

Microbially corrected amino acid composition of rumen-undegraded feed protein and amino acid degradability in the rumen of feeds enclosed in nylon bags

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1. In the previous work (Varvikko & Lindberg, 1985), ¹⁵N-labelled rapeseed (*Brassica napus*), barley, ryegrass (*Lolium perenne*) and barley straw were incubated in the rumen in nylon bags for 5, 12 and 24 h and microbial nitrogen in the residues was quantified using the feed ¹⁵N-dilution method. In the present study, residual amino acids (AA) of these feeds were analysed, and microbially corrected AA of feed origin (feed AA) were estimated as the difference between total residual AA and respective microbial AA, assuming a constant AA composition for the microbial protein.

2. In barley and barley-straw residues, and also in ryegrass incubated in the rumen for 24 h, very large enrichment by microbial N and AA-N was found. The microbial enrichment was rather small in rapeseed residues and ryegrass incubated for 5 or 12 h. During the rumen incubation, feed N and AA-N (g/kg feed dry matter (DM)) decreased very clearly in all the feeds, and feed and incubation time effects were always statistically significant ($P < 0.001$).

3. The slow degradation of essential (E) feed AA compared with the respective non-essential (NE) AA degradation increased the proportion of feed EAA (g/kg determined feed AA) in barley and barley-straw residues. In rapeseed and ryegrass, residual feed EAA:NEAA remained very similar to the original. Branched-chain (Br) AA tended to increase proportionally in all the feed residues, suggesting these AA to be, on average, more resistant against microbial degradation in the rumen than other AA. Similarly, lysine was clearly increased in barley residues. A rumen degradation faster than the average rate caused decreased residual feed glutamic acid in rapeseed; methionine, alanine and glycine in barley; arginine and alanine in ryegrass; and methionine, asparagine and tyrosine in barley straw. Feed and incubation time effects were significant ($P < 0.05$ – 0.001) for feed AA (g/kg determined feed AA) grouped as EAA, BrAA or NEAA, and for most individual AA, as well as for feed AA disappearance (%) and relative amounts (%) of feed AA in the respective residual AA.

4. According to present findings, AA composition of the rumen-undegraded vegetable feed residues may markedly differ, either quantitatively or qualitatively (or both), from their original AA composition. When determining the feed AA composition of nylon-bag residues, the microbial error may be very large with starchy or fibrous feeds of low protein content. The microbial AA do not, however, considerably confuse the AA determination of protein-rich feeds.

Since amino acid (AA) composition of rumen microbial protein is fairly constant and independent of the diet given to the ruminant animal (Weller, 1957; Purser & Buechler, 1966; Meyer *et al.* 1967; Bergen *et al.* 1968; Williams & Dinusson, 1973; Burris *et al.* 1974; Czerkawski, 1976; Storm & Ørskov, 1983), variation in the AA composition of the digesta entering the duodenum should be mainly due to variation in the AA composition and quantity of feed protein escaping rumen degradation. Experiments conducted *in vitro* (Chalupa, 1976; Scheifinger *et al.* 1976; MacGregor *et al.* 1978; Craig & Broderick, 1984) and *in vivo* (Tamminga, 1979; Stern *et al.* 1983) indicated that feed AA are not degraded equally by the rumen microbes, suggesting accordingly that residual AA composition of feed is different from the original. Analyses of feed residues in nylon bags are not uniformly consistent with this conclusion. Crooker *et al.* (1981) and Rooke *et al.* (1984) reported that differences exist in the AA profile between the ingested feed protein and the rumen-undegraded feed protein. Several other studies in which feed protein was introduced into the rumen in porous synthetic fibre bags did not, however, indicate selective degradation of feed AA in the rumen (Ganev *et al.* 1979; Varvikko *et al.* 1983; Weakley *et al.* 1983; Setälä & Syrjälä-Qvist, 1984–5).

It has been shown that residues of vegetable feed supplements in nylon bags can be markedly contaminated by microbes during rumen incubation (Mathers & Aitchison, 1981; Kennedy *et al.* 1984; Rooke *et al.* 1984; Varvikko & Lindberg, 1985). The AA originating from the attaching microbial matter are, therefore, likely to modify the AA composition of the undegraded feed residues. The purpose of the present study was to estimate feed AA profiles in residues left in porous nylon bags suspended in the rumen for four different types of vegetable feed supplements. Estimates of feed AA degradability were made, with correction of values for rumen microbial AA contribution.

MATERIALS AND METHODS

Experimental procedures

The present nylon-bag study was a direct continuation of previous work (Varvikko & Lindberg, 1985). Since details of the experimental procedures, conventional chemical analyses and ^{15}N determination, as well as calculation of the rumen microbial nitrogen (RMN) and microbially corrected (feed) dry matter (DM) in the residues have been described earlier, only a brief summary of the experimental procedures is given.

One rumen-cannulated, non-lactating cow of Swedish red and brown breed was used. The cow was fed daily with legume-grass silage (2.3 kg DM) and hay (2.3 kg DM), in two equal meals at 07.00 and 15.00 hours.

The experimental feeds used were rapeseed (*Brassica napus*), barley grain, ryegrass (*Lolium perenne*) and barley straw. The feeds, cultured in 5 l pots, were fertilized with ^{15}N -labelled ammonium nitrate (10 atom %) as the only N source. Rapeseed and barley were separated into seeds and straw at harvest. The feeds were dried at 40° for 3 d. The rapeseeds were crushed and diethyl-ether extracted before further use.

Bags with a pore size of 40 μm were used. Rapeseed, barley, ryegrass or barley straw (5 g), milled to pass a 1.0 mm screen, were weighed into nylon bags. The bags were incubated in the rumen for 5, 12 or 24 h. Four replications were collected for the feeds on each incubation time during four consecutive 2 d periods, with one replication for each feed and time on the same 2 d period.

DM was determined on micro-samples (100 mg) after drying at 105° overnight. The N content of the residues was analysed according to the modified Kjeldahl method and ^{15}N was determined from the titrated N distillates using a mass spectrometer (MM 622; VG Micromass, England). RMN in the residues was estimated using feed ^{15}N dilution as an indicator of RMN contamination as described by Varvikko & Lindberg (1985).

AA analyses

The AA of the feed residues were determined from their *n*-heptanofluorobutyric *n*-propyl ester derivatives after hydrolysing the samples with 6 M-hydrochloric acid at 110° (constant boiling) for 20 h, using a gas-liquid chromatograph (HP Model 5710 A). Pipecolic acid was used as an internal standard. The procedure, originally reported by March (1975), is described in detail by Näsi & Huida (1982).

Calculations

To estimate the microbial AA in the residues, an assumption was made that in the microbial AA-N pool ($0.8 \times \text{RMN}$; Storm & Ørskov, 1983), N proportions of individual AA (AA-N g/kg AA-N) were similar to those given by Storm & Ørskov (1983). Accordingly, individual AA of feed origin (g) in the residues were calculated as a difference between total residual AA and estimated microbial AA:

$$\frac{(\text{residual N} \times \text{residual AA}) - (0.8 \times \text{RMN}) \times \text{microbial AAN}}{16} \quad \text{NAA}$$

where residual N is g N in residue in bag, residual AA is g AA/16 g N in residue, microbial AA-N is g specific amino acid N/kg total amino acid N, NAA is g N/kg specific amino acid. In these calculations, negative values obtained for feed AA were regarded as zero.

Statistical analyses

The experimental design was 4 × 3 factorial (feeds, incubation times) and values were subjected to analysis of variance. When analysing the N, AA-N or AA composition of the feed samples, values from the original unincubated feeds were included.

The standard errors were derived from the respective interactions between replicates and treatments.

RESULTS

Uncorrected (total) and microbially corrected (feed) N and AA-N contents (total, g/kg DM; feed, g/kg feed DM) of the rumen-incubated feed supplements are presented in Table 1, and feed AA compositions (g/kg determined feed AA) are given in Table 2. Disappearance (%) of feed AA is given in Table 3, and relative amounts (%) of individual feed AA in the respective residual AA are presented in Table 4.

N and AA-N

Feed and incubation-time effects were always statistically significant ($P < 0.001$) for N and AA-N (Table 1). The total N and AA-N in the residues were higher than respective feed N and AA-N, the difference between uncorrected and corrected values being very large with barley and barley-straw residues, as well as with ryegrass incubated in the rumen for 24 h. With rapeseed residues, the influence of microbial contribution to N or AA-N was rather small. With rapeseed, barley and ryegrass residues, feed N decreased with increasing incubation time, while with barley straw it decreased to half the original sample during the 5 h rumen incubation and remained unchanged after that. The feed AA-N always decreased with increasing incubation time.

Feed AA

Statistically significant ($P < 0.01$ – 0.001) feed and incubation-time effects were found for microbially corrected feed AA (g/kg determined feed AA) grouped as essential (E), branched-chain (Br) or non-essential (NE) AA (Table 2). Except for arginine, significant ($P < 0.05$ – 0.001) feed effect was found for the individual feed AA, and except for lysine, phenylalanine, threonine, aspartic acid, glutamic acid and tyrosine, incubation-time effect was always significant ($P < 0.05$ – 0.001) for the AA. For the feed AA disappearance (%) (Table 3) as well as for relative amounts (%) of individual feed AA in the respective residual AA (Table 4), feed and incubation-time effects were always significant ($P < 0.05$ – 0.001).

The slower degradation of feed EAA compared with the respective NEAA degradation (Table 3) caused elevated feed EAA:NEAA in barley and barley straw residues (Table 2). With rapeseed and ryegrass, residual EAA:NEAA remained at the original level, although a slightly decreasing trend was found for ryegrass.

The increase with time in BrAA (isoleucine, leucine and valine) content (g/kg determined feed AA) found for all the feeds (Table 2) was very marked with barley and barley straw. Lysine was clearly increased in barley residues due to the rumen incubation. Feed AA showing an obvious decrease, notable already after 5 h, were glutamic acid in rapeseed; methionine, alanine and glycine in barley; arginine and alanine in ryegrass; and methionine, asparagine and tyrosine in barley straw.

Table 1. *Uncorrected (total) and microbially corrected (feed) nitrogen and amino acid (AA)-N contents (total, g/kg dry matter (DM); feed, g/kg feed DM) of original rapeseed (Brassica napus), barley, ryegrass (Lolium perenne) and barley-straw samples and their residues after 5, 12 and 24 h rumen incubation in nylon bags*

(Each value is the mean of four replicates)

Feed... Incubation period (h)...	Rapeseed			Barley			Ryegrass			Barley straw			SEM (45 df)
	0	5	12 24	0	5	12 24	0	5	12 24	0	5	12 24	
Total	53.1	44.3	23.3 20.6	18.4	25.1	20.2 13.8	31.9	32.6	26.8 24.2	6.1	6.4	7.3 10.6	0.44
Feed	53.1	42.3	20.8 18.6	18.4	10.6	8.2 6.4	31.9	29.5	22.6 13.6	6.1	3.3	3.5 3.5	0.51
AA-N	45.7	35.9	15.2 13.3	15.7	21.6	15.5 11.4	23.6	26.6	21.1 20.2	3.3	4.5	4.9 8.0	0.68
Feed	45.7	34.4	12.8 11.4	15.7	8.4	3.8 3.7	23.6	23.3	17.0 8.6	3.3	1.9	1.3 1.1	0.83

Table 2. Microbially corrected (feed) amino acid (AA) composition (g/kg determined feed AA) of original rapeseed (*Brassica napus*), barley, ryegrass (*Lolium perenne*) and barley-straw samples and their residues after 5, 12 and 24 h rumen incubation in nylon bags
(Each value is the mean of four replicates)

Feed ... Incubation period (h) ...	Rapeseed						Barley						Ryegrass						Barley straw						SEM (45 df)		
	0		5		12		24		0		5		12		24		0		5		12		24				
	58	17	59	24	24	34	58	27	66	52	62	62	59	16	21	8	41	59	35	39	41	46	18	46		2	0
Arginine	28	50	82	66	19	49	57	60	61	470	193	47	89	179	54	71	49	41	530	89	530	530	530	530	530	530	
Histidine	50	55	92	56	20	57	56	73	66	482	213	51	100	143	54	65	58	73	518	93	518	518	518	518	518	518	
Isoleucine	82	92	66	56	19	49	57	60	61	470	193	47	89	179	54	71	49	41	530	89	530	530	530	530	530	530	
Leucine	66	56	19	49	57	60	61	470	193	47	89	179	54	71	49	41	530	89	530	530	530	530	530	530	530	530	
Lysine	49	57	60	61	470	193	47	89	179	54	71	49	41	530	89	530	530	530	530	530	530	530	530	530	530	530	
Methionine	49	57	60	61	470	193	47	89	179	54	71	49	41	530	89	530	530	530	530	530	530	530	530	530	530	530	
Phenylalanine	49	57	60	61	470	193	47	89	179	54	71	49	41	530	89	530	530	530	530	530	530	530	530	530	530	530	
Threonine	49	57	60	61	470	193	47	89	179	54	71	49	41	530	89	530	530	530	530	530	530	530	530	530	530	530	
Valine	49	57	60	61	470	193	47	89	179	54	71	49	41	530	89	530	530	530	530	530	530	530	530	530	530	530	
EAA	470	482	466	463	392	469	546	430	482	474	471	451	440	550	537	565	565	565	565	565	565	565	565	565	565	565	
BrAA	193	213	218	218	156	176	248	167	204	232	225	223	216	281	330	353	353	353	353	353	353	353	353	353	353	353	
Alanine	47	51	42	41	51	3	15	9	90	77	72	37	81	77	85	43	43	43	43	43	43	43	43	43	43	43	
Aspartic acid	89	100	95	106	66	86	55	132	94	97	102	125	102	68	75	45	45	45	45	45	45	45	45	45	45	45	
Glutamic acid	179	143	110	100	235	230	223	244	120	121	126	149	148	114	89	121	121	121	121	121	121	121	121	121	121	121	
Glycine	54	54	64	69	49	26	7	13	65	65	61	51	60	33	50	8	8	8	8	8	8	8	8	8	8	8	
Proline	71	65	104	105	121	127	88	71	58	63	58	73	65	68	72	110	110	110	110	110	110	110	110	110	110	110	
Serine	49	58	73	72	52	39	41	81	49	54	54	63	69	68	81	95	95	95	95	95	95	95	95	95	95	95	
Tyrosine	41	47	46	44	34	20	25	20	42	49	56	50	35	22	11	13	13	13	13	13	13	13	13	13	13	13	
NEAA	530	518	534	537	608	531	454	570	518	526	529	539	560	450	463	435	435	435	435	435	435	435	435	435	435	435	
(EAA:NEAA) × 100	89	93	87	87	64	88	120	75	93	90	89	82	79	122	116	130	130	130	130	130	130	130	130	130	130	130	

EAA, BrAA and NEAA are sums of essential, branched-chain and non-essential AA respectively.

Table 3. Microbially corrected feed amino acid (AA) disappearance (%) from rapeseed (*Brassica napus*), barley, ryegrass (*Lolium perenne*) and barley straw incubated in the rumen in nylon bags for 5, 12 and 24 h
(Each value is the mean of four replicates)

Feed... Incubation period (h)...	Rapeseed			Barley			Ryegrass			Barley straw			SEM (33 df)
	5	12	24	5	12	24	5	12	24	5	12	24	
	Arginine	69.7	97.7	97.5	87.3	97.4	97.5	76.0	86.4	96.8	42.1	64.3	
Histidine	80.7	95.8	97.9	91.4	99.3	100.0	53.4	90.0	100.0	100.0	100.0	100.0	1.16
Isoleucine	64.2	93.5	94.8	86.9	91.2	97.8	48.3	74.4	93.8	33.9	54.4	60.8	4.69
Leucine	64.5	94.7	96.0	87.8	97.2	97.6	51.3	76.0	95.7	35.2	61.5	73.2	2.69
Lysine	70.7	95.7	96.5	82.7	91.9	96.1	76.2	80.6	95.7	54.8	85.6	86.1	5.01
Methionine	66.6	94.4	97.0	92.9	99.3	99.6	54.2	78.2	97.3	78.6	100.0	100.0	3.42
Phenylalanine	59.1	93.9	95.0	86.1	96.9	97.9	54.7	79.1	96.5	52.5	73.5	80.4	2.65
Threonine	63.0	92.5	94.3	92.5	97.2	98.1	50.8	75.9	95.7	46.4	66.2	75.2	3.53
Valine	63.0	93.9	94.2	93.9	96.3	98.5	49.1	73.1	95.9	42.5	53.6	81.4	3.64
EAA	66.8	94.7	95.9	89.1	96.3	98.1	57.1	79.3	96.4	54.0	73.2	83.7	2.14
BrAA	63.9	94.0	95.0	89.5	94.9	98.0	49.6	74.5	95.1	37.2	56.5	72.1	3.08
Alanine	66.6	95.5	96.6	99.2	99.3	99.6	66.1	84.3	98.3	56.4	68.9	91.2	2.76
Aspartic acid	65.0	94.3	95.0	86.9	97.6	96.0	57.0	77.1	94.3	64.0	78.4	88.9	3.20
Glutamic acid	73.6	96.7	97.6	90.0	97.3	98.1	54.7	75.9	94.7	65.2	83.5	83.6	3.38
Glycine	69.1	94.0	94.9	93.6	99.6	99.3	59.1	80.3	96.9	72.7	74.1	97.2	4.59
Proline	69.1	91.6	93.2	88.3	97.7	99.0	56.8	78.5	95.8	51.7	68.2	72.1	3.11
Serine	64.3	92.3	94.0	90.8	97.7	96.8	54.7	77.3	95.2	54.0	70.7	78.4	2.54
Tyrosine	63.3	93.9	95.4	93.6	98.1	98.9	58.2	77.7	96.3	75.0	91.2	95.2	2.65
NEAA	67.3	94.1	95.2	91.8	98.2	98.2	58.1	78.7	95.9	62.7	76.4	86.7	2.38
Total AA	67.0	94.4	95.6	90.2	97.1	98.2	57.5	79.0	96.2	57.8	74.7	85.0	2.02
Feed N	66.7	92.9	94.3	89.9	95.1	97.4	61.9	80.0	95.4	58.6	61.1	72.0	1.64

EAA, BrAA, NEAA and total AA are means of essential, branched-chain, non-essential and total AA respectively.

Table 4. Feed amino acids (AA) (%) of respective total residual AA) in rapeseed (*Brassica napus*), barley, ryegrass (*Lolium perenne*) and barley-straw residues after 5, 12 and 24 h rumen incubation in nylon bags

(Each value is the mean of four replicates)

Feed ... Incubation period (h) ...	Rapeseed			Barley			Ryegrass			Barley straw			SEM (33 df)
	5	12	24	5	12	24	5	12	24	5	12	24	
	Arginine	91.6	59.1	75.1	70.8	19.8	39.0	68.5	65.4	33.0	52.1	26.8	
Histidine	90.3	83.9	76.0	34.2	8.1	0.0	92.4	59.9	0.0	0.0	0.0	0.0	10.75
Isoleucine	90.9	81.9	84.0	27.5	29.2	22.5	80.3	74.6	39.6	48.7	34.4	24.1	5.34
Leucine	92.3	82.1	82.6	33.3	20.6	33.6	86.3	80.9	44.3	47.4	32.6	19.0	2.95
Lysine	86.7	67.2	74.8	34.8	29.3	32.8	60.4	64.5	30.3	40.6	9.3	9.7	6.55
Methionine	88.0	77.2	72.1	32.3	4.4	9.2	79.7	71.6	24.7	13.3	0.0	0.0	8.32
Phenylalanine	93.6	80.8	83.3	42.8	21.0	30.0	84.7	79.5	34.0	41.1	24.5	13.9	4.36
Threonine	91.8	85.2	86.5	17.5	14.5	30.2	81.9	75.6	38.7	46.9	30.3	17.9	3.77
Valine	92.3	85.9	87.6	19.2	20.8	25.1	84.0	77.9	33.7	53.5	43.5	15.5	5.25
EAA	90.8	78.2	80.2	34.7	18.6	24.7	79.8	71.2	30.9	38.2	18.5	12.1	2.89
BrAA	91.8	83.3	84.7	26.7	23.5	27.1	83.5	77.8	39.2	49.9	36.8	19.5	3.85
Alanine	87.6	71.0	72.6	2.3	5.4	5.1	82.3	72.2	24.7	41.5	29.4	7.7	5.38
Aspartic acid	94.2	76.3	82.8	16.1	10.2	32.1	76.3	71.8	36.8	27.1	16.2	10.2	4.20
Glutamic acid	91.0	77.4	77.8	36.8	33.6	44.6	79.4	74.0	38.8	35.7	18.4	10.7	5.21
Glycine	90.7	83.5	85.7	18.5	3.0	18.8	83.8	77.6	34.4	27.5	25.3	2.5	5.39
Proline	94.2	92.6	92.5	60.4	35.6	43.1	86.2	83.3	50.5	54.2	38.7	27.4	4.95
Serine	92.7	87.4	87.6	26.5	18.6	44.6	83.8	78.2	44.0	50.2	34.8	20.1	3.66
Tyrosine	90.9	80.2	81.3	35.2	11.9	16.0	83.8	86.8	36.8	24.1	15.6	3.2	6.36
NEAA	91.6	81.2	82.9	28.0	16.9	29.2	82.2	78.1	38.0	37.2	25.5	11.7	3.34
Total AA	91.2	79.5	81.4	31.8	17.9	26.7	80.9	74.2	34.0	37.7	20.4	11.9	2.89

EAA, BrAA, NEAA and total AA are means of essential, branched-chain, non-essential and total AA respectively.

DISCUSSION

In a previous study (Varvikko & Lindberg, 1985) it was concluded that not only bacteria but probably also other microbes contribute to the N contents of the vegetable feed residues in nylon bags (with a pore size of 40 μm) during rumen incubation. The AA composition of mixed rumen bacteria and protozoa is known to be very constant irrespective of animal feeding. Also, individual strains of rumen bacteria have been shown to have a uniform AA composition (Purser & Buechler, 1966). Higher levels of EAA, particularly lysine, have been reported for protozoa compared with bacteria (Weller, 1957; Meyer *et al.* 1967; Bergen *et al.* 1968). Czerkawski (1976), on the other hand, found that different rumen microbial fractions generally were similar in their AA compositions, and of seventeen AA only glycine, alanine (both more in bacteria), lysine and glutamic acid (both more in protozoa) showed marked differences between the two microbial fractions.

In the present study, individual feed AA were determined as the difference between analysed residual AA and estimated microbial AA. Errors in these calculated feed AA values might result either from a discrepancy between real and estimated microbial AA in the residues or from inaccuracy in analysing the residual AA. As discussed earlier, only minor errors should be expected to be found in the microbial matter resulting from a quantitative or qualitative shift in bacterial:protozoal values in the residual RMN. The contribution from anaerobic fungi is, however, not considered and could probably be of significance in ryegrass and straw. Low estimated values for individual microbial AA compared with the real microbial AA in the residues could not be established, but overestimated levels for microbial AA or inaccuracy in analysing the residual AA might result in negative residual feed AA values. Systematically negative values (all four replications negative) were obtained only for histidine (irrespective of incubation time) and methionine (12 h and 24 h residues) in barley-straw residues, i.e. AA with low levels in the original feed sample. With other feeds or AA, negative values were occasional and rare.

Generally, the decrease in feed N and AA-N (g/kg feed DM) indicated that feed particles avoiding rumen degradation contained proportionately less feed protein than the feeds originally ingested. The lower feed AA-N content compared with the respective feed N content suggested that the decrease in the true feed protein content might be even more distinct than could be concluded from the decreasing residual feed N. Therefore, quantitative changes in the AA composition of vegetable feeds are highly probable during the protein degradation in the rumen.

Only small differences in the AA composition between residues incubated in the rumen for 9 h and original soya-bean meal, groundnut meal, sunflower meal and fish meal were found by Ganey *et al.* (1979). However, with the exception of soya-bean meal, a lowered N content in the feed residues was indicated. In the experiment reported by Varvikko *et al.* (1983), the N content of untreated rapeseed meal decreased during 5, 12 or 24 h rumen incubation, but with formaldehyde(HCHO)-treated rapeseed meal or with untreated or HCHO-treated soya-bean meal, residual N was not decreased. Generally the residual AA composition was not markedly changed in the feeds. This was also the conclusion made by Setälä & Syrjälä-Qvist (1984-5) with rapeseed meal.

Incubating the bags in the rumen for 12 h, Crooker *et al.* (1981) reported a larger total residual AA content compared with the original soya-bean meal, distillers' dried grains or lucerne (*Medicago sativa*) meal mixed with ground maize, but lowered residual AA contents compared with the original fish meal mixed with ground maize. Rooke *et al.* (1984) found decreased total N and AA-N in residues compared with the original grass silage and also a marked change in microbially corrected residual AA composition after 2 h rumen incubation.

Contamination of feed residues by microbial AA shown in the present study, and also

earlier by Rooke *et al.* (1984), would obviously have affected the results referred to previously. However, the microbial error seems small with protein-rich feeds. In the study by Varvikko *et al.* (1983), HCHO-treatment probably stabilized the N and AA contents of the treated feeds. Larger microbial contamination alone cannot explain the higher residual AA (or AA-N) content of untreated rapeseed compared with the present study. Differences in the processing or variety of rapeseed used might also explain some of these discrepancies. In the present study, the crushed diethyl-ether-extracted Ante variety was used, while in the study by Varvikko *et al.* (1983) the industrially processed Tower variety was used.

Based on increased contents (g/kg determined feed AA) in the feed residues, the BrAA seemed to be, on average, rather resistant to microbial degradation. Notable proportional changes found in the individual feed AA also indicate that qualitative alterations occurred during the course of rumen degradation.

The very marked decrease in residual glutamic acid of rapeseed, indicating a rapid degradation in the rumen, has been reported previously (Varvikko *et al.* 1983; Setälä & Syrjäjä-Qvist, 1984–5). A similar decrease in glutamine content of several vegetable-protein feeds, especially with sunflower meal, has been reported (Ganev *et al.* 1979). The rapid degradation of methionine in rapeseed (Varvikko *et al.* 1983; Setälä & Syrjäjä-Qvist, 1984–5) could not, however, be confirmed in the present experiment.

According to present findings, the AA composition of the rumen-undegraded vegetable feed residues may differ markedly, either quantitatively or qualitatively (or both), from the original feed AA composition. Microbial contamination has probably only a slight influence on the AA composition of undegraded nylon-bag residues of protein-rich feeds, e.g. rapeseed used in the present study. The errors, however, may be large with fibrous or starchy feeds of lower protein content, and the need for proper microbial correction becomes obvious with these feeds. More detailed information on the progressive AA degradation should be obtained using shorter incubation periods, since the major part of feed protein was degraded within 5 h. Of most relevance to the animal, however, are changes in the AA composition of actually undegraded feed protein, for which estimates both of rates of AA degradation and effective residence times of proteins in the rumen are needed.

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