merit cows has remained stable, whereas genetic merit of high-merit cows has continued to increase (Jones et al., 1994). Coefficients of inbreeding are not allowed to exceed 6.25% for low or high-merit cows (Hansen, 2000).

Table 1. Ingredients and formulated composition of the diet.

Item	Contribution
Ingredients (% of DM)	
Alfalfa haylage	30.3
Corn silage	19.6
Ground corn	21.8
Soybean meal/vitamin/mineral mix[1]	13.8
Whole cottonseed	9.7
Alfalfa hay	4.8
Formulated composition	
Dry matter (%)	54.8
CP (% of DM)	17.3
NDF (% of DM)	30.1
ADF (% of DM)	21.1
NE_L (Mcal/kg DM)	1.71

[1]Soybean meal-vitamin-mineral mix contained 5.7% distillers grain, 2.8% soybean meal, 1.5% blood meal, 0.8% sodium bicarbonate, 0.6% limestone, 0.6% tallow, 0.6% Megalac (Church and Dwight Co., Inc., Princeton NJ), 0.3% yeast, 0.3% potassium chloride, 0.2% trace mineral salt, 0.2% magnesium oxide, 0.1% vitamin A, D, and E, 0.1% dicalcium phosphate, and 0.04% niacin.

Milk yield of the multiparous CL (6890 ± 403 kg/305-d lactation) and SL (11,078 ± 329 kg/305-d lactation) cows differed by more than 4100 kg during this study. Cows (10 CL, 12 SL; calving within a 5-mo period) from 7 CL sires and 10 CL dams and from 8 SL sires and 12 SL dams were fed the same TMR. The TMR was formulated to meet predicted requirements of cows in early lactation (NRC, 2001; Table 1) and ingredients and formulated composition did not differ (data not shown) during the experiment. Dry matter intakes were not measured in the present study; however, previous data (Crooker et al., 2001) using the same herd indicated that SL cows consume more feed than their CL counterparts.

Data Collection and Sample Analyses

Cows were milked at 12-h intervals. Milk yield was recorded daily, and weekly averages were used for statistical analysis. Twice-daily milk samples were obtained from each cow on 1 d during wk 1, 4, 8, 12, and 16 of lactation. Milk samples from morning milkings were analyzed for fat, lactose, and protein by infrared spectroscopy and for somatic cells by a cell counter (Minnesota DHIA Laboratory, Zumbrota, MN). Evening milk samples from wk 1, 8, and 16 were stored at –20°C without preservative and analyzed for fatty acid composition.

Fatty Acid Analysis

Milk fat was extracted according to Hara and Radin (1978) and fatty acid methyl esters were prepared by