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Nutrient digestibility, digesta volatile fatty acids, and intestinal bacterial profile in growing pigs fed a distillers dried grains with solubles containing diet supplemented with a multi-enzyme cocktail

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ABSTRACT

This study investigated the effects of adding a multi-enzyme cocktail (MC) to a distillers dried grains with solubles (DDGS)-containing diet on energy and nutrient coefficients of apparent ileal (CAID) and total tract (CATTD) digestibility, digesta volatile fatty acids (VFA) concentration, and gut bacterial profile using ileal-cannulated barrows ($n = 9$; 62.7 ± 6.4 Kg initial body weight). Three isocaloric/isonitrogenous diets based on corn and soybean meal with 0 (control) or 30% DDGS (DDGS diet) and DDGS diet supplemented with MC (DDGS + MC) were used. The 3 diets were fed to pigs in a 2-period change over design to obtain 6 observations per diet. A casein–cornstarch-based diet was used in a separate period to determine basal endogenous N and AA losses to estimate standardized ileal digestibility (SID) of AA. All diets contained titanium dioxide as a digestibility marker. Ileal digesta and feces were used for VFA and bacterial profile determination, respectively. The CAID for DM, N, starch, and energy were greater ($P < 0.05$) in pigs fed the control diet than in pigs fed the DDGS diet. Addition of MC to the DDGS diet improved ($P < 0.05$) the CAID for DM, starch, and energy, but not N ($P > 0.10$). The DDGS diet also decreased ($P < 0.05$) the CAID and SID for AA and the MC improved ($P < 0.05$) the CAID and SID of some of the AA. Further, the DDGS diet decreased ($P < 0.05$) the CATTD for DM, N, and energy and tended to decrease ($P < 0.10$) the CATTD for NDF, whereas the MC improved ($P < 0.05$) the CATTD for DM and energy, but not ($P > 0.10$) for N and NDF. However, diet had no effect ($P > 0.10$) on hindgut nutrient disappearance. Diet did not influence ($P > 0.10$) digesta pH and VFA concentrations except for isovalerate concentration, which was greatest ($P < 0.05$) in the DDGS + MC-fed pigs. *Bacteroides–Prevotella–Porphyromonas* and *Enterobacteriaceae* abundance were greatest ($P < 0.05$) in the feces of the DDGS + MC-fed pigs. Additionally, the abundance of the β-xylosidase gene, xynB, from the Bacteroidetes group increased ($P < 0.05$) when the MC was added to the DDGS diet. However, the DDGS-fed pigs had the greatest abundance ($P < 0.05$) of Firmicutes. The abundance of *Lactobacillus* spp. was not affected

Abbreviations: AA, amino acids; BW, body weight; CAID, coefficient of apparent ileal digestibility; CATTD, coefficient of apparent total tract digestibility; CCS, casein–cornstarch-based; CP, crude protein; DDGS, distillers dried grains with solubles; EC, exogenous carbohydrase; GE, gross energy; MC, multi-enzyme cocktail; NSP, non-starch polysaccharides; ME, metabolizable energy; N, nitrogen; NDF, neutral detergent fiber; PCR, polymerase chain reaction; SBM, soybean meal; SID, standardized ileal digestible; VFA, volatile fatty acids.

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($P > 0.10$) by diet. In conclusion, adding MC to the DDGS diet improved the digestibility of DM, starch, most AA, but not NDF and N digestibility. The results show that addition of MC to the DDGS diet stimulated the growth of intestinal bacteria with xylanolytic and cellulolytic activities.

1. Introduction

Distillers dried grains with solubles (DDGS), a co-product of the ethanol industry, is used extensively in pig diet because of its availability, low cost and high nutrient composition (Stein and Shurson, 2009). However, like all co-products, it has high NSP content and its incorporation into pig diet has been reported to depress energy and nutrient utilization (Nyachoti et al., 2005; Stein and Shurson, 2009; Urriola and Stein, 2010). Thus, exogenous enzymes (EE) have been used as a strategy to improve the nutritive value of diets containing DDGS in pigs (Kerr et al., 2013; Swiatkiewicz et al., 2015). However, the use of EE to improve nutrient digestion in DDGS-containing diets has yielded inconsistent results (Swiatkiewicz et al., 2015) probably due to the complex structure of the fiber in DDGS (Pedersen et al., 2014) and the use of single enzymes or enzyme activities, which may not be suitable for effective hydrolysis of such components (Kerr et al., 2013). Therefore, an enzyme matrix containing different enzyme combinations might be required to effectively hydrolyze the fiber in DDGS-containing diet to improve nutrient digestibility.

In vitro studies have shown that oligosaccharides derived from cell wall polysaccharides are fermented by intestinal bacteria, and bateroides are able to degrade xylans (van Laere et al., 2000). In addition, using in vitro model of the pig gastrointestinal tract, Bindelle et al. (2010) showed that cereal grains with high insoluble NSP contents stimulate the growth of acetate-producing cellulolytic bacteria and xylanolytic bacteria. The fiber in DDGS is predominantly insoluble because of its high insoluble arabinoxylans, cellulose and lignin contents (Pedersen et al., 2014) and is mostly resistant to hindgut fermentation (Urriola et al., 2010; Urriola and Stein, 2010). Exogenous enzymes have been reported to degrade complex NSP structure into lower molecular weight that are accessible for microbial fermentation and thereby influence intestinal microflora composition and microbial metabolite production (Kiarie et al., 2009; Bindelle et al., 2011; Bedford and Cowieson, 2012). Therefore, addition of EE to DDGS-containing diets is expected to generate oligosaccharides that will promote the growth of cellulolytic and xylanolytic bacteria and volatile fatty acids (VFA) production. However, there is dearth of information on the influence of multi-enzyme cocktail (MC) supplementation of DDGS-containing diets on gut microbial profile and microbial metabolites.

The first objective of this study was to evaluate the effect of supplementing a diet containing 30% DDGS with MC on coefficients of apparent ileal (CAID) and total tract (CATTD) energy and nutrient digestibility. The second objective was to test the hypothesis that addition of MC to a DDGS-containing diet will stimulate the growth of fiber-fermenting bacteria and volatile fatty acid (VFA) production. Fecal samples were used for the intestinal microbial composition analysis and the bacterial groups determined were selected based on the results from previous studies (Guo et al., 2008; Bindelle et al., 2011; Ivarsson et al., 2014) showing that these bacteria have xylanolytic and cellulolytic activities, responsive to dietary changes and composition, and are the most abundant bacterial groups in the pig gut.

2. Material and methods

2.1. Animals, housing, and experimental diets

The experimental protocols used in this study were reviewed and approved by the University of Manitoba Animal Care Committee and pigs were cared for according to the Canadian Council on Animal Care guidelines (CCAC, 2009).

Nine Yorkshire × Hampshire × Duroc barrows surgically fitted with a T-cannula in the distal ileum were used for this experiment. Because the pigs were used in an experiment before the present study, they were standardized on a commercial grower diet for 7 d before the commencement of the present experiment to offset any carryover effect from the previous study as described in the experiment by Ayoade et al. (2012). At the commencement of the present study, pigs had an average body weight of 62.7 ± 6.4 kg. Pigs were housed individually in pens (1.5 × 1.2 m) with plastic-covered expanded metal sheet flooring equipped with a nipple drinker and a stainless steel feeder in a temperature-controlled room. The pens were partitioned with metal walls that allowed visual contact with pigs in adjacent pens.

Three experimental diets were fed in this study. The diets were based on corn and soybean meal (SBM; control) and corn-SBM with 30% DDGS to manufacture the DDGS diet. The DDGS was produced from the fermentation of equal proportions of corn and wheat and was obtained from a commercial plant (NorAmera Bio Energy, Weyburn, SK, Canada). The third diet (DDGS + MC) was the DDGS diet supplemented with MC to supply 4400 xylanase, 175 β-glucanase, 3000 protease, 1500 α-amylase, and 30 pectinase U/kg of feed (Porzyme® TP100HP; DuPont Industrial Biosciences, Marlborough, Wiltshire, UK). The experimental diets were formulated to contain similar calculated metabolizable energy (ME) and standardized ileal digestible (SID) lysine contents, and all other nutrients were supplied according to NRC (1998) requirements for growing pigs (Table 1). Additionally, a casein–cornstarch-based diet (CCS, Table 1) was included in this experiment and used to