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Chemical and ruminal in vitro evaluation of Canadian canola meals produced over 4 years[1]

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ABSTRACT

To test the effects of year and processing plant on the nutritional value of canola meal (CM), 3 CM samples/yr were collected from each of 12 Canadian production plants over 4 yr (total = 144). Samples of CM were analyzed for differences in chemical composition and for in vitro ruminal protein degradability using the Michaelis-Menten inhibitor in vitro (MMIIV) method. In the MMIIV method, protein degradation rate (k_d) was estimated by 2 methods: from net release (i.e., blank corrected) of (1) ammonia plus AA determined by *o*-phthaldialdehyde fluorescence (OPA_F) assay or (2) ammonia, AA, plus oligopeptides determined by *o*-phthaldialdehyde absorbance (OPA_A) assay; rumen-undegradable protein (RUP) was computed assuming passage rates of 0.16 and 0.06/h for, respectively, soluble and insoluble protein. Casein, solvent soybean meal (SSBM), and expeller soybean meal (ESBM) were included in all incubations as standard proteins. Differences among years and plants were assessed using the mixed procedures of SAS. Small but significant differences were found in CM among years for chemical composition, including N solubility; some of these differences may have been related to changes in our analytical methods over time. However, adjustment of degradation activity of individual in vitro incubations based on the mean degradation activity over all incubations yielded k_d and RUP that did not differ by year using either assay. Simultaneously incubating CM samples from 2 yr in the same in vitro runs confirmed that no year effects existed for k_d or RUP. Differences existed in chemical composition of CM among the 12 processing plants over the 4 yr of sample collection. Moreover, consistent differences in k_d and RUP were observed among plants: k_d ranged from 0.069 to 0.113/h (OPA_A assay) and 0.075 to 0.120/h (OPA_F assay), and RUP estimates ranged from 51 to 43% (OPA_A assay) and 49 to 41% (OPA_F assay). Regression of k_d on insoluble N content of CM yielded correlation coefficients (R^2) = 0.40 (OPA_A assay) and 0.42 (OPA_F assay), and regressions of k_d on NDIN and N-fraction B_3 yielded $R^2 < 0.02$. Mean estimates from both OPA_A and OPA_F assays for casein, SSBM, ESBM, and CM were, respectively, k_d = 0.764, 0.161, 0.050, and 0.093/h and RUP = 18, 33, 56, and 45%. A range of 8 percentage units from lowest to highest RUP suggests that substantial differences exist in metabolizable protein content of CM produced by different processing plants.

Key words: canola meal, chemical composition, ruminal degradation, rumen-undegraded protein

INTRODUCTION

Increased production of canola has resulted in greater availability of canola meal (**CM**) as an alternative to soybean meal (**SBM**) for protein supplementation of lactating dairy cows (Hickling, 2008). Meta-analyses of published findings showed that replacing SBM with CM significantly increased milk protein yield (Martineau et al., 2013) and increased feed intake and yield of milk and milk components (Huhtanen et al., 2011). We observed numeric increases in milk and protein yield when CM replaced supplemental protein from SBM in 16.5% CP diets in dairy cows (Brito and Broderick, 2007). Brito et al. (2007) found that the proportion of RUP in CM was numerically greater than that in SBM. Huhtanen et al. (2011) also concluded that CM contributed amounts of RUP and MP that were at least equal to SBM. Ruminal in situ studies conducted by Maxin et al. (2013a) showed that SBM had a more rapid degradation rate, higher effective degradability, and lower RUP than CM. More recently (Broderick et al., 2015),

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increased DMI and yield of milk and milk protein were associated with reduced ruminal concentrations of ammonia and branched-chain VFA in cows fed CM versus SBM, suggesting lower ruminal degradation of CM protein. The National Research Council (NRC, 2001) model indicates ruminal protein degradation rates of 7.5%/h for 48% SBM and 10.4%/h for CM, and RUP values of 43% for 48% SBM and 36% for CM (at DMI = 4% of BW with 50% dietary DM fed as forage). These NRC (2001) data appear to be inconsistent with the greater RUP in CM reported by Maxin et al. (2013a) and the reduced ruminal ammonia and branched-chain VFA concentrations observed by Broderick et al. (2015) when CP from CM replaced equal CP from SBM.

Other evidence indicates that CM may be a more effective protein supplement than certain byproduct feeds such as distillers dried grains plus solubles (**DDGS**): Swanepoel et al. (2014) observed that replacing corn DDGS with CM increased both milk and true protein yield. Although milk and protein yield were not different, Acharya et al. (2015) found that replacing corn DDGS with CM significantly improved efficiency of MP utilization. Mutsvangwa et al. (2016) reported that substituting CM for wheat DDGS gave a numeric yield increase of 1.1 kg of milk/d plus increased omasal flow of Thr and Trp and tended to increase omasal flow of His and Lys.

Growing conditions experienced in canola production vary substantially from year to year, and we speculated that these differences might alter the nutritional quality of CM for ruminants. Therefore, the objectives of this study were to (1) determine if year of CM production had a significant effect on chemical composition and ruminal protein degradability; (2) determine if CM production plant led to significant differences in chemical composition and ruminal protein degradability; and (3) assess the relative ruminal degradability of protein in CM and SBM.

MATERIALS AND METHODS

Protein Samples

Canola meal samples were collected over 4 yr (2011, 2012, 2013, and 2014), 3 per year, from each of 12 Canadian canola processing plants (total = 144 samples). The 12 plants accounted for the entire CM production in Canada when the studies began; however, a 13th plant has recently come online. About 80% of the CM produced in North America derives from these plants (Carson Callum, Canola Council of Canada, Winnipeg, MB, personal communication). At 11 plants, oil was removed from crushed canola seed by prepress solvent extraction; oil was removed by expeller extraction at 1 plant. The 144 CM samples were identified by plant number (1–12), production year (2011–2014), and replicate within year (1–3). Prior to chemical and in vitro analysis, samples were ground using a laboratory mill fitted with a 1-mm screen (Udy cyclone mill, Udy Corporation, Fort Collins, CO). Three standard proteins were also included in all in vitro incubations: casein (no. C-5890, Sigma Chemicals, St. Louis, MO), solvent-extracted SBM (**SSBM**), and expeller-extracted SBM (**ESBM**). These same standard proteins had been incubated in earlier in vitro studies (Colombini et al., 2011).

Donor Animals and Diets

Ruminal inocula used in the incubations were obtained from 2 lactating Holstein donor cows surgically fitted with ruminal cannulas (Bar Diamond, Parma, ID) and fed a diet composed of 40% alfalfa silage, 20% corn silage, 31.3% ground shelled corn, 8.0% SSBM, 0.4% sodium bicarbonate, and 0.2% salt plus vitamins and trace minerals (on a DM basis) and formulated to 16.5% CP and 1.6 Mcal NE_L/kg DM (at 3× maintenance; NRC, 2001). About 5 min elapsed between collection of inocula and the start of strained ruminal fluid (**SRF**) pre-incubation for incubations conducted in 2011, 2013, and 2014. The University of Wisconsin facility housing donor animals was not available in 2012, necessitating that donor animals be maintained at the US Dairy Forage Research Center farm, which is 40 km from the laboratory. Thus, inocula used in incubations conducted in 2012 were obtained from 2 lactating Holstein donor cows, similarly fitted with ruminal cannulas and fed the same basal diet; however, about 50 min elapsed between collection of inocula and the start of SRF pre-incubations. Surgical care and general maintenance of the animals was as outlined by the guidelines of the University of Wisconsin institutional animal care and use committee.

Chemical Analysis

The CM samples were chemically analyzed in duplicate during the year of collection. Composition data of the 3 standard proteins (casein, SSBM, and ESBM) determined in 2011 were used in computations over all 4 yr. All samples were analyzed for total N (Leco FP-2000 N Analyzer; Leco Instruments, Inc., St. Joseph, MI), DM (method 967.03; AOAC, 1990), ash and OM (method 942.05; AOAC, 1990), sequentially for NDF, ADF, and ADIN using heat stable α-amylase and Na_2SO_3 (Van Soest et al., 1991; Hintz et al., 1996), and for NDIN omitting α-amylase and Na_2SO_3 during