

## Symposium: Forages and Pastures: Fiber Fermentation: Influence of Supplemental Nonstructural Carbohydrates

**37 Factors affecting activity of cellulolytic microbes in the rumen.** P. J. Weimer\*<sup>1,2</sup>, <sup>1</sup>USDA-ARS, Madison, WI, <sup>2</sup>University of Wisconsin, Madison.

Ruminant diets that contain high levels of readily fermentable carbohydrates often display reduced fiber digestibility, but separating direct from indirect effects has proven difficult. Laboratory culture studies have revealed that the most widely studied ruminal fibrolytic bacteria cannot use starches, and while often capable of using simple sugars, cannot compete effectively for these with typical saccharolytic ruminal bacteria. Glucose and cellobiose are known to inhibit cellulase enzymes *in vitro*, but their effect *in vivo* appears to be reduced by their low concentrations and by the fact that polysaccharide hydrolase enzyme complexes of the fibrolytic bacteria are cell-bound and somewhat protected from the bulk rumen liquid phase. At high sugar concentrations *in vitro*, rapid sugar fermentation appears to lengthen lag time before initiation of fiber digestion, without necessarily reducing digestion rate. Low ruminal pH (<5.9) inhibits growth of the most well-studied ruminal fibrolytic bacteria, but studies with mixed ruminal microflora *in vitro* suggest that cellulose degradation continues at substantially lower pH, apparently due to cellulose hydrolysis by cellulase complexes of nongrowing fibrolytic bacteria, coupled with rapid consumption of the released sugars by more acid-tolerant, noncellulolytic bacteria. Cellulose hydrolysis decreases rapidly at pH values < 5.3, apparently due to loss of adherence to cellulose fibers by the fibrolytic bacteria. Unlike starches, pectin does not appear to reduce fiber digestibility, in part because it is degradable by some fibrolytic bacteria, and because its fermentation does not result in dramatic declines in ruminal pH. Available data suggest that complex interactions among the microflora modulate the effects of concentrates on fiber digestion. Moreover, recently developed molecular techniques for characterizing bacterial populations suggest that most ruminal bacterial species have eluded isolation in pure culture, introducing the possibility that additional species may contribute to ruminal fiber digestion.

**Key Words:** Cellulose, Fiber Digestion, Rumen

**38 The source and degradability of dietary starch influences forage and fiber utilization by lactating dairy cows.** D. P. Casper\*, D. Schauff, D. Kleinschmit, D. Jones, E. Lanka, and G. Ayangbile, *Agri-King, Inc., Fulton, IL.*

Milk production by the modern lactating dairy cow is often limited by the intake and supply of nutrients through digestion and absorption in both the rumen and intestine. Optimal nutrient intake and supply is achieved through ration formulation and orchestration of forages, feeds, and feeding management on the farm to maximize digestion and absorption. The lactating dairy cow is well adapted to use forages to meet these nutrient requirements. However, the range in forage quality and subsequent ruminal fiber digestion can be quite dramatic based on forage types, environmental conditions, varieties, harvest management, etc. Ultimately, it is the rate and extent of ruminal fiber digestion of the forage that will determine the maximum nutrient supply by the ration to the lactating dairy cow. Starch sources are used in the ration to supply the difference between the nutrient requirements of the cow

and the nutrients supplied by the forages. However, the rate and extent of starch digestion of these sources can negatively or positively influence ruminal fiber digestion. The objective of this presentation will be to discuss the interactions between the rate and extent of various starch sources (corn, barley, wheat, etc.) and their interaction on ruminal fiber digestion from various forage sources to meet the nutrient requirements for milk production. For example, our work with summarizing the data from the USDA-ARS Energy Metabolism Unit Database demonstrates that lactating dairy cows exhibiting symptoms of ruminal acidosis (inverted fat and protein ratios) caused by excessive ruminal starch digestion resulted in significant reductions in ruminal fiber digestion when fed different forage sources. These reductions in ruminal fiber digestibility also lead to a lower supply of nutrients, milk production, milk components and feed efficiency by the lactating dairy cow.

**Key Words:** Forages, Starch, Digestibility

**39 Manipulation of rumen microflora to improve ruminant production.** R. J. Forster\*, K. A. Beauchemin, and S. Ohene-Adjei, *Agriculture and Agri-Food Canada, Lethbridge, AB, Canada.*

The addition of large quantities of non-structural carbohydrates to the diet of ruminants has often been associated with increased risks for ruminal acidosis and decreased activity of cellulolytic bacteria. Previously, the commonly accepted scenario for the occurrence of rumen acidosis was the overgrowth of lactic acid producing *Streptococcus bovis* and a decrease in lactate-utilizing bacteria. The subsequent accumulation of lactic acid and drop in rumen pH would then adversely affect the acid sensitive cellulolytic bacteria. However, recent studies utilizing molecular techniques to quantify rumen bacterial populations have not supported the theory that *S. bovis* always increases dramatically when starch is supplemented to cattle. Furthermore, lactic acid does not necessarily accumulate in rumen fluid of animals experiencing rumen acidosis. The inoculation of lactate-utilizing bacteria into the rumen before the onset of increased starch supplementation has had some success in establishing these bacteria before natural populations can increase. Recent studies of the microbial diversity of the rumen have shown that most of the rumen bacteria have not been cultivated and that even coherent phylogenetic groups can vary widely in their functional attributes. This presents challenges for the interpretation of results based on the characterization and enumeration of a few cultivated strains. It has also been found that populations of bacteria traditionally thought to be dominant in the rumen of cattle (such as the *Prevotella* and *Butyrivibrio* groups) may not always be present in significant numbers. To fully understand how the rumen microflora can be manipulated to ameliorate the effects of excess starch on fiber fermentation, we must obtain a thorough knowledge of the bacteria present under different dietary regimens and how they respond to dietary stress. Molecular techniques are being developed and are helping to better understand the dynamics of rumen microbial populations and how they may be manipulated to improve animal production.

**Key Words:** Rumen Ecology, Acidosis, *Prevotella*