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Metabolic Characteristics of the Proteins in Yellow-Seeded and Brown-Seeded Canola Meal and Presscake in Dairy Cattle: Comparison of Three Systems (PDI, DVE, and NRC) in Nutrient Supply and Feed Milk Value (FMV)

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ABSTRACT: To the authors' knowledge, there is little research on metabolic characteristics of the protein in newly developed yellow and brown types of canola meal and canola presscake. The objectives of this study were to (1) identify differences in the metabolic characteristics of the protein among yellow-seeded (*Brassica juncea*) and brown-seeded (*Brassica napus*) canola meal and brown-seeded (*B. napus*) canola presscake modeled for dairy cattle, (2) determine the extent of ruminal and intestinal digestion and absorption of the protein, (3) determine feed milk value, and (4) compare three evaluation systems in modeling nutrient supply to dairy cattle, namely, the DVE/OEB system (DVE, truly absorbed protein in the small intestine; OEB, degraded protein balance), the National Research Council (NRC) 2001 model, and the PDI system (protein truly digestible in the small intestine). Comparison was made in terms of (1) ruminally synthesized microbial protein, (2) truly absorbed protein in the small intestine, (3) endogenous protein, (4) total metabolizable protein, and (5) degraded protein balance. The results showed that there were significant differences in the truly absorbed protein supply, protein degraded balance, and feed milk value ($P < 0.05$) among the different types of canola meal. Yellow-seeded canola meal had significantly higher ($P < 0.05$) intestinal digestibility of rumen undegraded crude protein (%dRUP) than brown-seeded canola meal and presscake (%dRUP, 90 vs 75 and 60%, respectively). Yellow-seeded canola meal also had higher ($P < 0.05$) total metabolizable protein predicted by all three models (DVE, 312 vs 192 and 128 g/kg DM; MP, 287 vs 193 and 168 g/kg DM; PDIA, 264 vs 168 and 137 g/kg DM, respectively), lower ($P < 0.05$) degraded protein balance (OEB, 84 vs 104 and 102 g/kg DM; DPB, 49 vs 60 and 57 g/kg DM, respectively), and higher ($P < 0.05$) feed milk value (6.3 vs 3.9 and 2.6 kg milk/kg feed, respectively) than the brown-seeded canola meal and presscake. In the model comparison, the supply of endogenous protein predicted by the DVE/OEB system was higher ($P < 0.05$) than that predicted by the NRC-2001 model. Moreover, a high proportion of the variability in truly absorbed rumen-undegraded feed protein in the small intestine and the total metabolizable protein predicted by the DVE/OEB system was found that can be accounted for by the equivalent parameters predicted by the NRC-2001 model. The truly absorbed rumen-synthesized microbial protein values predicted from the PDI system were 19% lower than those predicted from the DVE/OEB system. Between the two latest mentioned models, no differences were detected in truly absorbed rumen-undegraded feed protein, microbial protein supply based on available energy, and degraded protein balance. All of the parameters predicted by the PDI system can be accounted for by the equivalent parameters predicted by the DVE/OEB system. When the PDI system and NRC-2001 model were compared, the overall means for microbial protein supply based on energy and truly absorbed rumen-synthesized microbial protein were found to be lower than those predicted by the NRC-2001 model. Although the factors used in quantifying calculations as well as the evaluation system's concepts differ among each other, all three protein evaluation systems employed in this study efficiently predict the potential nutrient supply to the animal from feedstuffs as affected by processing. In conclusion, the yellow-seeded canola meal provided the highest total metabolizable protein and the lowest degraded protein balance.

KEYWORDS: *canola, protein metabolic characteristics, nutrient modeling*

INTRODUCTION

Canola is a major oilseed crop in western Canada and was developed from rapeseed by Canadian plant breeders in the 1970s. Unlike with traditional rapeseed, canola contains low levels of "erucic acid" in the oil portion (<2% of total fatty acids in the oil) and low levels of antinutritional compounds called "glucosinolates" in the meal portion (<30 μmol).[1] Canola meal includes the newly developed yellow-seeded and brown-seeded varieties; hulls from newly developed yellow-seeded types have been reported to have lower fiber content compared to those from brown-seeded types.[2−4] The intermediate product in the manufacturing process of canola oil and canola meal is called canola presscake.[5]

In ruminants, canola coproducts are good protein sources with high protein quality. However, metabolizable protein information is lacking for canola coproducts, particularly newly developed yellow-type canola coproducts. The metabolizable

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protein value is contributed from three sources: absorbed rumen bypassed protein, absorbed microbial protein synthesis, and indigenous protein sources, which are important in ruminant nutrient supply.

Ruminants can convert feeds into animal products under widely varying conditions worldwide; thus, there is a need to systematically evaluate the nutritive value of each feed. Improving ruminant nutrition could be pursued by enhanced productivity, whereas further improvements in ruminant production efficiency will result from the use of models; the latest models are able to predict nutrient requirements and feed utilization in specific production settings.

In terms of protein nutrition, the level of microbial protein synthesis and the amount of digestible protein in the intestine are important determinants of the response and efficiency with which dietary nitrogen is used for milk production. These points are taken into account in the most advanced protein evaluation systems, such as the NRC-2001 model,[7] the DVE/OEB system,[11] and the PDI system.[16]

So far, little research has been conducted to determine metabolic characteristics of the protein, potential nutrient supply, and feed milk value of canola coproducts by employing and comparing different evaluation systems. Although the principles of these models (DVE/OEB, PDI, and NRC-2001) are similar, some of the factors used in quantifying calculations and some concepts differ. The objectives of this study were to (1) identify differences in the metabolic characteristics of the protein and energy among yellow-seeded (*Brassica juncea*) and brown-seeded (*Brassica napus*) canola meal and brown-seeded (*B. napus*) canola presscake modeled for dairy cattle, (2) determine the extent of ruminal and intestinal digestion and absorption of the protein, (3) determine feed milk value, and (4) compare the three evaluation systems in modeling nutrient supply, namely, the DVE/OEB system (DVE, truly absorbed protein in the small intestine; OEB, degraded protein balance), the National Research Council (NRC) 2001 model, and the PDI system (protein truly digestible in the small intestine).

MATERIALS AND METHODS

The experiment was approved by the Animal Care Committee of the University of Saskatchewan, and all animals were cared for in accordance with the guidelines of the Canadian Council on Animal Care.[6]

Coproducts from Canola Processing. Different types of canola meal (CM) and canola presscake (CPC) were used in this study as protein sources. Canola coproduct samples of solvent-extracted yellow-seeded (*B. juncea*) canola meal (CM_Y) and brown-seeded (*B. napus*) canola meal (CM_B) from two different places were obtained from Bunge Altona (MB, Canada) and Lethbridge Research Center (AB, Canada). Moreover, brown-seeded (*B. napus*) canola presscake (CPC_B) was produced using a physical press method only and obtained from Milligan Biotech (Foam Lake, SK, Canada).

Animals and Diets. Three dry Holstein cows fitted with a rumen cannula, with an internal diameter of 10 cm (Bar Diamond, Parma, ID, USA), were used for the in situ rumen degradation parameters. Cows were housed in the research barn at the University of Saskatchewan during the whole study period. Cows were given ad libitum access to water and individually fed 15 kg (as fed) of a totally mixed ration twice daily (7.5 kg/feeding) at 8:00 a.m. and 4:00 p.m. formulated according to nutrient requirements of the NRC.[7] The total mixed ration consisted of 57% barley silage, 10% alfalfa hay, 5% dehydrated alfalfa pellets, and 28% concentrates (containing barley, wheat, oats, canola meal, soybean meal, wheat dried distillers grains with soluble, corn gluten meal, molasses, golden flakes, canola oil, minerals, and vitamins).

Rumen Incubation Procedure. Seven grams of individual ground samples was weighed into each preweighed and numbered nylon bag (10 × 20 cm; Nitex 03-41/31 monofilament open mesh fabric, Screentec Corp., Mississauga, ON, Canada) with the pore size of 40 μm. These bags were tied about 2 cm below the top, allowing a ratio of sample size to bag surface area of 19 mg/cm^2. Samples were incubated in the rumen for 0, 2, 4, 8, 12, 24, and 48 h. Rumen incubations were performed according to the "gradual addition/all out" schedule.[8] In this technique, the bags assigned for the longest incubation time (48 h) are put in the rumen first and then, after 24 h, because the first bags have been incubated in the rumen, the next bags with the next longest incubation time (24 h) are added and so on. The multiple bags for each treatment at each incubation time in each experiment run were 2, 2, 2, 2, 4, 4, and 5 bags for incubation times of 0, 2, 4, 8, 12, 24, and 48 h, respectively. The maximum number of bags in the rumen at any one time was 28.[8] Treatment samples were randomly assigned to the three dry rumen fistulated Holstein cows in two experimental runs. After the incubation, the bags were removed from the rumen and rinsed under a cold stream of tap water without detergent to remove excess ruminal contents and subsequently dried at 55 °C for 48 h and reweighed to complete the calculation. The 0 h incubation samples were only washed under the same conditions. The dried samples were kept in a refrigerated room (4 °C) until chemical analysis was performed. The residues of the nylon bags, from both two experimental runs, were collected according to the sample, incubation time, in situ run, and treatment.

Rumen Degradation Characteristics. In situ rumen degradation kinetics of CP were determined using the first-order kinetics equation described by Ørskov and McDonald[9] and modified by Robinson et al.[10] to include lag time:

$$R(t) = U + (100 - S - U) \times e^{-K_d \times (t - T_0)}$$

$R(t)$ = residue present at time h incubation (%); S = soluble fraction (%); U = undegradable fraction (%); T_0 = lag time (h); and K_d = degradation rate (%/h). The results were calculated using the PROC NLIN (nonlinear) procedure of SAS (SAS Institute, Cary, NC, USA) with iterative least-squares regression (Gauss−Newton method).

On the basis of the nonlinear parameters estimated by the above equation (S, U, and K_d), rumen-degraded feed CP (RDP) and rumen undegraded CP (RUP) were predicted according to the NRC-2001 model as

$$\text{RDP (g/kg of DM)} = S + (D \times K_d)/(K_p + K_d) \text{ and}$$

$$\text{RUP (g/kg of DM)} = U + (D \times K_p)/(K_p + K_d)$$

where D = potentially degradable fraction (%) and $D = 100 - S - U$ (%) and K_p is the estimated rate of outflow of digesta from the rumen (%/h), which was assumed to be 6%/h. [11]

Intestinal Digestibility of Rumen Undegraded Feed Protein. Intestinal digestibility of rumen undegraded feed protein (dRUP) was determined according to ruminants' protocol.[12] Briefly, dried ground rumen residues containing 15 mg of N after 12 h of ruminal incubation were exposed for 1 h to 10 mL of 0.1 N HCl solution containing 1 g of pepsin/L. The pH was then neutralized with 0.5 mL of 0.5 mol NaOH/L and 13.5 mL of pH 7.8 phosphate buffer containing 37.5 mg of pancreatin, which were added to the solution and incubated at 38 °C for 24 h. After 24 h of incubation, 3 mL of a 100% (w/v) trichloroacetic acid solution was added to precipitate undigested proteins. The samples were centrifuged, and the supernatant was analyzed for N (Kjeldahl method, AOAC 984.13). Intestinal digestion of protein was calculated as TCA-soluble N divided by the amount of N in the 12 h residue sample.

Nutrient Supply with the DVE/OEB System. On the basis of the DVE/OEB system provided by Tamminga et al. in 1994[11] and in 2007,[13] the detailed explanations and calculation were given in the following to understand how to calculate and predict protein supply to the small intestine of dairy cows as a result of feeding the above concentrates. The DVE/OEB system constitutes a two-part system in which each feed has a DVE and an OEB value. The DVE value

comprises digestible feed protein, microbial protein, and an endogenous protein loss correction. The DVE value was calculated as DVE = $AMCP^{DVE}$ + $ARUP^{DVE}$ − ENDP, where $AMCP^{DVE}$ is the absorbable fraction of microbial crude protein (MCP^{DVE}), $ARUP^{DVE}$ is the absorbable fraction of ruminally undegraded feed protein, and ENDP is a correction factor for endogenous protein lost during the digestion process.

The OEB value or degradable protein balance of a feed is the difference between the potential MCP synthesis based on RDP ($MCP_{RDP}{}^{DVE}$) and the potential MCP synthesis based on energy extracted from anaerobic fermentation (MCP_{FOM}). Therefore

$$OEB = MCP_{RDP}{}^{DVE} - MCP_{FOM}$$

where MCP_{RDP} was calculated as MCP_{RDP} = CP × [1 − (1.11 × RUP (% CP)/100)]. The factor 1.11 in the formula was taken from the French PDI system[14] and represents the regression coefficient of in vivo, on in situ degradation data.[11,13]

Microbial Protein Synthesis in the Rumen and Truly Absorbable Rumen Synthesized Microbial Protein in the Small Intestine. MCP_{FOM} was calculated as MCP_{FOM} = FOM × 0.15, where the factor 0.15 means that for each kilogram of rumen fermented OM (FOM), 150 g of microbial protein CP is assumed to be synthesized in the rumen.[11]

The FOM in the rumen was calculated as FOM (g/kg of DM) = DOM − Cfat − RUP − RUST − FP, where DOM = digestible organic matter, Cfat = ether extract, RUST = ruminally undegraded feed starch, and FP = fermentation products for conserved forages. FP and RUST were assumed to be zero for canola meal and canola presscake. Truly absorbable microbial protein synthesized in the rumen ($AMCP^{DVE}$) was calculated as $AMCP^{DVE}$ (g/kg of DM) = 0.75 × 0.85 × MCP_{FOM} (g/kg of DM), where 0.75 and 0.85 are constants representing the assumed amount and digestibility of the true protein contained in MCP_{FOM}, respectively.[11]

Rumen Undegraded Feed Protein and Truly Absorbed Rumen Undegraded Feed Protein in the Small Intestine. The content of truly absorbed rumen undegraded feed protein in the small intestine ($ARUP^{DVE}$) is based on the content and digestibility of RUP. The RUP^{DVE} was RUP^{DVE} (g/kg of DM) = 1.11 × [CP (g/kg of DM) × RUP^{DVE} (% CP)/100], so $ARUP^{DVE}$ was then calculated as $ARUP^{DVE}$ (g/kg of DM) = [dRUP (%) × RUP^{DVE} (g/kg of DM)] /100, where dRUP was estimated according to the method of Calsamiglia and Stern.[12]

Endogenous Protein Losses in the Small Intestine. Endogenous protein losses (ENDP) in the small intestine are associated with the amount of undigested dry matter (UDM), which was calculated as UDM (g/kg of DM) = (ash ×0.35) + [OM − ((OM × dOM)/100)]. In the equation, 0.35 is the constant utilized by CVB,[15] indicating that 35% of ash is not digested, and dOM = OM digestibility after 120 h of rumen incubation.[11] According to DVE/OEB, 75 g of protein will be absorbed per kilogram of undigested dry matter (UDM) to compensate for endogenous losses. Therefore, ENDP was calculated as ENDP (g/kg of DM) = 0.075 × UDM (g/kg of DM).

Truly Digested and Absorbed Protein in the Small Intestine and the Degraded Protein Balance. Truly digested and absorbed protein in the small intestine (DVE) is contributed by (1) feed RUP^{DVE}, (2) microbial protein synthesized in the rumen (MCP_{FOM}), and (3) a correction from ENDP. Therefore, the DVE value was calculated as DVE (g/kg of DM) = $ARUP^{DVE}$ + $AMCP^{DVE}$ − ENDP. The DPB value, which shows the balance between potential microbial synthesis based on rumen-degraded protein and potential protein synthesis based on energy extracted during anaerobic fermentation of OM in the rumen, was calculated as DPB^{OEB} (g/kg of DM) = $MCP_{RDP}{}^{DVE}$ − MCP_{FOM}.

Nutrient Supply with the NRC-2001 Model. On the basis of the NRC-2001 model,[7] the detailed explanations and calculation are given in the following.

Microbial Protein Synthesis in the Rumen. Potential ruminally synthesized microbial CP was calculated as MCP_{TDN} (g/kg of DM) = 0.13 × TDN (discounted) in the case that RDP exceeded 1.18 × TDN-predicted MCP (MCP_{TDN}). However, when RDP was less than 1.18 × TDN-predicted MCP (MCP_{TDN}), then MCP was calculated as 0.85 of RDP ($MCP_{RDP}{}^{NRC}$). The factor 0.13 means that 130 g of microbial CP is assumed to be synthesized per kilogram of discounted TDN.

Intestinal Digestion of Feed and Microbial Protein. In NRC-2001, true protein and digestibility of ruminally synthesized microbial CP are assumed to be 800 g/kg; therefore, the amount of truly absorbed MCP ($AMCP^{NRC}$) was calculated as $AMCP^{NRC}$ (g/kg of DM) = 0.80 × 0.80 × MCP_{TDN}. Truly absorbed rumen-undegraded protein in the small intestine was calculated as $ARUP^{NRC}$ = RUP^{NRC} × dRUP, where dRUP was estimated according to the method of Calsamiglia and Stern.[12]

Rumen Endogenous Protein in the Small Intestine. Rumen endogenous protein in the small intestine (ECP^{NRC}) was calculated as ECP (g/kg of DM) = 6.25 × 1.9 × DM. The 6.25 represents the protein/N conversion factor, and 1.9 indicates that 1.9 g of endogenous N is originated from 1 kg of DM. Assuming that 500 g/kg of rumen endogenous CP passes to the duodenum and 800 g/kg of rumen endogenous CP is true protein (NRC, 2001), the truly absorbed rumen endogenous protein in the small intestine (AECP) value was calculated as AECP (g/kg of DM) = 0.50 × 0.80 × ECP.

Total Metabolizable Protein. Total metabolizable protein (MP) in the NRC-2001 model is contributed by (1) ruminally undegraded feed CP (RUP^{NRC}), (2) ruminally synthesized microbial CP (MCP), and (3) rumen endogenous CP (ECP), calculated as MP (g/kg of DM) = $ARUP^{NRC}$ + $AMCP^{NRC}$ + AECP.

Degraded Protein Balance. Degraded protein balance (DBP^{NRC}), based on data from the NRC-2001 model, reflects the difference between the potential microbial protein synthesis based on RDP and the potential microbial protein synthesis based on energy (discounted TDN) available for microbial fermentation in the rumen. The DBP^{NRC} was calculated as DPB^{NRC} (g/kg of DM) = RDP^{NRC} − 1.18 × MCP_{TDN}.

Nutrient Supply with the PDI System. The principle of the PDI system (Verity and Geay, 1987; INRA, 1978)[24,25] has been used in this study to calculate the true protein truly digestible in the small intestine (PDI) value for different feed materials. The PDI content of a diet is the sum of two fractions: PDIA, the dietary protein undegraded in the rumen, but truly digestible in the small intestine; and PDIM, the microbial true protein, which is truly digestible in the small intestine. Each feed contributes to microbial protein synthesis by both the degradable and the available energy it supplies to the rumen microorganisms. Thus, each feed is characterized by two PDIM values: (1) PDIMN, which corresponds to the amount of microbial protein that could be synthesized in the rumen from the degraded dietary N, when energy and others nutrients are not limiting and (2) PDIME, which corresponds to the amount of microbial protein that could be synthesized from the energy available in the rumen, when degraded N and other nutrients are not limiting.

The value of each feed is given directly as the sum of PDIA and PDIM, considering separately each of the two possible situations:

$$PDIN = PDIA + PDIMN \text{ and } PDIE = PDIA + PDIME$$

The PDI values were obtained from four individual feed characteristics: (1) CP content, (2) degradability of crude protein (RDP^{PDI}) obtained from the rumen incubation procedure, (3) fermentable organic matter content (FOM) calculated from the total digestible organic matter (DOM) content after subtraction of the contents of ether extract and undegradable dietary protein in the feed and fermentation products in silage, and (4) true intestinal digestibility (TId) of rumen-undegraded dietary true protein (RUP^{PDI}).

Estimation of Microbial Protein Synthesis in the Rumen Based on Available Energy or on Ruminally Degraded Protein and Truly Absorbable Rumen Synthesized Microbial Protein in the Small Intestine. The microbial protein synthesis was predicted from FOM. Fermentable organic matter content was calculated as follows: FOM = DOM − EE − RUP^{PDI} (%CP). PDIME was calculated as PDIME = FOM × 0.145 × 0.8 × 0.8. The factor 0.145 represents the yield of microbial protein that is assumed to be 145 g CP/kg of FOM with regard to energy substrates; the amino acid content of both microbial

Table 1. Predicted Values of Potential Nutrient Supply to Dairy Cattle from Brown Canola Meal (CM, *B. napus*) and Yellow Canola Meal (CM, *B. juncea*) in Comparison with Brown Canola Presscake (CPC, *B. napus*) Using the Dutch DVE/OEB System[a]

	type of canola product					contrast, *P* value
item (g/kg of DM)	CM_Y *B. juncea*	CM_B *B. napus*	CPC_B *B. napus*	SEM[b]	*P* value	CM vs CPC
absorbable microbial protein synthesis in the rumen ($AMCP^{DVE}$)[c]						
FOM	579.8a	533.0a	434.8b	14.18	0.012	0.006
MCP_{FOM}	87.0a	80.0a	65.2b	2.13	0.012	0.006
$MCP_{RDP}{}^{DVE}$	171.1a	184.1a	167.2a	3.88	0.110	0.117
$AMCP^{DVE}$	55.5a	51.0a	41.6b	1.36	0.012	0.006
endogenous protein in the small intestine (ENDP)[d]						
ENDP	12.9b	20.2a	20.5a	0.27	0.001	0.001
truly absorbable rumen-undegraded protein in small intestine ($ARUP^{DVE}$)[e]						
RUP^{DVE}	250.2a	185.3b	167.2b	3.94	0.001	0.002
dRUP	903.8a	749.1b	601.4c	0.007, 24.40	0.005	
$ARUP^{DVE}$	269.7a	161.7b	107.6b	9.44	0.003	0.003
total truly digested protein in small intestine (DVE value)[f]						
DVE	312.2a	192.5b	128.6c	10.79	0.003	0.003
degraded protein balance (OEB value)[g]						
DPB^{DVE}	84.2b	104.1a	102.0a	1.76	0.007	0.035

[a]Means within a row with different letters differ ($P < 0.05$). [b]SEM, standard error of mean. [c]FOM, organic matter fermented in the rumen; MCP_{FOM}, microbial protein synthesized in the rumen based on available energy; $MCP_{RDP}{}^{DVE}$, microbial protein synthesized in the rumen based on rumen degraded feed crude protein; AMCP, truly absorbed rumen synthesized microbial protein in the small intestine. [d]ENDP, endogenous protein losses in the digestive tract. [e]RUP^{DVE}, ruminally undegraded feed CP, calculated according the formula in DVE/OEB system; $ARUP^{DVE}$, truly absorbed bypass feed protein in the small intestine. [f]DVE, truly absorbed protein in the small intestine 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). [g]DPB^{DVE}, reflects the difference between the potential microbial protein synthesis based on rumen degraded feed crude protein (CP) and that based on energy (rumen fermented OM) available for microbial fermentation in the rumen.

protein and their true digestibility in the small intestine are assumed to be constant and equal to 0.8.

The PDIMN was calculated as PDIMN = CP × (1 − 1.11 (1 − RDP^{PDI})) × 0.9 × 0.8 × 0.8, where 0.9 is the efficiency of conversion of degraded N to rumen microbial N and, as mentioned before, the amino acid content of microbial protein and their true digestibility in the small intestine are 0.8 and 0.8, respectively. The truly absorbable rumen synthesized microbial protein in the small intestine (MPS^{PDI}) was calculated as MPS^{PDI} (g/kg of DM) = CP × RDP^{PDI}/DOM.

Estimation of Rumen Undegraded Feed Protein and Truly Absorbed Rumen Undegraded Feed Protein in the Small Intestine. The RDP^{PDI} was assessed from the disappearance of protein from nylon bags, assuming a rumen particle outflow rate equal to 0.06 h^{-1}. The PDIA was calculated as PDIA = CP × (1.11 (1 − RDP^{PDI})) × TId, where the effective rumen bypass of protein is assumed to be 1.11 × (1 − RDP^{PDI}).

True Intestinal Digestibility of Rumen Undegraded Dietary Protein. The TId was calculated as TId (g/kg of DM) = 88.3 × 0.371 × CP − 0.0037 × CP^2 − 1.07 × ADL − 0.313 × UDOM, where CP and acid detergent lignin (ADL) are expressed in g/kg of DM and UDOM represents the indigestible organic matter.[16]

Estimation of the Degraded Protein Balance. Degraded protein balance (DPB^{PDI}) was calculated as DPB^{PDI} (g/kg of DM) = (PDIA + PDIMN) − (PDIA + PDIME).

To make the comparison of the microbial PDIME or PDIMN, with the DVE/OEB system and NR-2001 model, PDIME and PDIMN values were recalculated as

$$\begin{aligned} \text{PDIME} &= \text{FOM} \times 0.145, \ \text{PDIMN} \\ &= \text{CP} \times (1 - 1.11(1 - \text{RDP}^{\text{PDI}})), \text{ and PDIA} \\ &= \text{CP} \times (1.11(1 - \text{RDP})) \times \text{dRUP} \end{aligned}$$

The standard coefficients used to describe the digestive process were not used for the recalculation of the PDIME and PDIMN values. The reason was that with the DVE/OEB system and the NRC-2001 model, the efficiency of conversion of degraded N to rumen microbial N, the content of amino acids, and their digestibility are not taken into account. Also, PDIA was recalculated by using the value of dRUP, as used during the calculations for the other two models.

Feed Milk Value Determined on the Basis of Metabolic Characteristics of Protein. On the basis of the metabolic characteristics of protein from the DVE, NRC, and PDI models, the feed milk values were determined. The efficiency of use of metabolizable protein for lactation is assumed to be 0.67, and protein composition in milk is assumed to be 33 g protein/1000 g milk.

Statistical Analysis. Statistical analyses were performed using the MIXED procedure of SAS (version 9.2; SAS Institute, Inc., Cary, NC, USA; 2008). Data were analyzed with a CRD model: $Y_{ij} = \mu + T_i + e_{ij}$, where Y_{ij} was an observation of the dependent variable ij, μ was the population mean for the variable, T_i was the effect of feed sources, as a fixed effect (different samples as replications), and e_{ij} was the random error associated with the observation ij. Proc Univarite with Normal and Plot options was used to check residual assumption of CRD analysis.

Comparisons among the models were performed using the MIXED procedure of SAS 9.2 and analyzed with the multicomparison procedure. Regression analysis among the models was performed using the REG procedure of SAS. Proc Univarite with Normal and Plot options was used to check residual assumption of regression analysis.

The significance of differences between means was assessed using Tukey's test. For all statistical analyses, significance was declared at $P < 0.05$ and trends at $P \leq 0.10$.

RESULTS

Protein Supply to Dairy Cattle Using the DVE/OEB System. The effects of processing method and canola variety on protein supply to dairy cows obtained by using the DVE/OEB system are presented in Table 1. By comparison of CM_Y and CM_B, no significant differences were observed for FOM, MCP_{FOM}, and $MCP_{RDP}{}^{DVE}$. Consequently, $AMCP^{DVE}$ was not different between the two canola varieties used in this study. Canola presscake was lower ($P < 0.05$) compared to both

Table 2. Predicted Values of Potential Nutrient Supply to Dairy Cattle from Brown Canola Meal (CM, *B. napus*) and Yellow Canola Meal (CM, *B. juncea*) in Comparison with Brown Canola Presscake (CPC, *B. juncea*) Using the NRC-2001 Model[a]

	type of canola product					contrast, *P* value
item (g/kg of DM)	CM_Y *B. napus*	CM_B *B. juncea*	CPC_B *B. napus*	SEM[b]	*P* value	CM vs CPC
absorbable microbial protein synthesis in the rumen ($AMCP^{NRC}$)[c]						
MCP_{TDN}	89.0ab	77.8b	94.9a	2.24	0.027	0.024
$MCP_{RDP}{}^{NRC}$	158.8a	166.5a	163.6a	1.43	0.071	0.627
$AMCP^{NRC}$	56.9ab	49.8b	60.8a	1.43	0.027	0.025
absorbable endogenous true protein in the small intestine (AECP)[d]						
ECP	10.6b	10.5b	11.2a	0.04	0.002	0.001
AECP	4.2b	4.2b	4.5a	0.02	0.002	0.001
truly absorbable rumen-undegraded protein in small intestine ($ARUP^{NRC}$)[e]						
RUP^{NRC}	250.2a	185.3b	167.2b	3.94	0.001	0.002
dRUP	903.8a	749.1b	601.4c	24.40	0.007	0.005
$ARUP^{NRC}$	226.2a	138.8b	103.5c	5.34	0.001	0.001
total metabolizable protein (MP)[f]						
MP	287.3a	192.8b	168.8b	4.69	0.001	0.001
degraded protein balance (DPB^{NRC})[g]						
DPB^{NRC}	81.9a	104.0a	80.4a	4.21	0.048	0.094

[a]Means within a row with different letters differ ($P < 0.05$). [b]SEM, standard error of mean. [c]MCP_{TDN}, microbial protein synthesized in the rumen based on available energy (discounted TDN); $MCP_{RDP}{}^{NRC}$, microbial protein synthesized in the rumen based on available protein calculated as 0.85 of rumen degraded protein; $AMCP^{NRC}$, truly absorbed rumen-synthesized microbial protein in the small intestine. [d]ECP, rumen endogenous crude protein (CP); AECP, truly absorbed endogenous protein in the small intestine. [e]RUP^{NRC}, ruminally undegraded feed CP, calculated according the formula in NRC-2001 dairy model; dRUP, intestinal digestibility of rumen undegraded crude protein, estimated according to Calsamiglia and Stern;[12] $ARUP^{NRC}$, truly absorbed rumen-undegraded feed protein in the small intestine. [f]MP, metabolizable protein (true protein that is digested postruminally and the component amino acid absorbed by the intestine) contributed by (1) ruminally undegraded feed CP, (2) ruminally synthesized microbial CP, and (3) endogenous CP. [g]DPB^{NRC}, reflects the difference between the potential microbial protein synthesis based on ruminally degraded feed CP and that based on energy-TDN available for microbial fermentation in the rumen.

Table 3. Predicted Values of Potential Nutrient Supply to Dairy Cattle from Brown Canola Meal (CM, *B. napus*) and Yellow Canola Meal (CM, *B. juncea*) in Comparison with Brown Canola Presscake (CPC, *B. napus*) Using the French PDI System[a]

	type of canola product					contrast, *P* value
item (g/kg of DM)	CM_Y *B. juncea*	CM_B *B. napus*	CPC_B *B. napus*	SEM[b]	*P* value	CM vs CPC
absorbable microbial protein synthesis in the rumen (MPS^{PDI})[c]						
DOM	824.6a	731.6b	731.8b	3.14	<0.001	0.001
FOM	533.1a	496.9a	424.0b	11.30	0.014	0.007
PDIME	49.5a	46.1a	39.3b	1.05	0.014	0.007
PDIMN	98.6a	106.0a	96.3a	2.23	0.107	0.117
MPS^{PDI}	38.9b	44.9a	40.4ab	0.97	0.046	0.293
truly absorbable rumen undegraded protein in small intestine (PDIA)[d]						
RUP^{PDI}	250.2a	185.3b	167.2b	3.94	0.001	0.002
TId	883.6a	779.7b	768.8b	4.41	0.001	0.001
PDIA	263.6a	168.2b	137.2b	6.61	0.002	0.002
degraded protein balance (DPB^{PDI})[e]						
PDIN (= PDIA + PDIMN)	362.2a	274.2b	233.5b	8.65	0.004	0.004
PDIE (= PDIA + PDIME)	313.1a	214.3b	176.6b	7.20	0.002	0.002
DPB^{PDI} (= PDIN − PDIE)	49.1b	59.9a	57.0ab	1.52	0.038	0.278

[a]Means within a row with different letters differ ($P < 0.05$). [b]SEM, stardard error of mean. [c]DOM, digestible organic matter; FOM, fermentable organic matter in the rumen calculated from the DOM; PDIME, amount of microbial protein that could be synthesized from the available energy in the rumen, when degraded nitrogen (N) is not limiting; PDIMN, of microbial protein that could be synthesized in the rumen from the degraded dietary N when energy is not limiting; MPS, truly absorbed rumen synthesized microbial protein in the small intestine. [d]RUP^{PDI}, ruminally undegraded feed crude protein (CP); TId, true digestibility in the small intestine of the undegraded dietary true protein; PDIA, dietary protein undegraded in the rumen, [e]PDIN, digestible proteins in the small intestine where N is the limiting factor for rumen microbial activity; PDIE, digestible proteins in the small intestine where energy is the limiting factor for rumen microbial activity; DPB^{PDI}, balance between microbial protein synthesis from available rumen degradable CP and potential energy from anaerobic fermentation in the rumen.

canola meals (435 vs 556 mean value) and for FOM and MCP_{FOM} (65 vs 84 mean value), respectively. For CM_Y, endogenous protein loss in the small intestine was lower ($P < 0.001$) than for CM_B and CPC_B. The DVE value for CM_Y was nearly 2 times higher ($P < 0.05$) than that for CM_B. Comparison of the two varieties of canola meal (CM_Y and CM_B) with CPC_B revealed significant differences in truly digested protein in the small intestine, and CPC_B had a lower ($P < 0.05$) DVE value (Table 1). The OEB values for all treatments were determined to be positive with significant difference between CM_Y and CM_B. The OEB value was

Table 4. Feed Milk Value of Brown Canola Meal (CM, *B. napus*) and Yellow Canola Meal (CM, *B. juncea*) in Comparison with Brown Canola Presscake (CPC, *B. napus*) Based on Metabolic Characteristics of Protein Predicted by DVE, NRC, and PDI Systems[a]

	canola meal treatment					contrast, *P* value
item (kg milk/kg feed)	CM_Y *B. juncea*	CM_B *B. napus*	CPC_B *B. napus*	SEM[b]	*P* value	CM vs CPC
using DVE system	6.34a	3.91b	2.61c	0.22	0.003	0.003
using NRC system	5.83a	3.91b	3.43b	0.10	0.001	0.001
using PDI system	7.35a	5.57b	4.74b	0.18	0.004	0.004

[a]Means within a row with different letters differ ($P < 0.05$). The efficiency of use of metabolizable protein for lactation is assumed to be 0.67 (source NRC, 2001), and protein composition in milk is assumed to be 33 g protein/1000 g milk. [b]SEM, standard error of mean.

Table 5. Comparison of the DVE/OEB System, the NRC-2001 Model, and the PDI System in the Prediction of Protein Supply to Dairy Cows from the Feedstuffs Canola Meal and Canola Presscake[a]

	mean					contrast, *P* value			
item (g/kg of DM)	DVE/ OEB	NRC-2001	PDI	SEM[b]	*P* value	DVE vs NRC	DVE vs PDI	NRC vs PDI	NRC vs DVE + PDI
compared microbial protein supply based on available energy[c] MCP_{FOM} vs MCP_{TDN} vs PDIME	77.4ab	87.2a	70.3b	3.54	0.015	0.068	0.176	0.004	0.007
compared microbial protein supply based on ruminally degraded feed protein[d] MCP_{RDP} DVE vs MCP_{RDP} NRC vs PDIMN	174.1a	163.0a	174.1a	3.12	0.034	0.023	1.000	0.023	0.010
compared truly absorbed rumen-synthesized microbial protein[e] $AMCP^{DVE}$ vs $AMCP^{NRC}$ vs MPS^{PDI}	49.3a	55.8a	41.4b	2.09	<0.001	0.044	0.017	<0.001	0.001
compared truly absorbed rumen-undegraded feed protein[f] $ARUP^{DVE}$ vs $ARUP^{NRC}$ vs PDIA	179.6a	156.2a	180.6a	28.03	0.784	0.562	0.981	0.546	0.496
compared endogenous protein[g] ENDP vs AECP	17.9a	4.3b	–	1.11	<0.001	<0.001	–	–	–
compared total metabolizable protein[h] (truly absorbed protein) DVE vs MP	211.1a	216.3a	–	29.23	0.9025	0.9025	–	–	–
compared degraded protein balance[i] DPB^{OEB} vs DPB^{NRC} vs DPB^{PDI}	96.8a	88.8a	103.9a	4.34	0.078	0.212	0.265	0.026	0.046

[a]Means within a row with different letters differ ($P < 0.05$). –, not defined. [b]SEM, standard error of mean. [c]MCP_{FOM}, microbial protein synthesized in the rumen based on available energy; MCP_{TDN}, microbial protein synthesized in the rumen based on available energy (discounted TDN); PDIME, amount of microbial protein that could be synthesized from the available energy in the rumen, when degraded nitrogen (N) is not limiting. [d]MCP_{RDP}, microbial protein synthesized in the rumen based on available protein calculated as 0.85 of rumen degraded protein; MCP_{TDN}, microbial protein synthesized in the rumen based on available energy (discounted TDN); PDIMN, amount of microbial protein that could be synthesized in the rumen from the degraded dietary N when energy is not limiting. [e]$AMCP^{DVE}$, $AMCP^{NRC}$, truly absorbed rumen synthesized microbial protein in the small intestine; MPS^{PDI}, truly absorbed rumen synthesized microbial protein in the small intestine. [f]$ARUP^{DVE}$, $ARUP^{NRC}$, truly absorbed rumen undegraded feed protein in the small intestine; PDIA, dietary protein undegraded in the rumen, but truly digestible in the small intestine. [g]ENDP, endogenous protein losses in the digestive tract; AECP, truly absorbed endogenous protein in the small intestine. [h]DVE, truly absorbed protein in the small intestine contributed by (1) feed protein escaping rumen degradation (RUP), (2) microbial protein synthesized in the rumen (MCP_{FOM}), and (3) a correction for endogenous protein losses in the digestive tract (ENDP); MP, metabolizable protein (true protein that is digested postruminally and the component amino acid absorbed by the intestine) contributed. [i]DPB^{OEB}, reflects the difference between the potential microbial protein synthesis based on rumen degraded feed crude protein (CP) and that based on energy (rumen fermented OM) available for microbial fermentation in the rumen; DPB^{NRC}, reflects the difference between the potential microbial protein synthesis based on ruminally degraded feed CP and that based on energy-TDN available for microbial fermentation in the rumen; DPB^{PDI}, balance between microbial protein synthesis from available rumen degradable CP and potential energy from anaerobic fermentation in the rumen.

found to be higher ($P < 0.05$) for CM_B than for CM_Y (104 vs 84 g/kg DM)

Protein Supply to Dairy Cattle Using the NRC-2001 Model. Table 2 shows the results of using the NRC dairy model[7] to predict the potential nutrient supply of total metabolizable protein to dairy cattle from canola meal and presscake as affected by processing method. The $ARUP^{NRC}$ was significantly different between the two varieties of canola meal, and the higher value was obtained for CM_Y. Moreover, CM_B was significantly lower than CPC_B in MCP_{TDN} and, therefore, lower in $AMCP^{NRC}$. The CPC_B was significantly lower in RUP^{NRC}, which resulted in a lower ($P < 0.05$) value for the absorption of the $ARUP^{NRC}$ compared to canola meal (104 vs 183 mean values). Total metabolizable protein calculated from $AMCP^{NRC}$, AECP, and $ARUP^{NRC}$ was higher ($P < 0.05$) for CM_Y than for CM_B and CPC_B (Table 2). No significant differences were detected in DPB^{NRC} among the feedstuffs used in this study.

Protein Supply to Dairy Cattle Using the PDI System. Prediction of the potential nutrient supply to dairy cattle from canola coproducts, as affected by processing method, using the PDI system is shown in Table 3. Fermentable organic matter was higher ($P < 0.05$) for both canola meals than for CPC_B, which resulted in a higher amount of PDIME. Therefore, PDIME values were 50, 46, and 39 for CM_Y, CM_Bm and CPC_B, respectively ($P < 0.05$). The value of microbial protein synthesis in the rumen was significantly lower for CM_Y than the one for CM_B (Table 3). In relation with its higher ($P < 0.05$) RUP^{PDI}, the CM_Y had also a higher ($P < 0.05$) amount of PDIA, compared to the other treatments. The highest ($P < 0.05$) value of digestible protein in the small intestine was obtained for CM_Y compared to other treatments. Also, the balance between microbial protein synthesis, from available

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Table 6. Regression Equations for Prediction of Protein Supply from the DVE/OEB System Based on Values from the NRC-2001 Model for Feedstuffs Canola Meal and Canola Presscake

item (g/kg of DM)	linear regression equation			
	equation $Y = a\ (\pm SE) + b\ (\pm SE) \times x$	R^2	P value	RSD[a]
microbial protein supply based on available energy[b] MCP_{FOM} vs MCP_{TDN}	MCP_{FOM} = 137.93 (±45.56) − 0.69 (±0.52) × MCP_{TDN}	0.31	0.253	9.49
microbial protein supply based on ruminally degraded feed protein[c] $MCP_{RDP}{}^{DVE}$ vs $MCP_{RDP}{}^{NRC}$	$MCP_{RDP}{}^{DVE}$ = −85.54 (±142.34) + 1.59 (±0.87) × $MCP_{RDP}{}^{NRC}$	0.45	0.142	7.40
predicted truly absorbed rumen-synthesized microbial protein[d] $AMCP^{DVE}$ vs $AMCP^{NRC}$	$AMCP^{DVE}$ = 87.95 (±29.05) − 0.69 (±0.52) × $AMCP^{NRC}$	0.31	0.253	6.05
predicted truly absorbed rumen-undegraded feed protein[e] $ARUP^{DVE}$ vs $ARUP^{NRC}$	$ARUP^{DVE}$ = −24.93 (±7.28) + 1.31 (±0.0044) × $ARUP^{NRC}$	1.00	<0.0001	5.62
predicted endogenous protein[f] ENDP vs AECP	ENDP = −37.44 (±52.99) + 12.84 (±12.30) × AECP	0.21	0.355	3.80
predicted total metabolizable protein[g] (truly absorbed protein) DVE vs MP	DVE = −107.47 (±28.77) + 1.47 (±0.13) × MP	0.97	0.0003	16.30
predicted degraded protein balance[h] DPB^{OEB} vs DPB^{NRC}	DPB^{OEB} = 57.82 (±29.25) + 0.44 (±0.33) × DPB^{NRC}	0.31	0.250	9.28

[a]Residual standard deviation. [b]MCP_{FOM}, microbial protein synthesized in the rumen based on available energy; MCP_{TDN}, microbial protein synthesized in the rumen based on available energy (discounted TDN). [c]$MCP_{RDP}{}^{DVE}$, microbial protein synthesized in the rumen based on rumen degraded feed crude protein; $MCP_{RDP}{}^{NRC}$, microbial protein synthesized in the rumen based on available protein calculated as 0.85 of rumen degraded protein. [d]$AMCP^{DVE}$, $AMCP^{NRC}$, truly absorbed rumen synthesized microbial protein in the small intestine. [e]$ARUP^{DVE}$, $ARUP^{NRC}$, truly absorbed rumen undegraded feed protein in the small intestine. [f]ENDP, endogenous protein losses in the digestive tract; AECP, truly absorbed endogenous protein in the small intestine. [g]DVE, truly absorbed protein in the small intestine contributed by (1) feed protein escaping rumen degradation (RUP), (2) microbial protein synthesized in the rumen (MCP_{FOM}), and (3) a correction for endogenous protein losses in the digestive tract (ENDP); MP, metabolizable protein (true protein that is digested postruminally and the component amino acid absorbed by the intestine) contributed by (1) ruminally undegraded feed CP, (2) ruminally synthesized microbial CP, and (3) endogenous CP. [h]DPB^{OEB}, DPB^{NRC}, reflects the difference between the potential microbial protein synthesis based on rumen degraded feed crude protein (CP) and that based on energy (rumen-fermented OM) available for microbial fermentation in the rumen.

Table 7. Regression Equations for Prediction of Protein Supply from the PDI System Based on Values from the DVE/OEB System for Feedstuffs Canola Meal and Canola Presscake

item (g/kg of DM)	linear regression equation			
	equation $y = a\ (\pm SE) + b\ (\pm SE) \times x$	R^2	P value	RSD[a]
predicted microbial protein supply based on available energy[b] PDIME vs MCP_{FOM}	PDIME = 14.52 (±4.10) + 0.72 (±0.05) × MCP_{FOM}	0.98	0.0002	1.20
predicted microbial protein supply based on ruminally degraded feed protein[c] PDIMN vs $MCP_{RDP}{}^{DVE}$	PDIMN = (1.00 ± 0) × $MCP_{RDP}{}^{DVE}$	1.00	<0.0001	0
predicted truly absorbed rumen-synthesized microbial protein[d] MPS^{PDI} vs $AMCP^{DVE}$	MPS^{PDI}= 40.48 (±11.41) + 0.02 (±0.23) × $AMCP^{DVE}$	0.93	0.002	3.34
predicted truly absorbed rumen-undegraded feed protein[e] PDIA vs $ARUP^{DVE}$	PDIA = 4.16 (±2.58) + 0.98 (±0.01) × $ARUP^{DVE}$	1.00	<0.0001	2.24
predicted degraded protein balance[f] (PDIN − PDIE) DPB^{PDI} vs DPB^{OEB}	DPB^{PDI} = 22.55 (±12.62) + 0.84 (±0.13) × DPB^{OEB}	0.91	0.003	2.90

[a]Residual standard deviation. [b]PDIME, amount of microbial protein that could be synthesized from the available energy in the rumen, when degraded nitrogen (N) is not limiting; MCPFOM, microbial protein synthesized in the rumen based on available energy. [c]PDIMN, amount of microbial protein that could be synthesized in the rumen from the degraded dietary N when energy is not limiting; MCP_{RDP}, microbial protein synthesized in the rumen based on available protein calculated as 0.85 of rumen degraded protein. [d]MPS^{PDI}, truly absorbed rumen sythenesized microbial protein in the small intestine; $AMCP^{DVE}$, truly absorbed rumen synthesized microbial protein in the small intestine. [e]PDIA, dietary protein undegraded in the rumen, but truly digestible in the small intestine; $ARUP^{DVE}$, truly absorbed rumen undegraded feed protein in the small intestine. [f]DPB^{PDI}, balance between microbial protein synthesis from available rumen degradable CP and potential energy from anaerobic fermentation in the rumen; DPB^{OEB}, reflects the difference between the potential microbial protein synthesis based on rumen degraded feed crude protein (CP) and that based on energy (rumen-fermented OM) available for microbial fermentation in the rumen.

rumen degradable protein and potential energy in the rumen (DPB), was lower for CM_Y compared to CM_B ($P < 0.05$) and CPC_B ($P > 0.05$).

Feed Milk Value Determined on the Basis of Metabolic Characteristics of Protein. The feed milk values (kg milk yield/kg feed) of brown canola meal (CM, *B. napus*) and yellow canola meal (CM, *B. juncea*) in comparison with brown canola presscake (CPC, *B. napus*) based on metabolic characteristics of protein predicted by DVE, NRC and PDI system are shown in Table 4. Based on the MP value from the DVE system, the results show that CM_Y (*B. juncea*) had a higher ($P < 0.05$) feed milk value than CM_B (*B. napus*) and CPC_B (*B. napus*) (6.3 vs 3.9 and 2.6 kg milk, respectively). Similar trends were found for NRC and PDI prediction: CM_Y had a significantly higher feed milk value than CM_B or CPC_B.

Comparisons among DVE/OEB System, NRC-2001 Model, and PDI System in Prediction of Protein Supply to Dairy Cows. The averages of the predicted values for CM_Y, CM_B, and CPC_B, modeled according to the DVE/OEB system, the NRC-2001 model, and the PDI system, as well as the comparison among those models are presented in Table 5.

Comparison between the DVE/OEB System and the NRC-2001 Model in the Prediction of Protein Supply to Dairy Cows. Using the DVE/OEB system, the mean supply of endogenous protein was higher ($P < 0.05$) by 14 g/kg of DM than the value predicted with the NRC-2001 model. Moreover,

Table 8. Regression Equations for Prediction of Protein Supply from PDI System Based on Values from NRC-2001 Model for Feedstuffs Canola Meal and Canola Presscake

item (g/kg of DM)	linear regression equation			
	equation $y = a$ (±SE) + b (±SE) × x	R^2	P value	RSD[a]
predicted microbial protein supply based on available energy[b] PDIME vs MCP_{TDN}	PDIME = 113.11 (±33.57) − 0.49 (±0.38) × MCP_{TDN}	0.29	0.269	6.99
predicted microbial protein supply based on ruminally degraded feed protein[c] PDIMN vs MCP_{RDP}^{NRC}	PDIMN = −85.54 (±142.34) + 1.59 (±0.87) × MCP_{RDP}^{NRC}	0.45	0.142	7.40
predicted truly absorbed rumen-synthesized microbial protein[d] MPS^{PDI} vs $AMCP^{NRC}$	MPS^{PDI} = 68.37 (±8.66) − 0.48 (±0.15) × $AMCP^{NRC}$	0.71	0.035	1.80
predicted truly absorbed rumen-undegraded feed protein[e] PDIA vs $ARUP^{NRC}$	PDIA = −20.66 (±4.76) + 1.29 (±0.03) × $ARUP^{NRC}$	1.00	<0.0001	3.67
predicted degraded protein balance[f] (PDIN − PDIE) DPB^{PDI} vs DPB^{NRC}	DPB^{PDI} = 58.49 (±20.89) + 0.51 (±0.23) × DPB^{NRC}	0.55	0.093	6.63

[a]Residual standard deviation. [b]PDIME, amount of microbial protein that could be synthesized from the available energy in the rumen, when degraded nitrogen (N) is not limiting; MCP_{TDN}, microbial protein synthesized in the rumen based on available energy (discounted TDN). [c]PDIMN, amount of microbial protein that could be synthesized in the rumen from the degraded dietary N when energy is not limiting; MCP_{RDP}, microbial protein synthesized in the rumen based on available protein calculated as 0.85 of rumen degraded protein; AMCP, truly absorbed rumen-synthesized microbial protein in the small intestine. [d]MPS^{PDI}, truly absorbed rumen synthesized microbial protein in the small intestine; $AMCP^{NRC}$, truly absorbed rumen synthesized microbial protein in the small intestine. [e]PDIA, dietary protein undegraded in the rumen, but truly digestible in the small intestine; $ARUP^{NRC}$, truly absorbed rumen undegraded feed protein in the small intestine. [f]DPB^{PDI}, balance between microbial protein synthesis from available rumen degradable CP and potential energy from anaerobic fermentation in the rumen; DPB^{NRC}, reflects the difference between the potential microbial protein synthesis based on ruminally degraded feed CP and that based on energy-TDN available for microbial fermentation in the rumen.

even though the MCP_{TDN} and $AMCP^{NRC}$ values were 12.7 and 13.2%, respectively, greater in the NRC-2001 model than in the DVE/OEB system, differences between these values did not reach a significant level ($P > 0.05$) (Table 6).

Linear regression equations of the main average predicted nutritional values between the NRC-2001 model and the DVE/OEB system with the different types of canola meal are presented in Table 6. The results indicated that not all of the regression equations were significant ($P > 0.05$); however, a high proportion of the variability in truly absorbed rumen-undegraded feed protein in the small intestine ($R^2 = 1.00$) and predicted total metabolizable protein ($R^2 = 0.97$) according to the DVE/OEB system can be accounted for in the equivalent parameters predicted by the NRC-2001 model.

Comparison between the PDI System and the DVE/OEB System in the Prediction of Protein Supply to Dairy Cows. The results indicated that the predicted values from the PDI system were 19% lower ($P < 0.05$) in the truly absorbed rumen-synthesized microbial protein than the predicted values from the DVE/OEB system (Table 5). No significant differences were detected in terms of truly absorbed rumen-undegraded feed protein; microbial protein supply based on available energy and degraded protein balance between the two models.

Linear regression of the predicted nutritional values between the PDI and the DVE/OEB system are presented in Table 7. All the regression equations were significant ($P < 0.05$), and all of the parameters predicted by the PDI system can be accounted for by the equivalent parameters predicted by the DVE/OEB system.

Comparison between the NRC-2001 Model and PDI System and in Prediction of Protein Supply to Dairy Cows. The comparison between the NRC-2001 model and PDI system is presented in Table 5. The results showed that using the PDI system, the overall mean for microbial protein supply, based on energy and truly absorbed rumen-synthesized microbial protein, were lower (−17 and −14 g/kg of DM, respectively) than the same values predicted by the NRC-2001 model.

Linear regression of the main average predicted nutritional values between the PDI system and the NRC-2001 model are presented in Table 8. The regression equations were significant ($P < 0.05$) for the truly absorbed rumen-synthesized microbial protein ($R^2 = 0.71$) and the truly absorbed rumen-undegraded feed protein ($R^2 = 1.00$) predicted according to the PDI system.

DISCUSSION

Metabolic Characteristics of Protein in Canola Coproducts. Comparison of three types of canola coproducts revealed significant differences in the truly absorbed protein supply, protein degraded balance, and feed milk value. Yellow-seeded canola meal had significantly higher intestinal digestibility of rumen-undegraded crude, total metabolizable protein, and feed milk value, but lower degraded protein balance, than brown-seeded canola meal and presscake (Tables 1−3). All canola coproducts had higher metabolizable protein level than barley, oat, triticale, and wheat.[22,23] These results also showed that feed milk values are much higher than those of cereal grain (Table 4). Low protein degraded balance indicated lower potential N loss than those of cereal grains. All of these results indicate that canola coproducts, particularly yellow-type canola coproducts, are excellent metabolizable protein sources.

With the increased knowledge gained concerning ruminants' N metabolism, different evaluation systems have been developed to quantitatively predict protein nutrient supply to dairy cows. This study provides information on the prediction of protein supply to dairy cows by employing and comparing three different evaluation systems.

Prediction of Endogenous Protein. A notable difference is the concept and calculation of endogenous protein in the digestive process. In the DVE/OEB system, the truly digested and absorbed protein in the small intestine requires a correction for endogenous protein losses,[11] which are affected by undigested dry matter. According to the DVE/OEB system, 75 g of absorbed protein/kg undigested DM in fecal excretion is required to compensate for the endogenous losses. In the NRC-2001 model, calculation of the metabolizable protein (MP) value considers rumen endogenous protein (AECP)

passed on to the small intestine and contributes to the total metabolizable protein value. Also, the rumen endogenous protein is associated with dry matter content. Although the endogenous protein losses in the small intestine are taken into account by the NRC-2001 model, its value is added to requirements rather than subtracted from supply.

In our study the DVE value predicted by the DVE/OEB system was about 2.5% lower than the value obtained by using the NRC-2001 model. The same trend was found in forages (alfalfa and timothy)[17] in which the amounts of total absorbable protein supply to small intestine predicted by using DVE/OEB system (DVE values) were 15% lower than predictions by the NRC-2001 model (MP values). In agreement with these results, Heendeniya et al.[18] predicted that DVE values were lower than MP values for canola meal.

Furthermore, it should be mentioned that in the DVE/OEB system the endogenous protein (ENDP) is considered as a loss. Thus, a comparatively higher ENDP value was estimated from the DVE/OEB model for canola meal and presscake compared to AECP.

In contrast with the previously mentioned models, the PDI system does not consider the endogenous protein for the calculation of the truly absorbed protein in the small intestine. Therefore, no comparison was made between PDI and the other two evaluation systems, not only for endogenous but also for total metabolizable protein as well.

Prediction of Truly Absorbed Rumen-Undegraded Feed Protein. In all three models compared, the truly absorbed rumen-undegraded feed protein in the small intestine was calculated as the product of the rumen-undegraded feed protein and the digestibility of feed protein in the intestine. However, the prediction of rumen-undegraded feed protein differs among the models; whereas the DVE/OEB andPDI systems use a coefficient (1.11) to correct the in situ degradation data on in vivo results, no correction factor is used by the NRC-2001 model.

Prediction of Microbial Protein Synthesis in the Rumen Based on Available Energy. The prediction of the potential microbial protein synthesized in the rumen from all three models used in this study was based on available energy. The DVE/OEB system, as well as the PDI system, uses rumen-fermented OM as the energy base to predict microbial protein. However, the NRC-2001 model uses available TDN as its energy base. Furthermore, each model uses different factor parameters to calculate microbial protein synthesized in the rumen.

Another difference among the evaluation systems compared concerns the microbial protein synthesis. Specifically, the DVE/OEB system assumes 150 g of microbial protein to be synthesized/kg fermented OM, the PDI system assumes 145 g of microbial protein to be synthesized with regard to energy substrates, and the NRC-2001 model assumes 130 g of microbial protein CP is to be synthesized/kg TDN. Moreover, the amount of truly absorbable rumen-synthesized microbial protein was calculated differently among the models. In the DVE/OEB system, the amount of truly absorbed rumen-synthesized microbial protein in the small intestine was estimated as $0.85 \times 0.75 \times MCP_{FOM}$ as the system assumes that true digestibility of microbial protein is 85%[19] and 75% of microbial N is present in amino acids; the remaining is N in nucleic acids. In the NRC-2001 model, digestibility and true protein of ruminally synthesized microbial CP are assumed to be 80%; therefore, the amount of truly absorbed rumen-synthesized microbial protein in the small intestine was estimated as $0.80 \times 0.80 \times MCP$. Although the individual coefficients differ, the net result is essentially the same between the two models (0.85×0.75) vs (0.80×0.80). In our study no significant difference was detected in terms of the microbial protein supply based on available energy. This is in contrast with Yu et al.,[8] who found for different concentrate feeds (barley, beans, lupins, soybeans) that the overall average microbial protein supply, based on available energy, was 10% lower than that predicted by the NRC-2001 model. The reason for such a difference may be due to feed types.

In the PDI system, the PDIME was estimated as CP × RDP/DOM. This difference in quantifying calculation as well as the concept of the microbial protein supply based on available energy resulted in a lower PDIME value compared with MCP_{TDN} by almost 19%.

Prediction of Microbial Protein Supply Based on Ruminally Degraded Feed Protein. The concept and calculation for the prediction of microbial protein supply based on ruminally degraded feed protein among models is different. In the DVE/OEB system,[11] it is assumed that 100% ruminally degraded feed protein could be potentially converted to microbial protein if enough energy is provided. However, in the NRC-2001 model, it is assumed that only 85% of ruminally degraded feed protein could be potentially converted to microbial protein. In the PDI system, it is assumed that 90% of the rumen-degraded protein is converted to microbial protein because some unavoidable losses such as unusable N fraction or rumen outflow may occur.[20,21]

A comparison in the prediction of nutrient supply to dairy cows from forages between the DVE/OEB system and the NRC-2001 model has been carried out by Yu et al.[17] In that study it was found that AMCP and ARUP values derived from the DVE/OEB system were consistently higher that those derived from the NRC-2001 model, for both alfalfa and timothy samples. However, in our study, only the $ARUP^{DVE}$ value was observed to be numerically higher than that predicted by the NRC-2001 model. In agreement with our results, Heendeniya et al.[18] found that the AMCP and ARUP values predicted for canola meal using the DVE/OEB system were lower than those of the NRC-2001 model. Nevertheless, in the same study they noted that the opposite results were found for soy meal.

Prediction of Degraded Protein Balance (DPB). The DPB shows the (im)balance between microbial protein synthesis from available rumen-degradable CP and potential energy from anaerobic fermentation in the rumen. When the DPB in a ration is positive, it indicates the potential N-loss from the rumen, and when it is negative, microbial protein synthesis is predicted to be impaired because of a potential shortage of N in the rumen. The optimum DPB in a ration is, therefore, zero or slightly higher.[11] The DPB values predicted by the three models showed that all of the feedstuffs exhibited positive DPB values. This indicates that availability of feed protein exceeds the availability of energy (extracted during rumen fermentation) for microbial protein synthesis in all different types of canola samples, which results in a potential nitrogen loss in the rumen. [11]

Generally, on the basis of the findings of the current study and published results by others[18,22,23] it appears that these three models could interact with different factors such as feed type, processing method, or variety. Therefore, standardization of sample processing and analytical procedures and grouping the feeds into categories based on chemical and physical character-

istics may increase the predictability and accuracy of data extrapolation from one model to another.

Conclusion. Comparison of three types of canola coproducts showed significant differences in the truly absorbed protein supply, protein degraded balance, and feed milk value among the different types of canola meal. Yellow-seeded canola meal had significantly higher intestinal digestibility of rumen-undegraded crude, total metabolizable protein, and feed milk value, but lower degraded protein balance, than brown-seeded canola meal and presscake. When the DVE/OEB system was compared with the NRC-2001 model, not all of the regression equations were significant; however, a high proportion of the variability in truly absorbed rumen-undegraded feed protein in the small intestine and the total metabolizable protein predicted by the DVE/OEB system was found, which can be accounted for by the equivalent parameters predicted by the NRC-2001 model. The results show that the truly absorbed rumen-synthesized microbial protein values predicted from PDI system were 19% lower than those predicted from the DVE/OEB system. All of the parameters predicted by the PDI system can be accounted for by the equivalent parameters predicted by the DVE/OEB system. When the PDI system and NRC-2001 model were compared, the overall means for microbial protein supply based on energy and truly absorbed rumen-synthesized microbial protein were found to be lower than those predicted by the NRC-2001 model. By using all of the protein evaluation systems compared in this study, it is possible to predict the potential nutrient supply to the animal from feedstuffs as affected by processing. Due to the fact that the results reported here were outputs from models with inputs based on in vitro and in situ studies, the challenge is to apply the prediction and evaluate them in animal experiments. However, the number of such studies in this area available to challenge the model is extremely limited.

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Notes

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