Evaluation of mathematical models to describe protein fraction degradation kinetics of various oilseed meals

M Danesh Mesgaran, T Tashakkori, A Heravi Moussavi, S Danesh Mesgaran, A Vakili, A A Aslaminejad
Dept of Animal Science, Ecellence Centre for Animal Science, Ferdowsi University of Mashhad, Mashhad, Islamic Republic of Iran *Email: danesh@um.ac.ir*

Introduction *In situ* procedure is a direct method of measuring the rumen degradation kinetic of a feed nutrient. Data obtained by this technique are generally analysed using an exponential curve (Ørskov and McDonald, 1979). However, very low attention has been paid to choice of mathematical model to fit the curves and goodness-of-fit of the model. Lopez *et al.* (1999) pointed out that the disappearance of some feed components, particularly structural carbohydrates, exhibits a larger variety of forms than for crude protein (CP). In the present study, two different mathematical models of a straight line or a negative exponential (France *et al.*, 1990; and Ørskov and McDonald, 1979) were selected to evaluate *in situ* degradation kinetics of protein fractions including true protein (TP), neutral-detergent insoluble protein (NDIP) and acid-detergent insoluble protein (ADIP) of various oilseed meals (cottonseed meal (CSM), soyabean meal (SM) and rapeseed meal (RM)).

Materials and methods Samples of various oilseed meals including CSM, SM and RM were collected from oil industries located in east Iran during May-September, 2006. Four Holstein steers (330±15 kg body weight) were used. Animals fed a diet consisted of 1.7 kg wheat straw, 3.8 kg lucerne hay and 3.4 kg of a commercial concentrate (CP: 184 g/kg dry matter (DM)) at 0800 and 1800 h. In order to determine protein fraction degradability coefficients, 5 g DM equivalent of each sample (ground with a 2-mm screen mill) was placed in individual polyester bags (50 µm pore size and averaged 12 cm × 19 cm). Incubation times were 2, 4, 8, 16, 24, 48, 72 and 96 h. Bags were placed in the dorsal sac of the reticulorumen of each steer (2 bags per each sample in each steer). Immediately after incubation, the bags were hand washed thoroughly in cold running water. Two bags of each feed sample were washed without incubation in the rumen (0.0 h samples). The bags were dried in a forced-air oven (58 °C, 48 h). Crude protein and protein fraction concentrations of the rumen pre-incubated and incubated samples were determined as proposed by Licitra *et al.* (1996). Data of protein fraction degradations were adjusted to a straight line model [model I, P=a+ct, France *et al*., 1990)] or a negative exponential model [model II, $P=a+b(1-e^{-ct})$, Ørskov and McDonald, 1979], where P= fraction degraded in the time t, a= rapidly degradable fraction, b= slowly degradable fraction, c= fractional degradation rate and t= incubation time. Lag phase was not included in the models. Several statistics, including mean square prediction error (MSPE), root of MSPE (rMSPE, expressed as a percentage of the observed mean) and coefficient of determination (R-square) were used to evaluate goodness-of-fit of each model.

Results The results of protein fraction degradation kinetics of each sample using models I and II are shown in Table 1. In addition, for each model, the MSPE, rMSPE and R-square have been presented.

Table 1 *In situ* protein fraction degradation parameters estimated for various oilseed meals using models I (P=a+ct) and II ($P=a+b(1-e^{-ct})$)

Oilseed meals	Model I							Model II					
	Protein fractions	a	b	c	MSPE	rMSPE	R^2	a	b	c	MSPE	rMSPE	R^2
CSM	TP	0.61	0.33	0.06	0.0017	4.1	0.91	0.58	0.42	0.10	0.0011	3.1	0.96
	NDIP	0.18	0.67	0.01	0.0021	4.5	0.88	0.25	0.57	0.01	0.0012	3.4	0.94
	ADIP	0.36	0.40	0.09	0.0030	5.4	0.91	0.35	0.34	0.12	0.0009	3.0	0.97
SM	TP	0.36	0.66	0.06	0.0019	4.3	0.89	0.40	0.87	0.10	0.0015	3.8	0.96
	NDIP	0.06	0.71	0.04	0.0015	3.8	0.90	0.03	0.82	0.04	0.0014	3.7	0.98
	ADIP	0.01	0.83	0.06	0.0021	4.5	0.89	0.05	0.91	0.06	0.0016	4.0	0.94
RM	TP	0.36	0.44	0.06	0.0015	3.8	0.91	0.43	0.51	0.07	0.0014	3.7	0.98
	NDIP	0.11	0.61	0.04	0.0021	4.5	0.90	0.16	0.71	0.05	0.0018	4.2	0.99
	ADIP	0.10	0.33	0.05	0.0015	3.8	0.90	0.15	0.29	0.08	0.0012	3.4	0.97

Conclusions There were major differences among the oilseed meals for the different protein fraction degradation kinetics evaluated in the present study. The low values of ADIP degradation confirmed the previous results. In the CNCPS model, ADIP is believed to be more slowly degraded in the rumen than are TP and NDIP (Sniffen *et al.*, 1992). Results of the present experiment showed that, based on various statistical tests, MSPE and rMSPE, as indicators of model accuracy, of model II gave better fits to protein fraction degradation kinetics than model I. R-square showed that the variation was high for models I compared with model II, and values of rMSPE of Model II was sufficiently small to show that model parameters accurately. Therefore, the negative exponential model is well suited to describe the degradability patterns of protein fractions of TP, NDIP and ADIP.

References

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