Effects of bioethanol plant and coproduct type on the metabolic characteristics of the proteins in dairy cattle

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ABSTRACT

The dramatic increase in bioethanol production in Canada has resulted in millions of tonnes of different types of coproducts: wheat dried distillers grains with solubles (DDGS), corn DDGS, and blend DDGS (e.g., wheat:corn 70:30). The objectives of this study were 1) to investigate the effect of DDGS type and bioethanol plant on the metabolic characteristics of the proteins and the total truly digested and absorbed protein supply to dairy cattle using the DVE/OEB system and 2) to compare the metabolic characteristics of the proteins of original feedstock grains with their respective derived DDGS samples. The results showed that all types of DDGS are a good source of the truly digested and absorbed protein in the small intestine [DVE; 107 vs. 249 g/kg of dry matter (DM) for wheat and wheat DDGS; 108 vs. 251 g/kg of DM for corn and corn DDGS]. According to the DVE/OEB system, the predicted total DVE supply to dairy cattle differed among wheat DDGS (DVE = 249 g/kg of DM), corn DDGS (DVE = 251 g/kg of DM), and blend DDGS (DVE = 281 g/kg of DM) and, to a lesser extent, between the different bioethanol plants (DVE: 277 vs. 230 g/kg of DM for bioethanol plants 1 and 2). The results indicated the superior protein value of blend DDGS as well as that of the more optimum degraded protein balance (DPB) value for corn DDGS (DPB: 11 g/kg of DM in corn DDGS vs. 72 g/kg of DM in wheat DDGS and 55 g/kg of DM in blend DDGS). In addition, differences in the acid detergent-insoluble crude protein content of wheat DDGS samples were reflected in differing protein DVE values. In conclusion, it is inappropriate to assume fixed protein values for DDGS without considering factors such as DDGS type and bioethanol plant origin.

Key words: bioethanol coproduct, DVE/OEB system, protein evaluation, metabolic characteristic of protein

INTRODUCTION

Nutrition models are fundamental for the continued success of the dairy nutritionist. They are practical tools that provide information on the animal's performance in response to changes in the ration. With the increasing understanding of events occurring in the ruminant's digestive tract, as well as the development of *in vitro* techniques and mathematical approaches that mimic these events, nutrition models are able to estimate the availability of protein in the small intestine. This is advantageous from a research standpoint because the *in vivo* animal trial is labor intensive, expensive, and suitable for only a few treatments, whereas a model allows for the evaluation of a greater number of treatments.

The period from 1970 to 1995 saw the creation of various nutrition models (Satter and Roffler, 1975; Institut National de la Recherche Agronomique, 1978; Agriculture Research Council, 1984; Madsen, 1985; Nordisk Kontaktorgan for Jordbrugsforskning, 1985; NRC, 1985) and their corresponding updates (Verité and Geay, 1987; Madsen et al., 1995). These models were developed to predict the protein value for feeds and the requirements of dairy cattle in terms of truly digested and absorbed protein in the small intestine (DVE). Some of the principles and elements of these models were used to develop the framework of a more sophisticated model: the DVE/OEB system, which is a system not based on total digestible nutrients (TDN; Tamminga et al., 1994) currently being used in several European countries. For each feed ingredient or diet, this protein evaluation system predicts 2 major outputs: 1) the DVE and 2) the degraded protein balance (DPB^{OEB}). The prediction of these 2 outputs is based on the chemical profile, the rumen degradation characteristics of different feed components, and the intestinal digestibility of protein. The first output includes 1) the truly absorbable rumen-synthesized microbial protein in the small intestine, 2) the truly absorbed RUP in the small intestine, and 3) endogenous protein losses. The second output is a concept derived from the Nordisk Kontaktorgan for Jordbrugsforskning (1985) model and

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reflects the balance between available N and energy in the rumen (Tamminga et al., 1994). This balance is critical to achieve efficient synthesis of microbial protein, which ultimately contributes to the postruminal pool of true protein.

The dramatic increase in bioethanol production has resulted in millions of tonnes of different types of coproducts: wheat dried distillers grains with solubles (**DDGS**), corn DDGS, and blend DDGS (e.g., wheat:corn 70:30). There is an urgent need to systematically evaluate the nutritive value of different types of DDGS from different bioethanol plants to increase accuracy in ration formulation, particular for wheat DDGS and blend DDGS. In the recent study (Nuez-Ortín and Yu, 2009), the different types of DDGS and different bioethanol plants were compared in terms of detailed chemical profiles, mineral concentrations, protein and carbohydrate subfractions associated with different degradation rates, and energy values. However, information on the potential true protein supply to the small intestine of dairy cows from DDGS and the metabolic characteristics of DDGS protein affected by DDGS type and bioethanol plant origin is still lacking.

The objectives of the current study were 1) to investigate the effect of DDGS type and bioethanol plant origin on the metabolic characteristics of the proteins and the prediction of total DVE supply using the DVE/OEB system and 2) to compare the predicted protein supply of feedstock grains with their respective derived DDGS samples. This data will help nutritionists increase accuracy in the formulation of diet rations containing different types of DDGS.

MATERIALS AND METHODS

Different Types of DDGS and Original Cereal Grains

During May to December in 2007, 3 to 5 batches from each of wheat DDGS, blend DDGS (wheat:corn 70:30), and wheat samples were collected from 2 bioethanol plants, referred to as SK-plant 1 and SK-plant 2, located in western Canada. Both plants used local wheat feedstock for bioethanol production. During the same time frame, corn DDGS and corn samples produced by a bioethanol plant in North Dakota were obtained through Federated Co-Op Ltd. (Saskatoon, Saskatchewan, Canada). Prior to ruminal incubation, samples were processed using a Sven Roller Mill (Apollo Machine and Products Ltd., Saskatoon, Saskatchewan, Canada). The roller gap was adjusted to a size of 0.203 cm (coarsely rolling, industry practice) to equalize the particle size of all samples. The detailed chemical profiles were reported by Nuez-Ortín and Yu (2009).

Animals and Diets

Three nonlactating Holstein cows fitted with a rumen cannula (Bar Diamond Inc., Parma, ID) with an internal diameter of 10 cm were used in this study. The cows were individually fed twice daily at 0800 and 1600 h and received 14 kg (7 kg at each feeding time) of a TMR of 56.8% barley silage, 10.2% alfalfa hay, 4.5% dehydrated alfalfa pellets, 21.6% standard dairy concentrate (containing barley, wheat, oats, dairy supplement pellets, and molasses), and 6.8% fresh cow concentrate (containing barley, oats, canola meal, soybean meal, wheat DDGS, corn gluten meal, molasses, golden flakes, canola oil, minerals, and vitamins). The animal experiment was reviewed and approved by the Animal Care Committee of the University of Saskatchewan (Animal Use protocol no. 19910012), and the animals were cared for in accordance with the guidelines of the Canadian Council on Animal Care (1993).

Rumen Incubation Procedure

Rumen degradation parameters were determined using the in situ method described by McKinnon et al. (1995) and Yu et al. (2000). Seven grams of sample were weighed and placed into numbered nylon bags (Nitex 03-41/31 monofilament open mesh fabric, Screentec Corp., Mississauga, Ontario, Canada) measuring 10 cm × 20 cm with a pore size of 41 µm. The ratio of sample size to bag surface area equaled to 17.5 mg/cm², which is within the range recommended by previous reports (Ørskov and McDonald, 1979; Nocek, 1988). A polyester mesh bag (45 cm × 45 cm with a 90-cm length of rope to be anchored to the cannula) was used to hold the bags in the rumen. Sample bags were added into the polyester mesh bag according to the graduate addition-all out schedule and incubated for 48, 24, 12, 8, 4, 2, and 0 h. Data from Urdl et al. (2006) were used to determine the number of bags incubated from each sample, which increased in relation to incubation time. The maximum number of bags in the rumen at any one time was 30 (Goelema, 1999). A 5-d long in situ rumen incubation was carried out to estimate maximum digestibility of nutrient components in the feed according to the DVE/OEB system (Tamminga et al., 1994). All treatments were incubated in 2 runs to the 3 nonlactating cows. After incubation, the bags were removed from the rumen and, together with those representing 0 h, rinsed under cold water to remove excess ruminal contents. The bags were washed with cool water without detergent and subsequently dried at 55°C for 48 h. Dry samples were stored in a refrigerated room (4°C) until analysis.

Table 1. Comparison of wheat dried distillers grains with solubles (DDGS), corn DDGS, and blend DDGS (wheat:corn 70:30) and comparison of different bioethanol plants in rumen protein degradation kinetics and estimated protein intestinal digestibility.

Item	Feed source					Bioethanol plant ¹			
	Wheat	Corn	Wheat DDGS	Corn DDGS	Blend DDGS (W:C 70:30)	Feed source SEM	SK-plant 1	SK-plant 2	Bioethanol plant SEM
In situ rumen degradation kinetics of CP									
Degradation rate, %/h	18.50 ^a	3.90 ^b	4.56 ^b	4.19 ^b	3.75 ^b	0.641	3.54	5.24	0.763
RDP, % CP	73.63 ^a	40.13 ^{bc}	45.58 ^b	33.95 ^c	36.20 ^c	3.095	44.80	46.10	2.893
RUP, % CP	26.4 ^c	59.8 ^{ab}	54.4 ^b	66.1 ^a	63.8 ^a	3.21	55.2	53.9	2.89
Estimated intestinal digestibility of RUP ²	76.4 ^{bc}	69.3 ^c	81.3 ^b	82.5 ^b	93.9 ^a	3.26	89.4	75.9	4.18
Acid detergent insoluble crude protein, % CP	0.0 ^c	0.1 ^c	4.9 ^{ab}	6.4 ^a	1.2 ^{bc}	1.41	0.7 b	7.6 b	0.13

^{a-c}Means within a row with different superscripts differ significantly ($P < 0.05$).

¹Bioethanol plants located in western Canada. Both plants used local wheat feedstock for bioethanol production.

²Estimated intestinal digestibility of RUP using the 3-step in vitro procedure.

Chemical Analysis

The samples and rumen residues were ground through a 1-mm screen [Retsch ZM-1, Brinkmann Instruments (Canada) Ltd., Mississauga, Ontario, Canada] and analyzed for DM (AOAC, 1990; method 930.15), ash (AOAC, 1990; method 942.05), CP (Leco protein/N analyzer, model FP-528, Leco Corp., St. Joseph, MI), and NDF (Ankom A200 Filter Bag Technique, Ankom Technology, Fairport, NY). Amylase and sodium sulfite was used for NDF analysis. To prevent the high fat content of DDGS from giving inaccurately high values for NDF, fat was extracted by incubating the samples in acetone for 2 h. Dried rumen residues and original samples of wheat and corn were analyzed for total starch content using the Megazyme Total Starch Assay Kit (Megazyme International Ireland Ltd., Cambridge, UK). The acid detergent insoluble CP (**ADICP**) values were also determined in original samples (Licitra et al., 1996). All samples were analyzed in duplicate and repeated if the error was higher than 5%.

Rumen Degradation Model

The first-order kinetic degradation model described by Ørskov and McDonald (1979) and modified by Robinson et al. (1986) and Dhanoa (1988) was applied to describe the rumen degradation characteristics of DM, CP, and starch. Such a model was solved by the NLIN procedure of SAS (SAS Institute, Cary, NC) via iterative least squares regression (Gauss-Newton method) using the following equation:

$$R(t) = U + (100 - S - U) \times \exp^{-K_d \times (t - T_0)}, \quad [1]$$

where $R(t)$ = residue present (%) at t hours of incubation; U = undegradable fraction (%); S = soluble

fraction (%); K_d = degradation rate (%/h); and T_0 = lag time (h).

The degradation model of starch differs in that T_0 and U are assumed to be zero in the DVE/OEB system (Tamminga et al., 1994); thus,

$$R(t) = (100 - S) \times \exp^{-K_d \times t}. \quad [2]$$

Based on the parameters (S , U , D , K_d), rumen-undegraded feed CP and rumen-undegraded starch (**RUST**) were predicted as

$$\text{RUP (\%)} = U + (D \times K_d)/(K_p + K_d) \text{ and} \quad [3]$$

$$\text{RUST (\%)} = S \times 0.1 + (D \times K_p)/(K_p + K_d), \quad [4]$$

where $D = 100 - S - U$ (%); K_p is estimated rate of outflow of digesta from rumen (%/h) and was assumed to be 6%/h in the DVE/OEB system for concentrate feedstuffs (Tamminga et al., 1994); and factor 0.1 is a compensation factor between in situ and in vivo starch results indicating that 10% of the S fraction of starch escapes rumen degradation (Nocek and Tamminga, 1991; Tamminga et al., 1994; Yu et al., 2003). The in situ data were presented in Table 1.

Estimation of the Intestinal Digestibility of RUP

The estimation of intestinal digestibility of RUP is necessary to estimate the amount of absorbable RUP in the DVE/OEB system. The 3-step in vitro procedure was followed as described by Calsamiglia and Stern (1995). Briefly, dried ground residues containing 15 mg of N after 12 h of ruminal incubation (Tamminga et al., 1994; Yu et al., 2000) were exposed for 1 h in 10 mL of 0.1 N HCl solution containing 1 g/L of pepsin. The pH was neutralized with 0.5 mL of 1 N NaOH and 13.5 mL

of pH 7.8 phosphate buffer containing 37.5 mg of pantoic acid that was added to the solution and incubated at 38°C for 24 h. After incubation, 3 mL of a 100% (wt/vol) trichloroacetic acid solution were added to stop enzymatic activity and precipitate undigested proteins. Samples were centrifuged and the supernatant (soluble N) was analyzed for N (Kjeldahl method; AOAC, 1990; method 984.13). Intestinal digestion of protein is calculated as trichloroacetic acid-soluble N divided by the amount of N in the 12-h residue sample. The estimated intestinal digestibility of RUP is presented in Table 1.

DVE/OEB System

The DVE/OEB system is outlined in detail by Tamminga et al. (1994). Below is a summarized description of the concepts and calculations that the DVE/OEB system uses to predict the DVE supply and availability to the small intestine of dairy cows. The 2 major outputs of the model are 1) the DVE and 2) the DPB^{OEB}. The DVE value was calculated as follows:

$$\text{DVE (g/kg of DM)} = \text{AMCP}^{\text{DVE}} + \text{ARUP}^{\text{DVE}} - \text{ENDP}, \quad [5]$$

where AMCP^{DVE} is truly absorbable microbial protein synthesized in rumen; ARUP^{DVE} is truly absorbed undegraded feed protein in the small intestine; and ENDP is endogenous protein loss in the small intestine.

The DPB^{OEB} value, which shows the balance between potential microbial synthesis based on RDP and potential protein synthesis based on energy extracted during anaerobic fermentation of OM in rumen (non-TDN model), was calculated as

$$\text{DPB}^{\text{OEB}} \text{ (g/kg of DM)} = \text{MCP}_{\text{RDP}}^{\text{DVE}} - \text{MCP}_{\text{FOM}}, \quad [6]$$

where MCP_{RDP}^{DVE} is microbial synthesis from RDP and MCP_{FOM} is microbial protein synthesis from energy available from rumen-fermented OM. A positive DPB^{OEB} in a diet reveals a potential N loss from the rumen, whereas a negative value indicates a shortage of N that can impair microbial protein synthesis. Therefore, the optimal DPB^{OEB} in a diet is zero or slightly higher than zero. The calculation of the components contained in these 2 outputs was as described below.

Estimation of Fermented OM. The DVE/OEB system uses the content of fermented OM (FOM) in the rumen to estimate microbial protein synthesis in the rumen, thus the term of non-TDN model. According to Tamminga et al. (1994), FOM was calculated as

$$\text{FOM (g/kg of DM)} = \text{DOM} - \text{CFat} - \text{RUP} - \text{RUST} - \text{FP}, \quad [7]$$

where DOM is digestible OM; CFat = crude fat; RUP = rumen-escaped feed protein; RUST = rumen-undegraded starch; and FP = fermentation products that are assumed to be zero for concentrates.

Estimation of Microbial Protein Synthesis in the Rumen and Truly Absorbable Rumen-Synthesized Microbial Protein in Small Intestine. Microbial protein synthesis according to DVE/OEB system (MCP_{FOM}) is based on FOM; thus,

$$\text{MCP}_{\text{FOM}} \text{ (g/kg of DM)} = 0.15 \times \text{FOM} \text{ (g/kg of DM)}, \quad [8]$$

where 0.15 indicates that 150 g of microbial protein/kg of FOM is assumed to be synthesized (Tamminga et al., 1994).

The DVE/OEB system also considers microbial protein synthesized from RDP (MCP_{RDP}^{DVE}) for the estimation of DPB^{OEB}. The MCP_{RDP}^{DVE} value was calculated as

$$\text{MCP}_{\text{RDP}}^{\text{DVE}} \text{ (g/kg of DM)} = \text{CP (g/kg of DM)} \times \{1 - [1.11 \times \text{RUP (\% CP)}/100]\}, \quad [9]$$

where 1.11 represents the regression coefficient between in situ RUP and in vivo RUP according to the French PDI system (Verité and Geay, 1987).

The estimation of the truly absorbable microbial protein synthesized in rumen (AMCP^{DVE}) contemplates only MCP_{FOM}; therefore,

$$\text{AMCP}^{\text{DVE}} \text{ (g/kg of DM)} = 0.75 \times 0.85 \times \text{MCP}_{\text{FOM}} \text{ (g/kg of DM)}, \quad [10]$$

where 0.75 and 0.85 are factors representing the assumed amount and digestibility of the true protein, respectively, contained in MCP_{FOM} (Tamminga et al., 1994).

Estimation of Ruminally Undegraded Feed CP and Truly Absorbed RUP in the Small Intestine.

The content of truly absorbed RUP in the small intestine (ARUP^{DVE}) is based on the content and digestibility of ruminally undegraded feed CP (RUP^{DVE}), which was calculated as

$$\text{RUP}^{\text{DVE}} \text{ (g/kg of DM)} = 1.11 \times \text{CP (g/kg of DM)} \times \text{RUP (\% CP)}. \quad [11]$$

ARUP^{DVE} was then formulated as

$$\text{ARUP}^{\text{DVE}} (\text{g/kg of DM}) = \text{dRUP} (\%) \times \text{RUP}^{\text{DVE}} (\text{g/kg of DM}), \quad [12]$$

where dRUP = intestinal digestibility of rumen undegraded protein.

Estimation of Endogenous Protein Losses in the Small Intestine. The estimation of DVE is corrected for endogenous protein losses in the small intestine (ENDP) to consider N lost as a consequence of digestive processes. The ENDP is associated with the amount of undigested DM (UDM), which was estimated as

$$\text{UDM (g/kg of DM)} = (\text{ash} \times 0.35) + \{\text{OM} - [\text{OM} \times \text{dOM} (\%)]\}, \quad [13]$$

where 0.35 is the factor used by Centraal Veevoeder Bureau (1996) indicating the 35% of ash is not digested and dOM is OM digestibility after the 5-d longer rumen incubation (Tamminga et al., 1994).

Given that the model assumes that 75 g of absorbed protein/kg of UDM is required to compensate for the endogenous losses (Tamminga et al., 1994), ENDP was formulated as

$$\text{ENDP (g/kg of DM)} = 0.075 \times \text{UDM (g/kg of DM)}. \quad [14]$$

Statistical Analysis

Study on the Effect of DDGS Type. Statistical analyses were performed using the MIXED procedure of SAS. The model used for the analysis was $Y_{ij} = \mu + F_i + e_{ij}$, where Y_{ij} was an observation of the dependent variable ij ; μ was the population mean for the variable; F_i was the effect of feed sources, as a fixed effect, batch and runs as replications; and e_{ij} was the random error associated with the observation ij . The residual analysis was carried out to test the model assumptions using the UNIVARIATE procedure of SAS with NORMAL and PLOT options.

Study on the Effect of Bioethanol Plant. Statistical analyses were performed using the MIXED procedure of SAS. The model used for the analysis was $Y_{ij} = \mu + P_i + e_{ij}$, where Y_{ij} was an observation of the dependent variable ij ; μ was the population mean for the variable; P_i was the effect of bioethanol plant, as a fixed effect, batch and runs as replications; and e_{ij} was the random error associated with the observation ij . The residual analysis was carried out to test the model assumptions using the UNIVARIATE procedure of SAS with NORMAL and PLOT options.

Correlation Analysis. Relationship between ADICP and truly digested and absorbed protein values were performed using the CORR procedure of SAS using a Pearson correlation method because variable data are normal distributed. The normality tests were performed using the UNIVARIATE procedure of SAS with NORMAL and PLOT options. For all statistical analyses, significance was declared at $P < 0.05$ and trends at $P \leq 0.10$. Treatment means were compared using the Fisher's protected least significant difference method.

RESULTS

Effects of DDGS Type on the Metabolic Characteristics of the Proteins and Total True Digested and Absorbed Protein Supply to Dairy Cattle

Using the DVE/OEB system, the effects of DDGS type on the metabolic characteristics of the proteins and true digested and absorbed protein supply to dairy cattle is shown in Table 2. Microbial protein synthesis according to the DVE/OEB system is based on FOM. Given that wheat contained a greater ($P < 0.05$) amount of FOM than DDGS samples (Table 2), MCP_{FOM} and AMCP^{DVE} were also greater ($P < 0.05$) for wheat; however, no differences ($P > 0.05$) were observed between corn and DDGS products. The content and digestibility of RUP was greater in DDGS samples relative to feedstock grains (Table 1); consequently, ARUP^{DVE} values were on average 5 times higher ($P < 0.05$) for DDGS. The variation in UDM was equally detected in ENDP, being higher ($P < 0.05$) in DDGS samples than in feedstock grains. As a result of these differences, mainly in ARUP^{DVE} , DVE values for DDGS were on average 2 times greater than those for feedstock grains. Similarly, DPB^{OEB} values were higher ($P < 0.05$) for DDGS samples than for feedstock grains.

The results showed that the different types of DDGS had an effect on the potential nutrient supply to cattle (Table 2). As the amount of wheat in feedstock increased, FOM and consequently AMCP^{DVE} increased. A similar trend was observed in UDM and subsequently in ENDP. Blend DDGS had the highest ($P < 0.05$) ARUP^{DVE} resulting in the highest ($P < 0.05$) DVE. The DPB^{OEB} values were positive; wheat DDGS was the highest ($P < 0.05$), followed by blend DDGS and corn DDGS.

Effects of Bioethanol Plants on the Metabolic Characteristics of the Proteins and True Digested and Absorbed Protein Supply to Dairy Cattle

The effects of bioethanol plants on the metabolic characteristics of the proteins and true protein supply

Table 2. Comparison of wheat dried distillers grains with solubles (DDGS), corn DDGS, and blend DDGS (wheat:corn 70:30) and comparison of different bioethanol plants in truly absorbed rumen-synthesized microbial protein, truly absorbed rumen-undegraded feed protein in the small intestine, endogenous protein losses in the digestive tract, prediction of nutrient supply to dairy cows, and degraded protein balance using the DVE/OEB system

Item ¹	Feed source					Feed source SEM	Bioethanol plant ²		Bioethanol plant SEM
	Wheat	Corn	Wheat DDGS	Corn DDGS	Blend DDGS (W:C = 70:30)		SK-plant 1	SK-plant 2	
Truly absorbed rumen-synthesized microbial protein in the small intestine, g/kg of DM									
FOM	792.5 ^a	562.6 ^{bc}	590.2 ^b	528.1 ^c	558.1 ^{bc}	15.85	563.2	608.1	19.83
MCP _{FOM}	118.8 ^a	84.4 ^{bc}	88.5 ^b	79.2 ^c	83.7 ^{bc}	2.38	84.5	91.2	2.98
RDP ^{DVE}	126.8 ^c	48.5 ^d	185.1 ^a	114.4 ^c	163.5 ^b	6.43	188.8	182.7	11.31
MCP _{RDP} ^{DVE}	122.1 ^b	40.6 ^d	160.6 ^a	89.9 ^c	138.8 ^b	6.87	163.2	158.9	12.20
AMCP ^{DVE}	75.8 ^a	53.8 ^{bc}	56.4 ^b	50.5 ^c	53.4 ^{bc}	1.52	53.9	58.2	1.90
Truly absorbed rumen-undegraded feed protein in the small intestine, g/kg of DM									
RUP ^{DVE}	47.1 ^c	80.1 ^b	247.3 ^a	247.1 ^a	249.5 ^a	9.38	258.1	240.1	18.58
ARUP ^{DVE}	35.6 ^c	55.8 ^c	199.7 ^b	204.0 ^b	234.6 ^a	9.42	230.8 ^a	178.9 ^b	11.86
Endogenous protein losses in the digestive tract, g/kg of DM									
UDM	59.6 ^b	24.3 ^c	97.6 ^a	51.5 ^b	94.8 ^a	5.06	103.9	93.5	8.36
ENDP	4.5 ^b	1.8 ^c	7.3 ^a	3.9 ^b	7.1 ^a	0.38	7.8	7.0	0.63
Total truly absorbed protein in the small intestine, g/kg of DM									
DVE	107.0 ^c	107.8 ^c	248.8 ^b	250.6 ^b	280.8 ^a	8.45	276.8 ^a	230.0 ^b	10.67
Degraded protein balance, g/kg of DM									
DPB ^{OEB}	3.3 ^c	-43.8 ^d	72.1 ^a	10.7 ^c	55.1 ^b	5.96	78.7	67.7	10.35

^{a-c}Means within a row with different superscripts differ significantly ($P < 0.05$).

¹FOM = OM fermented in the rumen (g/kg of DM; DVE/OEB); MCP_{FOM} = microbial protein synthesized in the rumen based on available energy (g/kg of DM; DVE/OEB); RDP^{DVE} = ruminally degraded feed CP, calculated according the formula in DVE/OEB system (g/kg of DM); MCP_{RDP}^{DVE} = microbial protein synthesized in the rumen based on rumen-degraded feed CP (g/kg of DM; DVE/OEB); AMCP^{DVE} = truly absorbed rumen-synthesized microbial protein in the small intestine (g/kg of DM; DVE/OEB); RUP^{DVE} = ruminally undegraded feed CP, calculated according the formula in DVE/OEB system (g/kg of DM); ARUP^{DVE} = truly absorbed rumen-undegraded feed protein in the small intestine (g/kg of DM; DVE/OEB); UDM = undigested DM (g/kg of DM); ENDP = endogenous protein losses in the digestive tract (g/kg of DM; DVE/OEB); DVE = truly absorbed protein in the small intestine (g/kg of DM), contributed by 1) feed protein escaping rumen degradation (RUP^{DVE}), 2) microbial protein synthesized in the rumen (MCP_{FOM}), and 3) a correction for endogenous protein losses in the digestive tract (ENDP; DVE/OEB). DPB^{OEB} reflects the difference between the potential microbial protein synthesis based on rumen-degraded feed CP and that based on energy (rumen-fermented OM) available for microbial fermentation in the rumen (DVE/OEB).

²Bioethanol plants located in western Canada. Both plants used local wheat feedstock for bioethanol production.

to dairy cattle are shown in Table 2. Between wheat DDGS from SK-plant 1 and SK-plant 2, difference was detected in the DVE value (277 vs. 230 g/kg of DM; $P < 0.05$), mainly because of the difference in $ARUP^{DVE}$ (231 vs. 179 g/kg of DM; $P < 0.05$). There was no difference ($P > 0.05$) in the DPB^{OEB} between SK-plant 1 and SK-plant 2.

DISCUSSION

The study showed significant effect of DDGS type (wheat DDGS, corn DDGS vs. blend DDGS) and bioethanol plant on the prediction of truly absorbed protein supply to dairy cows and DPB^{OEB} (Table 2). For truly absorbed rumen-synthesized microbial protein, wheat DDGS and corn DDGS were significantly different. The blend DDGS (wheat:corn 70:30) was in between. Comparing the grains and the DDGS samples, the DDGS samples were significantly lower in $AMCP^{DVE}$ than the original grains. This was mainly attributed to lower fermented OM in the DDGS sample compared with the original grains (Table 2). For truly absorbed RUP in the small intestine, the blend DDGS provided the higher $ARUP^{DVE}$ than the wheat DDGS and corn DDGS, although the RUP among 3 types of DDGS samples was similar (Table 2). This was mainly because the blend DDGS had highest estimated digestibility of RUP (Table 1). Comparing the grains and the DDGS samples, the DDGS samples were significantly higher in $ARUP^{DVE}$ than the original grains. This was mainly attributed to higher rumen effective degradability of CP in the grain samples (Table 1). For total truly absorbed protein in the small intestine, the blend DDGS provided the higher DVE value than the wheat DDGS and corn DDGS (Table 2), which indicated that the blend DDGS is a good source of metabolizable protein. Comparing the grains and the DDGS samples, the DDGS samples were significantly higher in DVE value than the original grains (Table 2). This was mainly attributed to lower ARUP value in the grain samples (Table 2).

The DVE values in Table 2 were the highest for blend DDGS and similar between wheat DDGS and corn DDGS. According to Tamminga et al. (1994), a lactating dairy cow producing 30 kg of milk with 3% CP requires DVE of 1,414 g/d of truly digested and absorbed protein in the small intestine, implying that 3 kg of wheat DDGS or 2.5 kg of blend DDGS in the ration (on a DM basis) would cover 50% of this requirement. In the prediction of the DPB^{OEB} , the DVE/OEB system assumes that 100% rumen-degraded dietary protein can potentially be converted to microbial protein if enough energy is supplied. The NRC (2001) model, however, assumes that only 85% of rumen-degraded dietary protein can be converted

by rumen microorganisms into protein, thus the factor ($1.18 = 100/85$) used in the NRC (2001) dairy model. Moreover, the concept and calculation of the predicted microbial protein synthesis in the rumen from available energy [FOM in the DVE/OEB vs. TDN in the NRC (2001) model] and the microbial protein synthesis in the rumen from available degraded protein differed. The MCP based on TDN contemplates more energy in the equation than MCP_{FOM} ; consequently, more N is required to achieve optimal rumen availability of N and energy according to the NRC (2001) model. The 1.11 correction factor is taken into consideration for the calculation of MCP_{RDP}^{DVE} but not for RDP in the NRC (2001) model.

The DVE of DDGS samples was on average 3 times higher than alfalfa and 3 times higher than barley (DVE: 84 vs. 249 g/kg of DM). Canola meal showed a lower protein value than wheat DDGS and corn DDGS (DVE: 180 vs. 249 vs. 251 g/kg of DM) besides showing a greater potential for N loss in the rumen. However, it was recently reported that canola meal can replace corn DDGS in dairy cattle diets without affecting animal performance (Mulrooney et al., 2009). This fact can be explained by the reduced availability of Lys in corn DDGS and the more desirable biological value of canola meal protein (Mulrooney et al., 2009). The protein value of soy meal was the closest to DDGS samples, particularly to blend DDGS (DVE: 291 vs. 281 g/kg of DM). Several studies showed that similar milk production is achieved when corn DDGS or soy meal are used as protein supplements (Nichols et al., 1998; Anderson et al., 2006). Differences in the AA availability between the 2 protein sources exist: DDGS are first limiting in Lys, whereas soy meal is first limiting in Met (Chandler, 1989; Kleinschmit et al., 2007).

There were significant plant effects on truly absorbed protein supply to dairy cattle ($ARUP^{DVE}$ and DVE) as shown in Table 1. These results indicated that different ethanol processing methods used in each plant (such as fermentation method, distillation, and DDGS drying method) or feedstock used in each plant, or both, may affect truly absorbed protein supply to dairy cattle.

The bioethanol plant effect was detected in the DVE values. The difference in the truly digested and absorbed protein values was largely contributed by the differences ($P < 0.05$) in the values of $ARUP^{DVE}$, which can be further attributed to a difference ($P < 0.05$) in ADICP content (0.7 vs. 7.6% CP; Table 1) between plants. Several studies (Arieli et al., 1989; McKinnon et al., 1995) have shown a negative relationship between the ruminal and postruminal availability of protein and the ADICP content resulted from heating. In DDGS, the relationship between ADICP and ruminal availability of protein has been found to be nonexistent

(Klopfenstein, 1996), to be moderate (Nakamura et al., 1994), or to be strong when ADICP levels were higher than 13% CP (Harty et al., 1998). In the present wheat DDGS samples, ADICP levels were different ($P < 0.05$) but lower than 13% CP, which explains the lack of effect on the protein disappearance in rumen. However, the difference in the ADICP content (Table 1) was reflected in tended differences ($P = 0.052$) in the digestibility of RUP (89.4 vs. 75.9% RUP; Table 1), which ultimately affected the intestinal availability of RUP as well as the predicted total postruminal protein supply and availability. As a result, the relationship between ADICP content and DVE for wheat DDGS was moderate and significant ($r = -0.74$; $P < 0.05$). This suggests a higher sensitivity of DDGS protein disappearance to low ADICP levels in the small intestine than in the rumen, as well as the important role of ADICP in the determination of truly absorbable protein in the small intestine. The difference in ADICP content and in the subsequent DVE values has also an economic impact. In this case, an extra 0.5 kg of wheat DDGS from SK-plant 2 would be required to meet 50% of the truly digested and absorbed protein in the small intestine required by a lactating dairy cow producing 30 kg of milk/d with 3% CP (DVE = 1,414 g/d; Tamminga et al., 1994). The variation in the metabolizable essential AA between bioethanol plants was not studied; however, Kleinschmit et al. (2007) concluded that for corn DDGS this variation was not as prominent as in the ruminal and postruminal availability of protein.

CONCLUSIONS

All types of DDGS are a good source of DVE. According to the DVE/OEB system, the predicted true protein supply differed among wheat DDGS, corn DDGS, and blend DDGS and, to a lesser extent, between different bioethanol plants. Therefore, it is inappropriate to assume fixed protein values for DDGS without considering factors such as DDGS type and bioethanol plant origin. The results showed the superior protein value (DVE) in blend DDGS and the more optimum DPB^{OEB} in corn DDGS. In addition, the difference in the ADICP content of wheat DDGS samples as a result of different operation philosophies between bioethanol plants was reflected in differing truly digested and absorbed protein value, suggesting the reliable use of ADICP as an indicator for the protein value of wheat DDGS for sample comparison purposes. It is important to remember that the current experiment evaluated DDGS as single ingredients and, thus, the modeling of a TMR containing different types and levels of DDGS would provide a more realistic approach of the differences in the ruminal and postruminal supply and availability of

protein as well as of the differences in the balance between available N and energy in rumen. Also, the DVE values do not contemplate the entire biological value of the protein. Therefore, other factors such as the availability of limiting AA must be carefully considered.

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