

ESTIMATION OF RUMINAL PROTEIN DEGRADATION AND BIOSYNTHESIS BY AN *IN VITRO* METHOD

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Introduction

Amino acid composition of feed proteins is modified within the rumen as a consequence of microbial degradation and biosynthesis. The *in situ* bag technique of Orskov (Mehrez and Orskov, 1977; Orskov and McDonald, 1979), devised for the estimation of protein degradability in the rumen, is widely applied and sufficiently reliable to estimate the potential value of feed proteins in ruminants.

If a simpler laboratory method for the estimation of feed proteins, giving also information on the amount of duodenal amino acid supply (DAAS) and on limiting amino acids, were available, it could be of help when rationing ruminants with high protein requirements.

Actually, *in vitro* methods have been proposed already (Dennison and Phillips, 1983; Broderick, 1987). The scope of the present work is to verify whether a well-known *in vitro* technique (Tilley and Terry, 1963) can adequately simulate the rumen environment and, therefore, be a valid laboratory tool for the estimation of feed protein values. In this communication some *in vitro* results are presented and compared with figures measured *in vivo*.

Materials and Methods

Forty one different feeds (7 green forages, 5 silages, 10 hays, 2 straws, 8 complete diets, fish meal, meat meal, maize gluten feed and 6 mixtures of these three latter concentrates with maize) were analyzed for their amino acid composition and digested *in vitro* (first stage of the Tilley and Terry method). The whole content of fermentation vessels was then hydrolyzed and analyzed for amino acids.

Ten feeds (3 green forages, 1 silage, 2 hays and 4 complete diets) were fed to dairy cows and growing lambs; rumen contents and faeces were collected and analyzed for amino acids. These ten feeds and the three protein concentrates were also degraded *in situ* in bags.

Cysteine and tryptophan were not determined and true protein (TP) was conventionally indicated as the sum of 16 amino acids.

The amount of residual proteins (RTP), synthesized plus undegraded, was expressed as the percentage of TP found in the fermentation vessels after 48 hours, corrected for the amount introduced with inoculum, as compared to feed TP. Digestible protein (DP) figures were then calculated as 80 % of RTP.

Results and Discussion

Figures of amino acid composition showed the qualitative differences among feeds (see table 1): glutamic acid (GLU) ranged from 9.17 to 21.04 % of TP, aspartic acid (ASP) from 5.38 to 14.26 %, glycine (GLY) from 2.48 to 15.04 %.

Figures of *in vitro* fermented feeds (table 2) were not so different from one another: mean values were close to the amino acid pattern of microbial protein and to the composition of rumen content withdrawn from dairy cows and lambs. Standard deviations were lower.

In all cases of wide ranges, extreme values were due to the poorly degradable proteins of fish meal, meat meal and maize gluten feed.

The amino acid composition of faeces, not presented in this paper, was very similar to that of rumen contents, presumably because intestinal digestion occurred without changes of ratios between amino acids.

The amount of residual proteins (RTP) within

TABLE 1. AMINO ACID COMPOSITION OF FEED PROTEINS (PERCENTAGES OF TRUE PROTEIN)

Amino acid	Range	Mean	SD
ASP	5.38 - 14.26	10.34	1.81
THR	3.12 - 5.80	5.00	0.76
SER	2.87 - 6.04	5.37	0.61
GLU	9.17 - 21.04	15.22	3.36
PRO	5.07 - 11.66	7.93	1.57
GLY	2.48 - 15.04	6.00	1.79
ALA	5.04 - 22.25	7.75	2.83
VAL	3.58 - 7.69	5.32	0.80
MET	1.27 - 3.25	1.83	0.38
ILE	2.64 - 5.48	4.13	0.50
LEU	5.99 - 15.95	9.19	1.58
TYR	2.16 - 5.30	3.74	0.57
PHE	3.33 - 8.15	5.16	0.97
HIS	1.24 - 3.54	2.23	0.44
LYS	1.85 - 8.54	5.09	1.13
ARG	2.49 - 7.77	5.70	1.15

TABLE 2. AMINO ACID COMPOSITION OF FERMENTED FEED PROTEINS (PERCENTAGES OF TRUE PROTEIN)

Amino acid	Range	Mean	SD
ASP	6.79 - 12.75	11.32	1.19
THR	3.95 - 6.22	5.60	0.67
SER	4.05 - 5.50	5.07	0.27
GLU	12.79 - 20.51	14.04	1.68
PRO	3.81 - 9.44	5.51	1.24
GLY	2.68 - 12.20	5.87	1.42
ALA	6.53 - 8.99	7.84	0.45
VAL	3.57 - 5.53	5.00	0.43
MET	1.75 - 3.03	2.24	0.32
ILE	3.47 - 5.10	4.60	0.37
LEU	6.96 - 15.25	8.80	1.57
TYR	2.87 - 5.89	4.62	0.51
PHE	3.49 - 8.48	5.32	0.93
HIS	1.85 - 3.25	2.18	0.32
LYS	2.30 - 8.42	6.82	1.12
ARG	3.31 - 6.69	5.17	0.68

the artificial rumens showed large differences, ranging from 55 %, as referred to starting alimentary TP; in the case of *Bromus* hay, up to 270 %; in the case of treated straw, rich in non protein nitrogen (table 3). Corresponding DP figures (y)

TABLE 3. EXTENT OF PROTEIN IN VITRO BIOSYNTHESIS. ONLY A PART OF RESULTS OF THE STUDIED FEEDS IS PRESENTED (RATIO: RESIDUAL TP & FEED TP)

Feed	Type of feed	Residual TP/Feed TP
<i>Dactylis glomerata</i>	F	0.74
Maize silage	S	0.90
<i>Festuca arundinacea</i>	F	0.73
<i>Phleum pratense</i>	F	1.05
<i>Medicago sativa</i>	F	0.81
Mixed hay	H	0.76
<i>Bromus catharticus</i>	H	0.55
Treated straw (NH ₃)	T	2.70
Fish meal	C	0.71
Meat meal	C	0.62
Maize gluten feed	C	0.83
Maize gluten feed + Maize 50:50	C	0.99
Maize gluten feed + Maize 25:75	C	1.09

*F - green forage; S - silage; H - hay;
T = treated forage; C = concentrate.

that resulted significantly correlated with those calculated from *in situ* degradabilities (x). The regression equation is:

$$y = 6.84 + 0.95 x; \quad R^2 = 0.98;$$

$$DSR = 21.27 \text{ g/kg.}$$

In conclusion, the proposed *in vitro* approach seems a valid laboratory tool to get reliable information on the nutritive values of feed proteins (quantities and qualities of proteins entering the duodenum). Further studies are needed to clarify the particular aspect of limiting amino acids.

(Key Words: Proteins, Rumen Degradability, In Vitro Techniques)

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