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Changes in ruminal microbial populations in transition dairy cows

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Abstract

We used four ruminally fistulated, multiparous, pregnant Holstein cows to delineate microbial adaptations in dairy cows as they experienced the transition from one lactation to the next. Diets consisted of typical far-off and close-up diets, a late lactation diet containing wet corn gluten feed (20% DM) and an alfalfa hay-corn silage based early lactation diet. Calculated NEL (Mcal/lb), measured crude protein (%), and diet digestibilities (%; based on steers fed at 2% of BW) were: 0.78, 18.7, 74.1; 0.70, 11.5, 66.2; 0.74, 15.6, 71.0; 0.73, 18.4, 70.7 for late lactation, far-off dry, close-up dry, and early lactation, respectively. Microbial samples were obtained on days 72 (late lactation), 51 (far-off dry), 23, and 9 (close-up dry) prepartum and days 6, 20, 34, 48, 62, 76, and 90 postpartum. We analyzed ruminal samples for ciliated protozoa and viable counts of bacteria and fungi. Changing from a high forage to a high concentrate diet impacted bacterial counts less than ciliated protozoal and fungal counts. Switching diets from high concentrate to high forage increased ciliated protozoa and fungal counts, and counts decreased when diets were switched from high forage to high concentrate. Bacterial and ciliated protozoa counts increased in early lactation and decreased as cows approached peak dry matter intake. Dietary changes with the onset of lactation led to virtual disappearance of fungi from the rumen. In general, ruminal microbial populations of dairy cows respond to changes in diet and intake. Changes in diet affected populations of protozoa and fungi, whereas changes in intake affected populations of bacteria, protozoa, and fungi.; Dairy Day, 2002, Kansas State University, Manhattan, KS, 2002;

Keywords

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CHANGES IN RUMINAL MICROBIAL POPULATIONS IN TRANSITION DAIRY COWS

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Summary

We used four ruminally fistulated, multiparous, pregnant Holstein cows to delineate microbial adaptations in dairy cows as they experienced the transition from one lactation to the next. Diets consisted of typical far-off and close-up diets, a late lactation diet containing wet corn gluten feed (20% DM) and an alfalfa hay-corn silage based early lactation diet. Calculated NE_L (Mcal/lb), measured crude protein (%), and diet digestibilities (%; based on steers fed at 2% of BW) were: 0.78, 18.7, 74.1; 0.70, 11.5, 66.2; 0.74, 15.6, 71.0; 0.73, 18.4, 70.7 for late lactation, far-off dry, close-up dry, and early lactation, respectively. Microbial samples were obtained on days 72 (late lactation), 51 (far-off dry), 23, and 9 (close-up dry) prepartum and days 6, 20, 34, 48, 62, 76, and 90 postpartum. We analyzed ruminal samples for ciliated protozoa and viable counts of bacteria and fungi. Changing from a high forage to a high concentrate diet impacted bacterial counts less than ciliated protozoal and fungal counts. Switching diets from high concentrate to high forage increased ciliated protozoa and fungal counts, and counts decreased when diets were switched from high forage to high concentrate. Bacterial and ciliated protozoa counts increased in early lactation and decreased as cows approached peak dry matter intake. Dietary changes with the onset of lactation led to virtual disappearance of fungi from the rumen.

In general, ruminal microbial populations of dairy cows respond to changes in diet and intake. Changes in diet affected populations of protozoa and fungi, whereas changes in intake affected populations of bacteria, protozoa, and fungi.

(Key Words: Transition, Dairy Cow, Microbial.)

Introduction

Bacteria, protozoa, and fungi comprise the majority of the ruminal microbial population. Changes in diet and intake can affect each group of microbes differently. Bacteria possess the shortest generation time, thus changes in diet and intake should impact their populations less than protozoa or fungi. Protozoa have the longest generation time, so changes in diet and intake can greatly affect their population in the rumen. Protozoa usually attach themselves to larger feed particles or the ruminal wall to overcome the long generation time, thus maintaining populations in the face of diet and intake changes. In addition, protozoa can use bacteria and fungi as a source of nutrients to maintain populations during periods of low intake or low quality diets. Fungi attach and feed on fiber particles

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then release fungal spores upon maturation; thus, diet and intake changes may drastically affect their population.

The two-tiered feeding system (far-off and close-up diets) for dry cows is structured to allow time for ruminal microbial populations to adjust to dietary changes and potentially reduce the incidences of ruminal and metabolic disorders after calving. Ruminal microbes also must respond to changes in intake as the cow makes the transition from late gestation into early lactation. Changes in intake include about a 20 to 30% reduction during the 3 weeks prior to parturition and an increase in intake during early lactation. Limited information exists on changes in ruminal microbial populations in dairy cows associated with diet and feed intake changes during late gestation and early lactation. Thus, our objective was to characterize ruminal microbial changes as the dairy cow makes the transition from a non-lactational to a lactational state.

Procedures

We used four-ruminally fistulated, multiparous, pregnant Holstein cows fed typical dairy diets for late lactation, far-off dry, close-up dry, and early lactation. Diets were offered as a total mixed ration twice daily in amounts sufficient to ensure ad libitum intake. Ruminal content samples were collected from the rumen on days 72 (late lactation), 51 (far-off), 23 and 9 (close-up); then on days 6, 20, 34, 48, 62, 76, and 90 postpartum. Samples for microbial enumeration were obtained from the rumen prior to the morning feeding on each sampling date. Measurements included counts of total bacteria and fungi, cellulolytic bacteria and fungi, and total ciliated protozoa. Bacterial and fungal counts were enumerated by the Most Probable Number (MPN) method. Ciliated protozoa were counted under a microscope using a counting chamber.

Results and Discussion

None of the cows experienced health disorders during the experimental period, thus microbial counts likely reflect a normal transition from one lactation to the next. All cows received total mixed rations (TMR) consistent with stage of lactation or gestation (Table 1).

The cows consumed about 3.1% of their body weight on a dry matter basis prior to dry-off and their dry matter intake (DMI) dropped to about 2.3% of their body weight during the far-off period. This decrease in DMI was attributed to cessation of lactation (less demand for nutrients) and switching from a high energy, low fiber to a low energy, high fiber diet. Total ciliated protozoa (Figure 1) and total fungi (Figure 2) increased as cows moved into the far-off period, cellulolytic fungi (Figure 3) decreased during this change, and cellulolytic (Figure 4) and total bacteria (Figure 5) exhibited little or no response, respectively, by day 8 after the diet change. Dry matter digestibility was lower during the far-off period than during late lactation, and this likely was due to the increase in prairie hay in the diet at the expense of more digestible components, corn grain and soybean meal.

The cows were switched to a close-up diet 28 days before expected calving to partially adjust the rumen to the lactation diet. The cows calved later than expected, so the close-up diet was introduced on average 32 days before calving. The increase in energy and protein concentrations of the close-up diet compared with the far-off dry diet was achieved by partially replacing prairie hay with alfalfa hay, corn silage, and expeller soybean meal. These changes increased dry matter digestibility of the diet but did not change DMI. Total ciliated protozoa and total fungal counts were lower, cellulolytic fungal and total bacterial counts were unchanged, whereas cellulolytic bacteria were elevated 5 days after

the switch to the close-up diet compared to their populations in samples collected during the far-off period. It is conceivable that the increase in cellulolytic bacteria and the decrease in total ciliated protozoa and total fungi could have occurred prior to the close-up sampling date because we did not evaluate a sample at the end of the far-off period. However, because the rumen had been exposed to the close-up diet for about 5 days prior to sampling it is assumed that the changes observed were associated with the diet change. The lack of change in total ciliated protozoa and total fungi between the first and second close-up period samples supports this assumption, but not the sharp decrease in cellulolytic bacterial counts between the two sampling dates. We theorize that the cellulolytic bacteria responded positively to the higher CP content in the close-up diet than the far-off diet at the first sampling date, but negatively to the decrease in DMI that occurred by the second sampling date. This theory is supported by the observed rebound in cellulolytic bacterial counts by day 6 after calving following the change to the lactation diet (higher CP content than the close-up diet) and an increase in DMI. The subsequent decrease in cellulolytic bacteria during lactation appears to be consistent with their accepted response to an increase in starch intake.

In addition to the aforementioned changes in cellulolytic bacteria, total bacterial counts on day 6 postpartum were similar to those on day 9 prepartum but increased by day 20 postpartum, likely due to an increase in starch fermenters. Total ciliated protozoa followed a pattern similar to total bacteria when the cows were switched from the close-up to the lactation diet. Total and cellulolytic fungal counts were low during the close-up and early lactation periods except for an increase in total fungi on day 6 postpartum.

In summary, ruminal microbial populations of dairy cows responded to changes in diet and intake. Changes in diet affected populations of protozoa and fungi, whereas changes in intake affected populations of bacteria, protozoa, and fungi. Focusing future research efforts on nutritional modulation to improve microbial populations during the transition period is warranted.

Table 1. Experimental Diets

	Diets (% of DM)			
Item	Late Lactation	Far-off	Close-up	Lactation
Ingredient				
Alfalfa hay	20.0	–	15.0	30.0
Prairie hay	–	48.4	20.0	–
Corn silage	10.1	19.8	30.0	15.0
Corn grain	27.7	22.4	18.7	32.0
Whole cottonseed	9.3	–	–	9.3
Fishmeal	1.3	–	–	1.3
Expeller soybean meal	7.7	–	9.4	3.3
48% soybean meal	–	8.4	4.4	4.4
Wet corn gluten feed	19.6	–	–	–
Molasses	1.3	–	–	1.0
Limestone	1.38	0.06	0.60	1.36
Dicalcium phosphate	0.05	0.40	0.74	0.88
Sodium bicarbonate	0.68	0.00	–	0.75
Trace mineral salt[1]	0.29	0.34	0.50	0.32
Magnesium oxide	0.20	–	0.50	0.21
Vitamin A,D,E[2]	0.12	0.11	0.12	0.13
Sodium selenite premix[3]	0.08	0.02	0.04	0.01
Nutrients				
Crude protein, %	18.7	11.5	15.6	18.4
RDP, %	11.6	7.3	10.3	11.7
ADF, %	17.5	25.2	22.0	18.2
NDF, %	29.9	42.9	34.4	27.0
Non-fiber carbohydrate, %	37.8	35.2	39.1	40.4
NE_L , Mcal/lb[4]	0.78	0.70	0.74	0.73
Crude fat, %	5.75	3.76	3.49	5.60

[1]Composition: not less than 95.5% NaCl, 0.24% Mn, 0.24% Fe, 0.05% Mg, 0.032% Cu, 0.032% Zn, 0.007% I, and 0.004% Co.

[2]Contributed 4912 IU vitamin A, 2358 IU vitamin D, and 24 IU vitamin E per kg diet DM.

[3]Contributed 0.06 mg Se per kg diet DM.

[4]Calculated based on NRC, 2001. Estimates of NE_L values from summation of individual ingredients (0.78, 0.66, 0.71, 0.77 for the late lactation, far-off, close-up, and lactation diets, respectively).

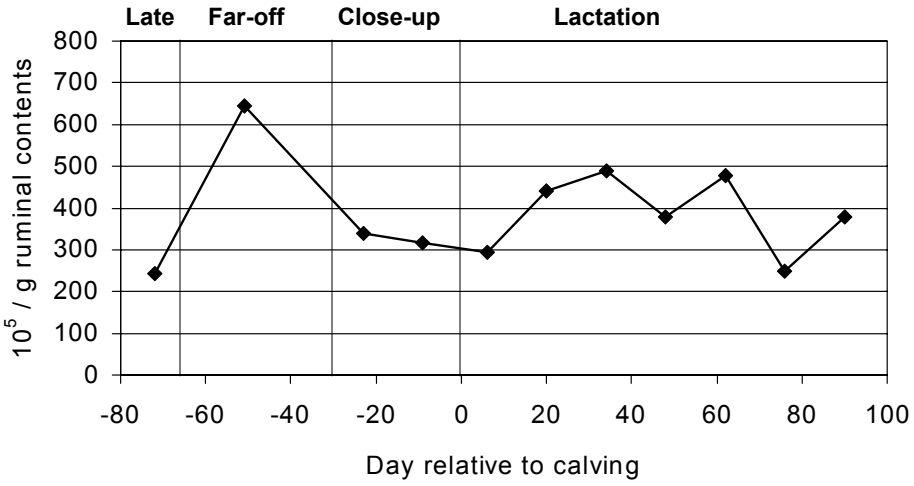

Figure 1. Total Ciliated Protozoal Counts.

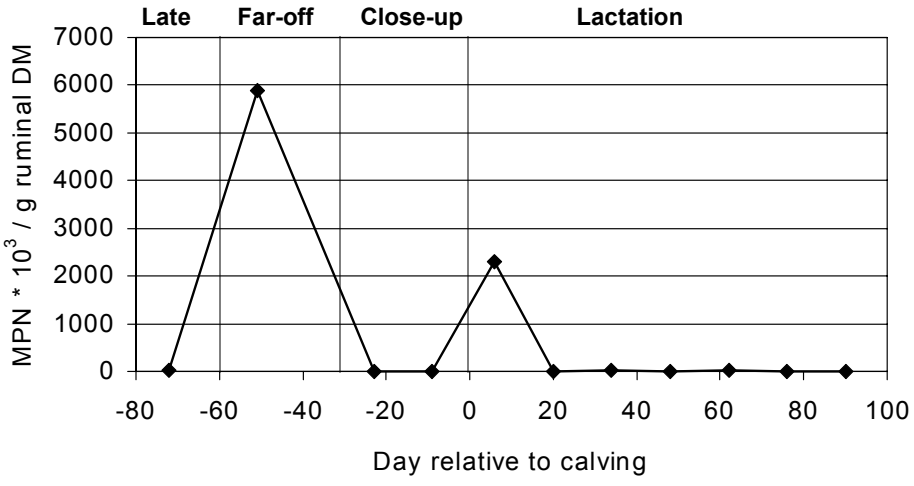

Figure 2. Total Fungal Counts.

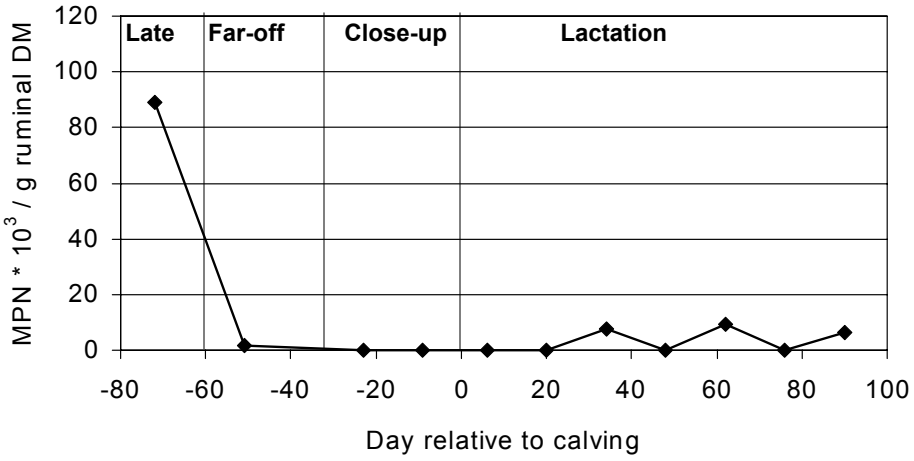

Figure 3. Cellulolytic Fungal Counts.

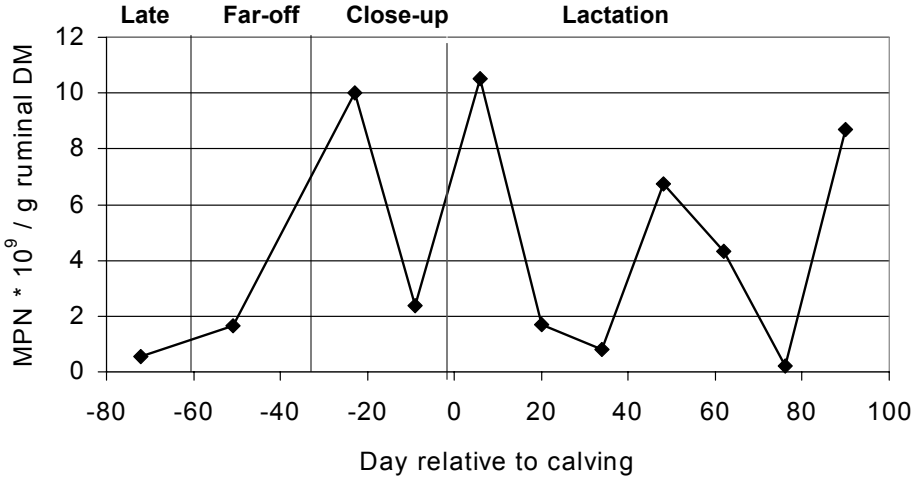

Figure 4. Cellulolytic Bacterial Counts.

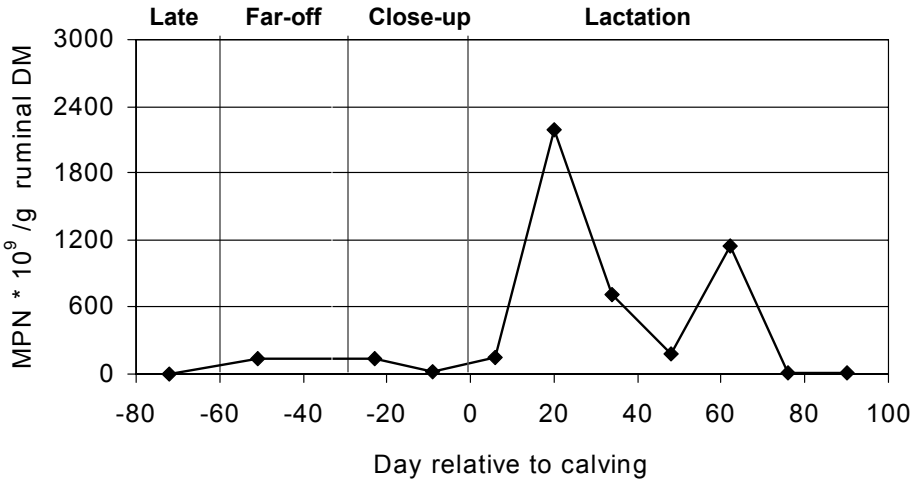

Figure 5. Total Bacterial Counts.