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Active dry *Saccharomyces cerevisiae* can alleviate the effect of subacute ruminal acidosis in lactating dairy cows

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ABSTRACT

The objective of the study was to determine the effect of active dry *Saccharomyces cerevisiae* (ADSC) supplementation on dry matter intake, milk yield, milk components, ruminal pH, and microbial community during a dietary regimen that leads to subacute ruminal acidosis (SARA). Sixteen multiparous, rumen-cannulated lactating Holstein cows were randomly assigned to 1 of 2 dietary treatments that included ADSC (Biomate; AB Vista, Marlborough, UK; 8×10^{10} cfu/head per day) or control. During wk 1 to 6, all cows received a high-forage (HF) diet (77:23, forage:concentrate). Cows were then abruptly switched during wk 7 to a high-grain (HG) diet (49:51, forage:concentrate) and remained on the HG until the end of wk 10. Feed intake and milk yields were recorded daily. Ruminal pH was recorded continuously using an indwelling system for 1 to 2 d per week during the pre-experimental phase, and wk 6, 7, and 10. Ruminal digesta samples were collected at the end of the experiment and analyzed for relative change in microbial communities using real-time quantitative PCR. Cows were considered to have SARA if the duration below pH 5.6 was ≥300 min/d. Ruminal pH during wk 6 (HF plateau) was not different across treatments (15 ± 46 min/d at pH <5.6). The dietary regimen successfully induced SARA during wk 7 (transition from HF to HG diet), and ruminal pH (551 ± 46 min/d at pH <5.6) was not different across treatments. However, cows receiving ADSC had an improved ruminal pH (122 ± 57 vs. 321 ± 53 min/d at pH <5.6) during wk 10 (HG plateau) compared with control. Additionally, cows receiving ADSC had a better dry matter intake (23.3 ± 0.66 vs. 21.6 ± 0.61 kg/d) and 4% fat-corrected milk yield (29.6 ± 1.2 vs. 26.5 ± 1.2 kg/d) than control cows during the HG phase (wk 8 to 10). During HG feeding, cows receiving ADSC had greater total volatile fatty acid and propionate concentrations (175 ± 7.5 vs. 154 ± 7.5 and 117 ± 6.1 vs. 94 ± 5.7 m*M* for ADSC and control, respectively) and lower acetate:propionate ratio (0.26 ± 0.5 vs. 0.36 ± 0.05 for ADSC and control, respectively). Microbial analyses conducted on samples collected during wk 10 showed that cows supplemented with *S. cerevisiae* had a 9-fold, 2-fold, 6-fold, 1.3-fold, and 8-fold increase in *S. cerevisiae*, *Fibrobacter succinogenes*, *Anaerovibrio lipolytica*, *Ruminococcus albus*, and anaerobic fungi, respectively, which suggested an increase in cellulolytic microbes within the rumen. Cows supplemented with ADSC had 2.2-fold reduction in *Prevotella albensis*, which is a gram-negative bacterium predominant during SARA. *Prevotella* spp. are suggested to be an important source of lipopolysaccharide responsible for inflammation within the rumen. Cows supplemented with ADSC had a 2.3-fold increase in *Streptococcus bovis* and a 12-fold reduction in *Megasphaera elsdenii*. The reduction in *M. elsdenii* may reflect lower concentration of lactic acid within the rumen for ADSC cows. In conclusion, ADSC supplementation to dairy cows was demonstrated to alleviate the condition of SARA caused by abrupt dietary changes from HF to HG, and can potentially improve rumen function, as indicated by greater numbers of cellulolytic microorganisms within the rumen.
Key words: *Saccharomyces cerevisiae*, subacute ruminal acidosis, rumen microbes, dairy cattle

INTRODUCTION

Subacute ruminal acidosis is a common digestive disorder in dairy cows caused by feeding rapidly fermentable carbohydrates. The condition is characterized by a diurnal depression in ruminal pH due to the accumulation of VFA, and to a lesser extent lactic acid, within the rumen (Oetzel, 2000). A research model using cannulated dairy cows has defined SARA as a decline in ruminal pH below 5.6 for approximately 300 min/d (AlZahal et al., 2007a). Symptoms of SARA are variable, but often include depressed intake, resulting in poor body condition and reduced production (Plaizier et al., 2008), and may predispose cows to milk fat depression (AlZahal et al., 2009, 2010).

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Ruminant nutritionists have used a spectrum of feed additives to improve ruminal pH and maximize fiber degradation, namely by directly feeding active dry bacteria and yeast and yeast culture products. Active dry yeast products are manufactured in a manner to maintain a specific number of live cells ($>1.5 \times 10^{10}$ cfu/g of DM), thus preserving the majority of the products' ability to ferment forages.

The mechanisms proposed to explain the mode of action of active dry yeast within the rumen are mainly focused on optimizing fiber digestion [see review by Chaucheyras-Durand et al. (2008)]. Active dry yeast was proposed to survive for a short period of time within the rumen by utilizing traces of dissolved oxygen, which can be directly involved in fiber digestion and (or) can create an optimal anaerobic environment for bacterial growth. Live yeast was also proposed to create optimal growth conditions for bacteria by preventing the accumulation of lactic acid within the rumen (Nocek, 1997). Most commercially available active dry yeasts are based on strains of *Saccharomyces cerevisiae*. Yeast culture products, on the other hand, do not contain a guaranteed live yeast cell level but rather yeast fermentation by-products. Those by-products have been suggested to affect the growth of ruminal microbes (Callaway and Martin, 1997).

Studies that examined the effects of active dry yeast, exclusively, on performance and digestive characteristics of lactating ruminants are scarce and inconclusive. It was reported that active dry yeast supplementation can increase DMI and milk yield in early-lactation dairy cows (Wohlt et al., 1991) and dairy goats (Stella et al., 2007), whereas others reported no difference in dairy cattle (Swartz et al., 1994; Chiquette, 1995; Kung et al., 1997; Soder and Holden, 1999). The main variations among studies are likely due to differences in manufacturing processes, dosages and strains, and production systems. Additionally, the majority of available reviews of the literature, both the qualitative and the quantitative, did not differentiate between active dry yeast and yeast culture products, which limited the reliability of the results of such reviews. Studies evaluating the effect of active dry yeast on fermentation characteristics, including pH, are limited to in vitro methods, which were considered inappropriate for studying the effect of yeast on pH due to its high buffering capabilities (Carro et al., 1992).

To our knowledge, no studies exist in the literature that directly examined the effect of active dry *S. cerevisiae* (**ADSC**) on mitigating SARA by utilizing a nutritional SARA induction model, and concurrently assessed changes in ruminal microbes. Therefore, the objective of the current study was to determine the effect of *S. cerevisiae* supplementation on ruminal pH, cow performance (DMI, milk yield, and milk components), and microbial community during a dietary regimen that leads to SARA.

MATERIALS AND METHODS

Animals, Treatments, and Feeding

Sixteen multiparous lactating Holstein cows (166 ± 30 DIM) were used in a randomized complete block design. Cows were randomly assigned into 1 of 2 blocks (n = 8 each) and then assigned to 1 of the 2 dietary treatments that included ADSC (Biomate; AB Vista, Marlborough, UK; strain 1242) or control. The layout of the experimental design and feeding regimen is depicted in Figure 1. The 2 blocks were conducted in a staggered manner with 1-wk difference to facilitate complex measurements. The daily allotments of ADSC were prepared weekly by mixing 4 g of the ADSC product (2×10^{10} cfu/g of DM) with 250 g of ground dry corn. The control diet contained the carrier only. Before starting the experiment, cows were maintained on a regular lactating-cow TMR fed twice daily (0700 and 1300 h) that consisted (DM basis) of 28% corn silage, 27% haylage, 6% straw, 20% high-moisture corn, and 19% protein supplement. The TMR included approximately 16% CP, 40% NFC, and 33% NDF. During the first 6 wk, all cows received a high-forage (**HF**) diet (Table 1). The HF diet was created by replacing 42% of the TMR (DM basis) with chopped hay. During wk 7, cows were switched abruptly to a high-grain (HG) diet (Table 1), and cows remained on the HG diet until the end of wk 10. The HG diet was created by replacing 20% of the TMR (DM basis) with wheat and barley pellets (1:1). Cows were allowed only 1 d of transition from the HF to the HG diet, where they received only 50% of the grain pellet allotment. The HF diet, transition diet, and HG diet were remixed in a Data Ranger (American Calan Inc., Northwood, NH) and fed twice daily as a TMR. The HG diet has been reported in previous studies to induce sustainable SARA [see, for example, AlZahal et al. (2009)], whereas the HF has been designed to induce optimal ruminal conditions. Cows were top-dressed during the morning feeding (wk 1 through 10) with either the ADSC or control diet. The amount of offered feed was adjusted daily to allow a maximum of 5 kg of orts/d (as-fed basis). Researchers and technical staff were blinded to the treatments. Ingredients and chemical analyses of TMR are presented in Table 1.

The cows were housed in a tie-stall facility at the Ponsonby Dairy Research Station (University of Guelph, Guelph, ON, Canada). All experimental procedures were approved by the University of Guelph