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Performance of Lactating Dairy Cows Fed Silage and Grain from a Maize Hybrid with the *cry*1F Trait Versus its Nonbiotech Counterpart

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ABSTRACT

Effects of feeding grain and maize silage from a non-Bt maize and a variety of Bt maize that contains *cry*1F (event TC1507, event DAS-Ø15Ø7-1), a gene that provides maize with insect resistance, on the health and performance of dairy cows were evaluated. In a crossover trial, 20 lactating Holstein cows were assigned to each of 2 dietary treatment groups and fed diets containing whole-plant maize silage plus maize grain from TC1507 or its near-isoline counterpart (control). Each period of the crossover trial lasted 28 d and was preceded by a 7-d adjustment period. To minimize variability due to stage of lactation, 2 blocks of 10 cows at 90 to 130 d of lactation at the start of the trial were used. Within each dietary treatment, 10 cows were from each of 2 genetic selection lines (high and average fat plus protein predicted transmitting ability). Diets were formulated to be isocaloric and isonitrogenous. Dry matter intake and daily production of milk, fat, protein, lactose, nonfat solids, and total solids did not differ between cows fed the TC1507 diet and cows fed the control diet. Furthermore, milk from cows in different dietary treatment groups did not differ in milk urea nitrogen concentration or somatic cell count. For milk fat percentage, a significant dietary treatment by genetic group interaction was detected although overall yield of milk and solids-corrected milk did not differ with diet. Physical measures of cow health including body weight, body condition score, temperature, pulse, and respiration rate were collected weekly; dietary treatment group means for these measures were not different. Blood chemistry and hematological analyses were conducted using blood samples collected from cows before the start of the trial and at the end of each period. Overall, the TC1507 and control groups did not differ in any of these indices of health status. Further, hematological profiles for cows in the dietary treatment groups were not different. In summary, no differences were detected in milk production, milk composition, or cow health as indicated by physical measures, blood chemistry, and hematological analyses between dairy cows fed diets containing maize grain plus whole-plant maize silage from TC1507 and dairy cows fed grain plus silage from its near-isoline counterpart.
Key words: *cry*1F gene, maize grain, maize silage, dairy cow

INTRODUCTION

Bacillus thuringiensis (**Bt**) is a common soil bacterium that produces proteins that are toxic to certain Lepidopteran pests. A new generation biotech maize (*Zea mays* L.) hybrid containing the *cry*1F gene (event TC1507) from *Bacillus thuringiensis* var. *aizawai* and the phosphinothricin acetyltransferase (*pat*) gene from *Streptomyces viridochromogenes* has been developed. The *cry*1F gene encodes the Cry1F protein that is insecticidal toward several lepidopteran pests of maize, including European corn borer, southwestern corn borer, fall armyworm, black cutworm, corn earworm, and western bean cutworm. The expressed PAT protein confers *in planta* tolerance to herbicides that contain the active ingredient glufosinate-ammonium (e.g., Liberty, Bayer Crop Science, Research Triangle Park, NC). This trait was developed through collaboration between Pioneer Hi-Bred International Inc. (Johnston, IA) and Dow AgroSciences LLC (Indianapolis, IN).

Maize serves as the major source of both energy and forage in diets for dairy cows in the United States. The use of biotech maize hybrids enhances yield under conditions of insecticidal pressure in the midwestern United States. Previous research by Faust and Miller (1997) and Folmer et al. (2002) demonstrated similar performance of dairy cows fed diets containing transgenic maize expressing the Cry1Ab protein from Bt events compared with diets containing their non-transgenic counterparts.

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The purpose of this study was to investigate dairy cow performance (milk and component yields) and health status of cows when fed a TMR containing silage plus grain produced from maize plants containing the *cry*1F gene (**TC1507**) vs. maize silage plus grain from plants of a similar genetic background, but not containing the *cry*1F gene.

MATERIALS AND METHODS

Maize Grain and Silage Sources

Pioneer Hi-Bred, a DuPont business (Johnston, IA) supplied maize grain and silage used in this study. Grain came from 2 isolated fields (separated by 201 m) in Richland, Iowa; forage was produced from the same 2 hybrids as the grain in 2 isolated fields near Polk City, Iowa. The TC1507 maize grain and forage came from plants that received 2 sequential applications of glufosinate-ammonium herbicide (Liberty, Bayer Crop Science, Research Triangle Park, NC). The respective maize forages were custom harvested, delivered to the Iowa State University Dairy (Ankeny, IA), and ensiled in separate Ag Bags (Miller-St. Nazianz, St. Nazianz, WI) awaiting the start of the lactation study. Forages were harvested on September 27, 2001, with all equipment being cleaned between hybrids to prevent cross-contamination. Length of cut of forage was within the recommend range of 10 to 19 mm (Mueller et al., 1987; Roth and Heinrichs, 2001), with kernels being processed. Samples of harvested forage were submitted to Dairyland Labs (Arcadia, WI) for particle size analysis (ASAE, 2001) and analysis by wet chemistry methods for the following nutrients: moisture (AOAC, 1995), CP (AOAC, 1995), crude fat (AOAC, 1995), ADF, NDF, and lignin (Goering and Van Soest, 1970), ash (AOAC, 1995), calcium, phosphorus, magnesium, potassium (AOAC, 1995), and starch (determined with a YSI 2700 Select Biochemistry Analyzer; Application Note 322, YSI Incorporated, Yellow Springs, OH).

Diet Components, Preparation, Administration, and Sampling

Two separate diets were prepared (Table 1) using whole-plant maize silage plus maize grain from either TC1507 or its near-isoline counterpart (Pioneer hybrid 33P66; control). Diets were formulated to meet or exceed all nutrient requirements for the lactating dairy cow (NRC, 2001). Soybean meal and whole cottonseed used in this trial were obtained from plants that were not transgenic. Maize grains and silages were analyzed for the presence of Cry1F protein using a specific ELISA to ensure that identity preservation was maintained throughout the study (Pioneer Hi-Bred). Grains were sampled before the start of the trial and submitted for wet chemistry analysis (Dairyland Labs) for the previously listed nutrients with the exceptions of lignin, starch, and ash. Silages were sampled before the start of the trial and submitted (Dairyland Labs) for wet chemistry analysis for the previously listed nutrients, protein solubility (Krishnamoorthy et al., 1982), acid detergent insoluble CP determined by analyzing ADF residues for nitrogen (AOAC, 1995), pH (Eaton et al., 1995; method 4500-H+), and fermentation products by HPLC (Siegfried et al., 1984, with modification). Samples of grains and silages were also submitted for mycotoxin analysis (North Dakota State University Veterinary Diagnostic Laboratory, Fargo). *Fusarium* mycotoxins in grains and silages (nivalenol, deoxynivalenol, 3-acetyldeoxynivalenol, 15-acetyldeoxynivalenol, fusarenon X, diacetoxyscirpenol, scirpentriol, 15-acetoxyscirpentriol, T-2 toxin, iso-T-2 toxin, acetyl-T-2 toxin, T-2 triol, t-2 tetraol, HT-2 toxin, neosolaniol, zearalenol, and zearalenone) were analyzed as trimethylsilyl ester derivatives of tricothecenes and estrogens by GC-MS (Shimadzu QP5050, Tokyo, Japan; Raymond et al., 2003); aflatoxins were derivatized with trifluoroacetic acid, and fumonisins were derivatized with *o*-phthaldialdehyde and analyzed in grain samples by HPLC (Luna C18, Phenomenex, Torrance, CA, and Discovery C18, Supelco, Bellefonte, PA, respectively).

Diets were formulated based on the analyses of respective silages and grains and average milk production

Table 1. Ingredient composition of diets formulated with whole-plant maize silage plus maize grain from TC1507 or control plants[1]

	Diet	
Ingredient, g/kg of diet DM	TC1507	Control
Maize silage	302.0	299.0
Concentrate mix[2]	385.0	382.0
Soybean meal	43.0	52.0
Whole cottonseed	90.0	89.0
Alfalfa hay	174.0	173.0
Dairy Supreme premix[3]	6.0	6.0

[1]TC1507 = maize plants containing the *cry*1F gene; Control = maize plants isogenic to TC1507 but not containing the *cry*1F gene.

[2]Concentrate mix contained percentage as-fed: ground maize, 70.2; Zinpro 4-Plex (Zinpro Corporation, Eden Prairie, MN), 0.068; fish meal, 2.7; animal fat, 1.4; soybean hulls, 4.5; sodium bicarbonate, 1.1; salt, 0.906; magnesium oxide, 0.226; limestone, 2.7; selenium, 0.226; urea, 1.1;vitamin E, 0.091; and AminoPlus (Ag Processing Inc., Omaha, NE), 14.7.

[3]Dairy Supreme premix (Land O'Lakes, St. Paul, MN): calcium (minimum 146,000 mg/kg); phosphorus (minimum 110,000 mg/kg); magnesium (minimum 60,000 mg/kg); potassium (minimum 30,000 mg/kg); sulfur (minimum 40,000 mg/kg); zinc (minimum 6,440 mg/kg); manganese (minimum 4,315 mg/kg); iron (minimum 1,160 mg/kg); copper (minimum 1178 mg/kg); iodine (minimum 99 mg/kg); cobalt (30 mg/kg); selenium (35.0 mg/kg) vitamin A (minimum 660,000 IU/kg); vitamin D3 (minimum 132,000 IU/kg); and vitamin E (minimum 2640 IU/kg).

of groups. Fresh feed was prepared daily and cows were fed diets as a TMR twice per day at 0730 and 1630 h. Cows were fed an excess of feed daily (8 to 10%) to ensure that feed was available at all times; refusals were collected, sampled, and discarded every third day. Duplicate weekly samples of silages, grains, and diets were composited by sample type to form representative samples for each feeding period. Pooled samples of refusals were collected weekly throughout the experiment for each diet and composited for analysis to determine whether any preferential sorting of feed was evident. All samples were analyzed (Dairyland Labs) for moisture, CP, crude fat, ADF, NDF, calcium, phosphorus, magnesium, and potassium by wet chemistry methods described previously.

Dairy Cow Lactation Period

Twenty Holstein cows from a dairy herd composed of 2 genetic groups were used in this trial using a crossover design. The genetic groups consisted of cows with either high or average genetic merit for PTA for milk fat and protein yield. Based on the variance observed in previous trials, the number of animal replicates per treatment, when fed individually, was determined to be adequate to detect at $P < 0.05$, a 5 to 10% difference between treatment means 80% of the time. This sensitivity is comparable to current guidelines published by the International Life Sciences Institute (2003). The trial consisted of two 28-d feeding periods replicated in 2 blocks. Each period was preceded by a 7-d acclimation period (pretrial and transition). Cows received the alternate diet during the second period. Two blocks in time were used to minimize differences among cows in days of lactation. Ten cows (6 with high genetic merit and 4 with average genetic merit) were selected according to DIM (91 to 129) for each block. Five cows within each block (3 from the high and 2 from the average genetic merit group) were assigned randomly to their respective treatment. Diet groups were equalized based on previous milk production, parity of cows (second parity and greater), and genetic group (3 cows with high genetic merit and 2 cows with average genetic merit per diet group within each block). The first block of cows was on trial from February 3, 2002, to April 7, 2002; the second block was on trial from March 9, 2002, to May 11, 2002.

Healthy cows with no metabolic disorders, mastitis, or udder conformation limitations were selected for this study. Management and care for cows in this experiment followed all guidelines recommended by FASS (1999). In addition, a protocol for the trial was filed with and approved by the Iowa State University (**ISU**) Animal Care and Use committee. A veterinarian from the Veterinary and Diagnostic Production Animal Medicine unit of the ISU College of Veterinary Medicine removed 1 cow from the trial during the last 2 wk of the second period after clinical examination. The cause of removal, chronic endometritis, was determined to not be diet related. Removal date, BW, BCS, and feed refusals were recorded when this cow was removed from the study. Data from this animal were excluded from statistical analysis.

Cows were housed in a free-stall barn bedded with sand and were trained to use individual Calan gate feeders (American Calan, Northwood, NH) before the start of the trial. Daily milk production was recorded. Health and physical characteristics measured included BW, body temperature, pulse rate, respiration rate, and BCS. These measurements were collected on consecutive Fridays before and during the trial; measurements collected before the start of the trial were used to establish baseline values. Cows were monitored regularly for mastitis and other abnormal health conditions. All health treatments and abnormal health observations were recorded. Routine treatments including vaccinations required by standard operating procedures at the farm were used. Posilac (bST) was not used in this study.

Clinical Chemistry and Hematology Assays

Blood samples were collected 7 d before the start of the trial and at the end of each experimental period (d 28 and 63, respectively). Pretrial samples were collected to establish baseline values. Serum and plasma samples were submitted for clinical chemistry profile and hematological analyses (ISU Veterinary Medicine Clinical Pathology Laboratory, Ames) to assess the health status of the cows during the experiment. Milk samples were collected on consecutive Fridays before and during the trial. Milk samples collected twice daily during each milking period were composited into a single daily sample per cow for analyses. These daily milk samples were submitted to Dairy Lab Services (Dubuque, IA) for compositional analysis (fat, protein, solids, lactose, SCC, and MUN) using infrared procedures (Foss North America, Eden Prairie, MN). Fat-corrected milk (3.5%) was calculated according to the Gaines formula with adjustments as described by Stoddard (1980); ECM was calculated using the formula described by Bernard (1997); SCM was calculated according to Tyrrell and Reid (1965).

Statistical Analysis

Results of nutrient analyses for all dietary ingredients, totally mixed diets, and refusals, along with pre-

Table 2. Nutrient composition of maize grain, harvested whole plant maize fresh forage and fermented forage[1]

Item	Maize grain		Fresh maize forage		Fermented maize forage	
	TC1507	Control	TC1507	Control	TC1507	Control
Particle size, mm	—	—	11.2	10.9	9.4	9.2
Nutrient analysis of maize grain, harvested whole plant maize forage, and silage						
pH	—	—	—	—	3.79	3.89
DM, g/kg	862.7	857.7	375.8	420.2	422.4	450.8
	g/kg					
CP	79.7	73.6	80.6	75.0	88.1	86.4
Acid detergent insoluble CP	—	—	—	—	7.1	8.2
Crude fat	44.9	41.7	29.4	30.4	31.7	31.7
ADF	42.6	39.4	258.1	264.7	277.7	294.4
NDF	90.3	80.8	461.4	380.4	439.5	452.5
Calcium	0.2	0.2	3.0	2.5	2.5	2.7
Phosphorus	3.1	3.1	1.7	1.9	2.2	2.2
Magnesium	1.4	1.4	3.2	2.8	2.2	2.4
Potassium	4.4	4.1	3.4	4.4	8.2	8.1
Lignin	—	—	53.5	33.6	33.4	36.6
Starch	—	—	289.3	335.1	261.8	265.1
Ash	—	—	32.5	36.5	48.0	50.8
Protein solubility, % of CP	—	—	—	—	43.87	41.70

[1]TC1507 = maize plants containing the *cry*1F gene; Control = maize plants isogenic to TC1507 but not containing the *cry*1F gene.

trial health and physical measures, milk production and components, and blood chemistry and hematology values, were summarized using PROC MEANS of SAS (version 8.2; SAS Institute Inc., Cary, NC). Cow performance, milk production and composition, and blood chemistry data were analyzed as a 2-period cross-over design using PROC MIXED of SAS. The model's fixed effects consisted of dietary treatment, genetic group, treatment × genetic group, sequence of treatment, and treatment × sequence; cow (genetic group block sequence) and block were treated as random effects. Planned comparisons were by Fisher's Protected Least Significant Difference; differences between treatment means were considered significant at $P < 0.05$.

RESULTS AND DISCUSSION

Maize Grain and Silage Characterization

Nutrient composition and fermentation analysis (Table 2 and Table 3, respectively) revealed that maize grain and silage components of TC1507 and control were similar. The slightly greater DM content of maize silage from the control compared with the TC1507 maize (450.8 vs. 422.4 g/kg of DM) parallels the difference in DM at harvest (420.2 vs. 375.8 g/kg of DM) and presumably reflects greater European corn borer infestation of the control maize. Mycotoxin analyses revealed a small amount of vomitoxin (0.7 to 1 mg/kg) and fumonisin (3 mg/kg, maize grain only) present in both TC1507 and control silage and grain. Concentrations in grain and silage were below the Food and Drug Administration action levels of 5 and 30 mg/kg, respectively, for dairy cows (FDA 2000). Presence of the expressed Cry1F protein was confirmed in TC1507 maize grain and maize silage. Concentrations of Cry1F protein in the control maize grain or silage for both blocks of cows during both feeding periods were below the level of detection. The absence of Cry1F protein in control grain and silage reflects adequate isolation of crops in the field (separation of 201 m) as well as proper care during harvest and storage to avoid cross-contamination.

Diet and Refusal Composition

Results of nutrient analyses of diets and refusals from each diet are shown in Table 4. Diets were similar in

Table 3. Fermentation products of whole plant maize fermented forage[1]

Item	Fermented maize forage	
	TC1507	Control
	g/kg	
Ammonia nitrogen	7.3	6.7
Lactic acid	37.5	31.7
Acetic acid	12.4	14.6
Propionic acid	0.0	2.1
Butyric acid	0.0	0.0
Isobutyric acid	0.0	0.0
Ethanol	0.9	1.6

[1]TC1507 = maize plants containing the *cry*1F gene; Control = maize plants isogenic to TC1507 but not containing the *cry*1F gene.

Table 4. Analyzed nutrient compositions of diets formulated with whole plant maize silage plus maize grain from TC1507 or control plants,[1] and diet refusals

	Diet		Diet refusals	
Item	TC1507	Control	TC1507	Control
DM, g/kg	603.2	633.2	571.7	609.3
	g/kg			
CP	164.5	164.2	157.3	143.6
Crude fat	48.0	46.7	50.4	42.6
ADF	234.1	227.2	297.8	330.8
NDF	322.4	331.6	404.1	458.8
Calcium	11.2	11.6	10.6	8.9
Phosphorus	4.4	4.6	4.3	3.7
Magnesium	3.8	3.8	3.8	3.4
Potassium	15.6	12.1	13.8	14.3

[1]TC1507 = maize plants containing the *cry*1F gene; Control = maize plants isogenic to TC1507 but not containing the *cry*1F gene.

nutrient composition. Fiber analyses of diet refusals indicated that some preferential sorting occurred; this was not considered to be related to treatment because sorting occurred with cows fed both diets.

Lactation Performance

Results of animal measurements and milk production are presented in Table 5. Cows fed the treatment diets were similar in all measures demonstrating that diet did not affect BW, BCS, temperature, pulse rate, or respiration rate. This is similar to results of previous trials in which no differences in BCS were detected when dairy cows were fed either genetically enhanced maize silage (Grant et al., 2003; Ipharraguerre et al., 2003) or genetically modified whole cottonseed (Castillo et al., 2001). Effects of feeding genetically modified feedstuffs on pulse and respiration rate of lactating dairy cows have not been reported previously. Cows fed the treatment diets did not differ in DMI, daily milk produc-

Table 5. Physical measures, milk production and production efficiency, and milk components of cows fed diets containing maize silage plus maize grain from TC1507 or control plants[1,2]

		Diet		
Item	Pretrial	TC1507	Control	SEM
Physical measures				
BW, kg	638.3	659.2	657.4	13.1
BCS	3.13	3.06	3.06	0.08
Body temperature, °C	38.7	38.6	38.6	0.1
Pulse, beats per minute	66.3	69.2	68.9	0.8
Respiration, breaths per minute	31.1	32.7	33.4	3.5
Milk production, kg/d				
DMI, kg/d	—	27.1	27.9	0.8
Daily milk	39.0	38.9	38.6	1.4
FCM	40.2	39.3	39.6	1.4
ECM	39.2	38.6	38.8	1.3
SCM	37.0	36.4	36.8	1.2
Production efficiency, kg of milk/kg of feed				
Milk efficiency	—	1.44	1.40	0.05
FCM efficiency[3]	—	1.46	1.44	0.05
Milk component, g/kg				
Protein	29.4	30.0	29.9	0.5
Fat[4]	37.3	36.1	36.5	1.4
Total solids	124.5	123.6	124.9	2.1
Other solids	59.4	58.0	57.6	0.7
Lactose	49.4	48.5	48.6	0.7
Milk component yield, kg/d				
Protein[3]	1.14	1.16	1.15	0.03
Fat	1.44	1.39	1.41	0.06
Total solids	4.83	4.79	4.82	0.21
Other solids	2.30	2.26	2.22	0.08
Lactose	1.92	1.89	1.87	0.07
Other milk components				
MUN, mg/dL	18.6	19.1	18.7	1.2
SCC, ×1,000	144.0	206.1	202.8	51.1

[1]TC1507 = maize plants containing the *cry*1F gene; Control = maize plants isogenic to TC1507 but not containing the *cry*1F gene.

[2]Treatment means did not differ ($P < 0.05$).

[3]Genetic group effect ($P < 0.05$).

[4]Treatment × genetic group interaction ($P < 0.05$).

Table 6. Chemical profile of blood samples collected from cows fed diets containing maize silage plus maize grain from TC1507 or control plants[1,2]

Item	Pretrial	Diets: TC1507	Diets: Control	SEM	Reference interval[3]
Sodium, mEq/L	140.7	141.8	141.2	0.6	132.0–152.0
Potassium, mEq/L	4.55	4.71	4.55	0.13	3.9–5.8
Chloride, mEq/L	99.8	99.8	99.4	1.0	100.0–115.0
Calcium, mg/dL	9.48	9.32	9.34	0.16	8.0–11.4
Phosphorus, mg/dL	5.48	7.39	7.22	0.35	5.6–8.0
Magnesium, mEq/L	2.25	2.33	2.39	0.06	1.50–2.90
Total carbon dioxide, mEq/L	27.8	25.5	25.4	0.5	21.0–31.0
BUN, mg/dL	20.6	23.2	20.5	2.1	10–25
Creatinine, mg/dL	0.76	0.95	0.86	0.10	0.1–1.8
Glucose, mg/dL	64.8	62.5	63.0	1.0	40.0–100.0
Total protein, g/dL	8.24	7.82	7.80	0.18	6.7–7.5
Albumin, g/dL	3.76	3.55	3.54	0.06	2.5–3.8
Aspartate aminotransferase, IU/L	94.8	100.4	95.3	5.4	55.0–125.0
Creatinine kinase, IU/L	235.1	212.8	203.0	29.5	1.0–350.0
Alkaline phosphatase, IU/L	44.6	41.7	42.3	2.9	25.0–250.0
Gamma glutamyltransferase, IU/L	32.5	27.8	28.2	1.9	1–50
Total bilirubin, mg/dL	0.17	0.19	0.17	0.03	0.10–1.60
Hemolytic indices, mg/dL	23.6	61.4	40.3	17.0	0–50
Lipemic indices, mg/dL	2.80	4.79	5.01	1.63	0–50
Icteric indices, mg/dL	1.05	0.44	0.40	0.12	0–2
Anion gap, mEq/L	17.8	21.4	20.9	0.5	NA[4]

[1]TC1507 = maize plants containing the *cry*1F gene; Control = maize plants isogenic to TC1507 but not containing the *cry*1F gene.

[2]Treatment means did not differ ($P < 0.05$).

[3]Reference intervals established at ISU Veterinary Medicine Clinical Pathology Laboratory, Ames, IA.

[4]NA = not available.

tion, or efficiency of production of FCM. Similarly, lactation performance of dairy cows was not altered by feeding Bt maize and silage (Folmer et al., 2002) or genetically modified whole cottonseed (Castillo et al., 2001). Dry matter intakes were high, reflecting the time of year that the trial was conducted (late winter through early spring) when requirements for NE_M are higher.

Milk Composition

Milk nutrient composition (Table 5) was similar between the 2 dietary treatment groups for all components measured. As expected, cows with high genetic merit for protein produced more milk protein per day than cows with average genetic merit (1.16 vs. 1.15 kg/d). A dietary treatment by genetic group interaction ($P < 0.05$) was observed for fat percentage in milk due to a greater difference between genetic groups when fed the control diet (38.2 and 34.8 g/kg for high and average groups, respectively) than when fed the TC1507 diet (35.8 and 36.4 g/kg for high and average groups, respectively). Within genetic groups, values between cows fed TC1507 and control were not significantly different. When fat percentage was averaged across genetic groups, the difference in fat content associated with diet (36.1 g/kg for cows fed the TC1507 diet vs. 36.5 g/kg for cows fed the control diet) was also not significant. Dietary treatment did not affect protein, total solids, other solids, lactose, or MUN concentrations or SCC. Donkin et al. (2003) similarly observed no change in milk composition when lactating cows were fed Bt (MON810)/glyphosate-tolerant (GA21) maize hybrids. Milk urea nitrogen values, although slightly above the recommended herd average range of 12 to 18 mg/dL (Drudik et al., 2007), may be typical for this herd as indicated by the high values during the preliminary period.

Blood Chemistry and Hematology

Results of blood chemistry and hematological analyses are presented in Tables 6 and 7, respectively. No significant treatment effect was observed for any of these traits. Values for most measures fell within the reference intervals for lactating dairy cows established by the ISU Veterinary Medicine Clinical Pathology Laboratory. Chloride values of pretrial, TC1507, and control samples and phosphorus values pretrial all fell below the lower limit of the reference interval. Total protein, mean corpuscular hemoglobin concentration, red cell distribution width, plasma protein, and fibrinogen values for cows fed TC1507 or control diets were above the upper limit of the reference intervals. However, pretrial values for those measures were also above the

Table 7. Hematological profile of blood samples collected from cows fed diets containing maize silage plus maize grain from TC1507 or control plants[1,2]

Item	Pretrial	Diet: TC1507	Diet: Control	SEM	Reference interval[3]
White blood cells, $\times 10^3/\mu L$	8.48	8.29	8.05	0.83	4.0–12.0
Red blood cells, $\times 10^6/\mu L$	6.15	6.35	6.29	0.12	5.0–10.0
Hemoglobin, g/dL	10.2	10.3	10.3	0.2	8.0–15.0
Hematocrit, %	27.7	28.0	27.8	0.5	24.0–46.0
Mean corpuscular volume, fL	45.1	44.2	44.2	0.5	40.0–60.0
Mean corpuscular hemoglobin, pg	16.7	16.2	16.3	0.2	11.0–17.0
Mean corpuscular hemoglobin concentration, g/dL	36.9	36.7	36.9	0.1	30.0–36.0
Automated platelet count, $\times 10^3/\mu L$	447.4	433.0	467.1	27.4	100–800
Neutrophils, $\times 10^3/\mu L$	3.35	3.36	3.03	0.25	0.6–4.0
AB BAND, $\times 10^3/\mu L$	0.008	0.003	0.005	0.006	0–0.12
Lymphocytes, $\times 10^3/\mu L$	4.39	4.28	4.50	0.66	2.5–7.5
Monocytes, $\times 10^3/\mu L$	0.46	0.32	0.24	0.05	0.1–0.9
Eosinophils, $\times 10^3/\mu L$	0.22	0.28	0.23	0.06	0.0–2.4
Basophils, $\times 10^3/\mu L$	0.05	0.05	0.04	0.02	0.0–0.2
Red cell distribution width, %	20.3	20.0	20.0	0.3	8.0–15.0
Mean platelet volume, fL	5.15	5.28	5.27	0.17	0.0–99.9
Nucleated red blood cells/100 cells	0.00	0.00	0.05	0.04	NA[4]
Plasma protein, g/dL	8.26	8.11	8.07	0.16	6.9–7.7
Fibrinogen, mg/dL	590.0	550.0	523.7	92.2	100–500

[1]TC1507 = maize plants containing the *cry*1F gene; Control = maize plants isogenic to TC1507 but not containing the *cry*1F gene.

[2]Treatment means did not differ ($P < 0.05$).

[3]Reference intervals established at ISU Veterinary Medicine Clinical Pathology Laboratory, Ames, IA.

[4]NA = not available.

upper limits and values did not differ ($P < 0.05$) between the TC1507 and control groups. Hemolytic indices from the TC1507 treatment were above the upper limit; however, values did not differ ($P < 0.05$) between dietary treatments; the greater values likely were related to differences between personnel that drew the blood samples. Blood urea nitrogen concentrations were reanalyzed using only period 1 values due to an observed effect ($P < 0.05$) of feeding sequence in the initial analysis that indicated the possibility of a carryover effect from period 1 to period 2. Reanalysis using period 1 data detected no significant effect of dietary treatment on BUN. The BUN values were reflected in the MUN values, a correlation that has been well established (Broderick and Clayton, 1997). The greater protein values may have been influenced by the presence of the high milk protein genetic merit group in this herd. Blood chemistry and hematological measurements indicated that feeding TC1507 did not statistically alter ($P < 0.05$) these values. No research data have been published previously evaluating blood chemistries of lactating dairy cows fed genetically enhanced feedstuff.

CONCLUSIONS

Health and productivity of lactating dairy cows were not different between cows fed TMR containing a new generation Bt maize silage plus grain and cows fed a control maize silage plus grain. Milk composition, clinical blood chemistries, and hematology indices were not affected by source of maize silage and grain.

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