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Comparison between *in sacco* and *in vitro* protein rumen degradability*

S Terramoccia [1], S Puppo [1], L Rizzi [2], F Martillotti [1]

[1] *Istituto Sperimentale per la Zootecnia, Via O Panvinio 11, 00162 Rome;*
[2] *Istituto di Zootecnia e Nutrizione Animale, Via S Giacomo 11, 40126 Bologna, Italy*

As *in sacco* protein rumen degradability (DT) involves a lot of work and time, an enzymatic procedure for DT determination could be a simpler method. A comparison between *in sacco* and *in vitro* determination is useful in order to assess the difference.

The study concerned 8 feeds : maize germ (MG), maize gluten meal (MGM), alfalfa dehy (AD), cottonseed meal (CSM), fish meal (FM), full fat soybean (FFSB), extruded soybean (ETSB), flaked soybean (FSB). Each feed was incubated either *in sacco* (3 fistulated dairy cows, 3 × 3 replications, nylon bags 16 × 10 cm – diam 41 µm, sample = 3 g – 2.5 mm ground) according to Ørskov and McDonald (1979) or *in vitro* (glass tube = 100 ml, sample = 1 g – 1 mm ground) with *Streptomyces griseus* protease at pH 8.00 (2 mg protease/g sample) according to the Aufrere and Cartailler method (1988) modified: N × 6.25 was determined on feed residue after filtration on crucible 2G2. The incubation times were: 0, 1, 2, 4, 8, 16, 24, 48, 72 h. Both protein degradability kinetics were computed by the Nocek and English procedure.

In conclusion, in all samples, zero time *a* of *in sacco* data was close enough to the *in vitro* data, except for the 2 full fat samples (FFSB and MG). The asymptotic data $a + b$ of the *in sacco* method are always higher than those determined *in vitro*; such a difference is due to a major number of protein cleavage sites to be attached by protease in the rumen for synergistic action of other enzymes (amylase, cellulase, hemicellulase, etc). None of the *in vitro* kinetics curves showed lag time; some of the *in sacco* kinetics had a more or less long lag time. The DT:% figures of the 2 methods were close enough for MG, MGM, AD, CSM, FFSB, but for the other samples the differences were over 10 %. The RSD of the *in vitro* method were always lower than that of the *in sacco* method.

Although some results are good, the enzymatic method needs to be improved; it seems that the protease, used alone, is not active enough for a complete protein degradation.

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Table I. *In sacco / in vitro* parameters of degradation and degradability of the feeds.

Feed	a	b	c	*RSD*	*DT/% (k = 0.05)*	*Diff %*
MG	40.1/67.5	58.9/13.4	0.091/0.155	1.7/1.6	78/78	–
MGM	12.7/ 1.7	84.7/52.3	0.038/0.051	9.5/1.7	29/28	3.4
AD	56.5/60.1	36.2/23.6	0.082/0.155	5.3/0.8	76/78	2.6
CSM	56.8/55.2	36.4/32.6	0.097/0.072	5.0/1.3	74/78	5.4
FM	30.8/27.9	56.9/56.5	0.029/0.037	6.5/3.3	46/52	13.0
FFSB	24.4/53.9	74.8/16.6	0.075/0.062	6.7/1.5	69/63	8.7
ETSB	12.3/12.2	87.6/56.7	0.057/0.058	8.7/2.7	53/42	20.7
FSB	30.6/30.0	68.5/30.6	0.183/0.105	4.3/1.7	72/51	29.2

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