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THE AMINO ACID COMPOSITION OF SELECTED SOUTH AFRICAN FEED INGREDIENTS

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OPSOMMING: DIE AMINOSUURSAMESTELLING VAN SEKERE SUID-AFRIKAANSE VOERBESTANDELE

Die aminosuursamestelling van 14 verskillende voerbestanddele wat in 'n plaaslike voermeul gebruik is, is bepaal op replikaat monsters wat van die meul getrek is oor 'n tydperk van 18 maande. Vir elke bestanddeel is die gemiddelde en standard fout van elke aminosuur aangetoon en ook, om die balans van die aminosure te kan bepaal, is elkeen aangetoon as 'n persentasie van die behoefte van braaikuikens tot op drieweke ouderdom.

Van die voerbestanddele was pluimveeneweprodukte-meel en lusern die wisselvalligste, en van die aminosure, het sistien, metionien en tirosien, in die algemeen, meer variasie getoon as die ander aminosure.

Die aminosuursamestelling van plaaslike voerbestanddele word met dié van ekwivalente Amerikaanse bestanddele vergelyk.

SUMMAPY:

The amino acid composition of 14 different feed ingredients used in a local feed mill were determined on replicate samples drawn from the mill at intervals over a period of 18 months. For each ingredient the mean and standard error of each amino acid is presented and also, as a means of assessing the balance of amino acids, each is presented as a percentage of the requirements of broilers up to 3 weeks of age.

Poultry by-product meal and lucerne proved to be the most variable ingredients and in general, cystine, methionine and tyrosine varied more than the other amino acids.

The amino acid composition of local feed ingredients is compared with that of equivalent American ingredients.

Optimum utilisation of available feed ingredients involves maximising the nutritive value of feed mixes while minimising their cost. In the feed industry this is usually achieved using linear programming techniques on electronic computors, but the validity of the results obtained cannot exceed that of the input data. The most useful indices of the nutritive value of a feed to monogastric animals are recognised as being its amino acid composition, especially with respect to the limiting amino acids, and its metabolisable energy content. At present, the values for amino acids and metabolisable energy of the various ingredients used in formulating local feeds are derived largely from published American values. However, several ingredients used locally are not reflected in the American tables and also the results of a number of preliminary analyses which we have undertaken led us to believe that the amino acid composition of local ingredients might differ from that of the corresponding American ingredients, where these can be identified. Furthermore, to our knowledge the report of du Toit & Boyazoglu (1975) provides the only published systematic study of the amino acid composition of local feedstuffs.

These observations provided the motivation for the present study, which was aimed at the analysis for amino acids of the major feed ingredients used in a local mill over a period sufficiently long as to give an

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indication both of the average amino acid composition and of the variability in composition of each ingredient. The same samples were also analysed for metabolisable energy content and this is reported elsewhere (Gous & Dennison, 1980).

The analytical methods used were selected as a compromise between the painstaking but potentially accurate methods commonly used in the structural analysis of individual purified proteins, and the practical requirements of a routine analytical method for the analysis of large numbers of feed ingredient samples, where the accuracy of the analysis is in any event compromised by the non-protein adulterants inevitably present. Thus, for example, hydrolysis techniques using a large excess of acid were considered impractical due to the expense of the system required and the time required for removal of the acid and, similarly, time studies of the release of refractory amino acids such as valine and the destruction of labile amino acids such as serine and threonine were not undertaken. On the other hand, in view of the nutritional importance of the total sulphur amino acids, a separate analysis for cystine was undertaken in an attempt to obtain a more accurate assessment of this amino acid. The analytical methods used for the analysis of the sulphur amino acids are discussed in more detail in a separate report (Dennison & Gous, 1980). Tryptophan, which is destroyed by acid hydrolysis was not measured in this study.

Materials and methods

Reagents

Sample buffer, pH 2,2. Sodium citrate. $2H_2O$ (19,6 g) conc. HCl (16,5 cm^3), thiodiglycol (20 cm^3) and caprylic acid (0,1 cm^3) were dissolved in approx. 900 cm^3 of distilled H_2O, the pH adjusted to 2,2 with HCl, and the solution made up to 1 dm^3.

Buffered neutralising solution (BNS). Sodium hydroxide (52,5 g) was made up to 500 cm^3 with pH 2,2 sample buffer.

Internal standards

(i) *Norleucine* A stock solution containing 6,25 μ moles cm^{-3} was prepared by dissolving norleucine (81,9 mg) in pH 2,2 buffer and making up to 100 cm^3.

(ii) *Ethanolaminephosphoric acid (EPA) (phosphoethanolamine).* A stock solution containing 12,5 μ moles cm^{-3} was prepared by dissolving EPA (176,4 mg) in pH 2,2 sample buffer and making up to 100 cm^3.

Procedure

Ingredients containing a high proportion of fat, viz. Fishmeal, full fat soya meal, poultry by-product meal (PBPM) and carcass meal were extracted with diethyl ether in a soxhlet apparatus. The low-fat and fat-extracted ingredients were milled to a fine powder in a Bleuler pulverising mill. Samples (25 mg) of each milled ingredient were measured in duplicate into rimless pyrex test tubes (12 × 150 mm).

One of each pair of tubes was for the analysis for all the amino acids except cystine and tryptophan. To this tube, 6 mol dm^{-3} — hydrochloric acid (3 cm^3) was added. The mixture was frozen in an acetone/dry ice mixture, evacuated to less than 0,1 mm Hg, thawed under vacuum, refrozen and the tube was sealed in a flame, while the pressure was less than 0,1 mm Hg. The vacuum was monitored with a pirani guage and it was found necessary to have a liquid air cold-trap in the vacuum line in order to achieve the stated low pressures. Hydrolysis of the sample was effected at 110° C for 24h and, after cooling, the tube was opened and norleucine stock solution was added and thoroughly mixed in (see below). The hydrolysate was filtered through glass fibre filter paper and evaporated twice to the point of dryness at 40-45° C under reduced pressure in a rotary evaporator before being made up to 5 cm^3 with pH 2,2 buffer. Samples (0,25 cm^3) were analysed using a single-column methodology on a Beckman 119 amino acid analyser. Norleucine internal standard was added to the samples, and the samples were diluted before application to the column as set out in Table I.

The other of each pair of tubes was for the analysis for cystine, and to this tube 3 cm^3 of 6 mol dm^{-3} hydrochloric acid, containing 0,35 mol dm^{-3} dimethylsulphoxide was added (Spencer & Wold, 1969). The tube was sealed without evacuation and hydrolysis of the sample was effected at 110° C for 24h. After cooling, EPA stock solution (0,4 cm^3) was added, well mixed in, and the solution was filtered through glass fibre filter paper. To 1 cm^3 of the filtrate, 2 cm^3 of BNS was added and the pH was adjusted, if necessary, to approximately pH 2,2. Cystine was assayed as cysteic acid on the long column of a Beckman 119 analyser using the first buffer only on an abbreviated analytical cycle (Dennison & Gous, 1980).

Table 1

Addition of internal standard and dilution of samples before analysis

Ingredient	Norleucine standard (cm^3)	Dilution before analysis
Bloodmeal Carcass meal Fishmeal Poultry by-product meal	1,2	1 cm^3 → 3 cm^3 apply 0,25 cm^3
Groundnut Soya	0,8	1 cm^3 → 2 cm^3 apply 0,25 cm^3
Brewers grain Lucerne Ricebran Sunflower Pollard	0,4	Apply 0,25 cm^3
Maize (Straight run No. 2) Sorghum Wheatbran Maize screenings	0,4	Apply 0,5 cm^3

The amino acid analyser and computing integrator system (Beckman System AA) were standardised to present results as g amino acid residue/100 g sample. This is done during the standardization runs simply by changing the way of expressing the concentration of each amino acid in the standard solution, from the more usual moles, to the corresponding "mass of amino acid residue". An amino acid residue is, of course, the amino acid as it occurs in the peptide chains of proteins and is equivalent to the free amino acid less the one molecule of water which is lost during formation of the peptide bond.

eg. 125 n moles lysine = 18,27μg free lysine = 16,02 μg lysine residues.

In the subsequent analysis of unknowns the results are expressed in the same units as used in the standard run. Using a similar rationale of manipulating the standard run, allowance for any dilution factors can be built into the colour constants generated during the standard run so that the subsequent print-outs will give results relating to a selected mass of sample.

We have elected to express results initially as g amino acid residue/100 g sample, so that summation of the individual amino acid residues yields the total residues, for comparison with the crude protein (N × 6,25) percentage, thus providing an indication of the recovery of amino acid residues, and thereby also providing some check on the validity of the analysis. On the other hand, dietary amino acid requirement standards are based upon free amino acids, rather than amino acid residues, and so from the mass of each amino acid residue, the mass of the corresponding amino acid liberated by hydrolysis is calculated from the equation,

$$\text{mass of amino acid} = \text{mass of residue} \times \frac{\text{amino acid molecular mass}}{\text{residue molecular mass}}$$

It is these values for amino acids yielded by hydrolysis which are presented in the accompanying tables (Tables 2 and 3).

An example of the computing integrator print-out and the primary amino acid analysis result sheet print-out is presented in Fig. 1 to underscore our procedure and to emphasise the distinction between amino acid residues and amino acids. In our experience this simple distinction is a source of fairly general confusion in amino acid analysis, in particular with respect to the fact that, theoretically, the mass of the amino acid residues should sum to the mass of the protein containing them, whereas the mass of the amino acids liberated from a protein by acid hydrolysis should sum to more than the mass of the protein from which they are derived, due to the water molecules added during hydrolysis.

For each ingredient the mean and standard error of the values obtained for each amino acid were calculated and the mean is also expressed as a percent of the requirement of broiler chickens to 3 weeks of age for the particular amino acid. The requirements used were those published by Thomas, Twining, Bossard and Nicholson (1978), assuming that the ingredient is incorporated in a diet having a metabolisable energy value of 12,55 MJ kg^{-1}. Expression of the amino acid content in terms of the requirement provides a ready means of identifying and ranking the limiting amino acids.

In the case of samples which were fat-extracted before analysis for amino acids, the results were corrected for the presence of fat.

Results and discussion

The results obtained for replicate analyses of 14 different feed ingredients used in a local feed mill and the results obtained for replicate control analyses of a single sample of maize are presented in Table 2. The average recovery of amino acids, expressed as the sum of amino acid residues as a percent of the protein (N × 6,25), was different for different ingredients and varied from a low of 80% for wheatbran, pollard and lucerne to a high of 105% for bloodmeal, the overall mean being approximately 90%. The high recovery of amino acid residues in the case of bloodmeal is considered to be an artifact of the analytical method, however, caused by the large amounts of leucine in this ingredient overlapping the norleucine internal standard and resulting in false low values for the recovery of the standard. In the summary of the average amino acid composition of the different ingredients, Table 3, therefore the values of bloodmeal have been corrected to accord with the more realistic figure of an 88,5% recovery of residues. The cystine value is not corrected since this is obtained by an independent analysis.

The variability of the amino acid values obtained for the different feed ingredients is shown in Table 5 in which, for ease of comparison, the coefficients of variation are presented. From Table 5, poultry by-product meal and lucerne emerge as the most variable ingredients while cystine, methionine and tyrosine emerge as the most variable amino acids. Comparison of the coefficients of variation obtained for these amino acids in the various ingredients with that obtained for the same amino acids in replicate analyses of the control maize sample suggests that in the case of cystine, a large part of the observed variability might be due to the analytical method, but this does not appear to be the case with methionine and tyrosine.

The initial motivation for the present study was provided by the apparent discrepancy between the results obtained for the amino acid composition of local feed ingredients and the published values used in formulating local mixed feeds. Based upon the more comprehensive data provided by the present study, a more exact assessment of the agreement between values obtained for local ingredients and published American values is presented in Tables 6 and 7. For certain ingredients, eg. Maize (corn) and bloodmeal, the present results agree fairly well with published American values, whereas for others, eg. lucerne and PBPM the agreement is not as good. In general, however, the agreement between the values published by different American authors is no better than their agreement with the present values.

A difficulty attending the decision as to what weight to apply to any given set of data lies in the fact that tables of amino acid values are often published as *ex cathedra* values without reference to the original analyses upon which these are based. There exists the possibility, therefore, that certain tables might in fact be founded upon the same original data. In other cases, differences might be due to the use of more or less rigorous analytical methods.

For the individual amino acids our values show a fairly close correlation with the American values except in the case of cystine, methionine and tyrosine (Table 7). As mentioned above, these are the same amino acids which we have found to be the most variable, but the exact significance of this coincidence is at present unknown.

Du Toit and Boyazoglu (1975) have published values for the amino acid composition of local feed ingredients, but there is not a close agreement between the values published by these authors and those obtained in the present study. However, two observations lead us to believe that our results might be more accurate. The first is that our recovery of amino acid residues is, on average, approximately 90% of the protein (N × 6,25) value. Du Toit and Boyazoglu report an average recovery of amino acids of 93,2% of the protein value, but it would appear from their communication that this figure does not refer to amino acid residues. The mass ratio of amino acids to amino acid residues is, on average, approximately 1,16 : 1,0 and therefore their recovery of residues is, in fact, 80,3% of their protein figure. Supporting this observation of lower recovery of amino acids is the fact that Du Toit & Boyazoglu consistently obtained a higher figure for ammonia than was obtained in the present study, suggesting that the conditions used by these authors for hydrolysis occasioned a greater destruction of amino acids than that used in the present study. Du Toit & Boyazoglu used a sample to acid ratio of 75 mg 6 cm^{-3} and hydrolysis under nitrogen gas at 120° C for 24h, contrasting with our use of a sample to acid ratio of 25 mg 3 cm^{-3} and hydrolysis in evacuated containers at 110° C for 24h.

AAA 1
78110076 ID

MAIZE M193

RUN PARAMETERS

3,0	PW
200,00	SS
20,0	TI
160,0	T2
,50	MA
2,0	WN
114,5	*T4
105,0	*T5

TIME	KF	CONC	
23,8	3034	43,41	
27,5	3626	25,29	I
29,1	4196	34,70	I
31,6	3026	143,72	L
37,2	1046	68,33	
40,4	2555	6,73	
44,4	7704	22,63	I
47,2	4513	52,51	L
54,7	3328	50,69	
58,0	3266	12,06	
61,3	2900	24,31	I
63,8	3684	99,45	I
66,5	2800	131,20	IL
75,5	2529	31,55	
80,7	2890	36,19	
99,5	3630	20,21	I
101,7	3986	19,69	L
118,8	8937	21,41	
154,4	2659	27,64	

PROTEIN CONTENT 8,60 PERCENT

AMINO ACID	AMINO ACID RESIDUES CONTAINED BY SAMPLE: PERCENT (a) OF SAMPLE	PERCENT OF TOTAL RESIDUES (b)	FACTORS (c)	AMINO ACIDS YIELDED BY SAMPLE UPON HYDROLYSIS: PERCENT (d) OF SAMPLE	PERCENT OF PROTEIN: SUM OF AAS	PERCENT OF PROTEIN: N × 6,25
ASP	0,43	5,77	1,156	0,49	6,68	5,77
THR	0,25	3,36	1,178	0,29	3,95	3,42
SER	0,35	4,70	1,207	0,42	5,67	4,91
GLU	1,44	19,35	1,139	1,64	22,04	19,07
PRO	0,68	9,13	1,185	0,80	10,83	9,36
CYS	0,10	1,34	1,176	0,11	1,58	1,36
GLY	0,23	3,09	1,315	0,30	4,06	3,51
ALA	0,53	7,12	1,253	0,66	8,92	7,72
VAL	0,51	6,85	1,182	0,60	8,10	7,00
MET	0,12	1,61	1,138	0,13	1,83	1,58
ILE	0,24	3,22	1,159	0,27	3,73	3,23
LEU	0,99	13,30	1,159	1,14	15,42	13,34
TYR	0,32	4,30	1,110	0,35	4,77	4,13
PHE	0,36	4,83	1,122	0,40	5,42	4,69
HIS	0,20	2,68	1,131	0,22	3,04	2,63
LYS	0,20	2,68	1,140	0,22	3,06	2,65
NH3	0,21	2,82	1,063	0,22	3,00	2,59
ARG	0,28	3,76	1,115	0,31	4,19	3,63

TOTAL OF AMINO ACID RESIDUES = 7,43 PERCENT

$(a) = \textit{Computing integrator print-out} \times {}^{1}/_{100}$

$(b) = \dfrac{\textit{Residue}}{\Sigma \textit{Residues}} \times 100$

$(c) = \dfrac{\textit{Amino acid molecular mass}}{\textit{Residue molecular mass}}$

$(d) = (a) \times (c)$

Fig. 1 Print-out from computing integrator and first computer print-out showing calculation of amino acid values from residue values

Table 2

Amino acid composition of feed ingredients (g amino acid yielded/100 g air-dry sample)

		Bloodmeal	Carcass meal	Fishmeal	PBPM	Groundnut	Brewers grain	Sunflower	Lucerne	Maize	Wheatbran	Pollard	Sorghum	Ricebran	Control maize
Number of analyses		9	6	8	10	11	10	11	9	13	6	8	7	11	5
ASP	X±SE	10,57± 1,02	5,92± 1,35	6,37± 0,92	4,39± 0,91	5,03± 0,65	1,74± 0,27	3,75± 0,60	1,82± 0,25	0,57± 0,09	0,99± 0,07	1,09± 0,07	0,53± 0,06	1,56± 0,28	0,53± 0,05
	range	9,07 – 12,27	3,52 – 7,47	4,39 – 7,79	2,43 – 6,03	4,13 – 6,62	1,34 – 2,16	2,61 – 4,73	1,51 – 2,41	0,45 – 0,75	0,92 – 1,14	0,99 – 1,22	0,41 – 0,63	1,22 – 2,19	0,46 – 0,63
THR	X±SE	4,95± 0,49	2,35± 0,47	2,81± 0,39	2,93± 0,58	1,23± 0,16	0,91± 0,15	1,45± 0,21	0,69± 0,14	0,32± 0,04	0,44± 0,03	0,51± 0,02	0,25± 0,03	0,66± 0,08	0,30± 0,01
	range	4,13 – 5,76	1,54 – 3,03	1,93 – 3,21	1,60 – 3,90	1,08 – 1,39	0,68 – 1,21	1,14 – 1,90	0,51 – 1,08	0,27 – 0,41	0,37 – 0,47	0,45 – 0,56	0,18 – 0,29	0,55 – 0,82	0,29 – 0,31
SER	X±SE	5,15± 0,48	2,63± 0,46	2,71± 0,42	5,88± 1,21	2,18± 0,30	1,28± 0,20	1,79± 0,24	0,75± 0,13	0,44± 0,07	0,60± 0,02	0,66± 0,04	0,56± 0,05	0,85± 0,12	0,40± 0,01
	range	4,58 – 5,85	1,84 – 3,40	1,77 – 3,29	3,15 – 8,28	1,85 – 2,86	1,03 – 1,72	1,38 – 2,29	0,65 – 1,11	0,37 – 0,63	0,55 – 0,63	0,59 – 0,73	0,25 – 0,42	0,66 – 1,12	0,38 – 0,43
GLU	X±SE	8,48± 0,81	7,88± 1,64	8,40± 1,27	6,48± 1,28	7,79± 1,20	5,43± 0,97	7,78± 1,10	1,53± 0,30	1,50± 0,23	2,24± 0,13	2,50± 0,15	0,47± 0,21	2,29± 0,35	1,49± 0,13
	range	7,51 – 10,18	5,08 – 10,32	5,59 – 9,98	3,61 – 8,40	6,33 – 10,79	4,25 – 7,46	6,12 – 10,08	1,25 – 2,32	1,32 – 2,15	2,02 – 2,36	2,19 – 2,71	1,09 – 1,83	1,75 – 2,93	1,37 – 1,66
PRO	X±SE	3,58± 0,45	4,22± 0,79	2,60± 0,32	5,03± 1,12	1,66± 0,28	2,34± 0,43	1,53± 0,21	0,72± 0,18	0,74± 0,10	0,71± 0,09	0,81± 0,07	0,55± 0,09	0,69± 0,08	0,68± 0,04
	range	2,70 – 4,44	3,05 – 5,28	2,12 – 2,94	2,41 – 7,05	1,30 – 2,28	1,76 – 3,22	1,26 – 1,94	0,46 – 1,11	0,55 – 0,94	0,52 – 0,81	0,65 – 0,88	0,39 – 0,69	0,54 – 0,85	0,63 – 0,74
CYS	X±SE	0,92± 0,36	0,55± 0,15	0,83± 0,17	1,93± 0,46	0,68± 0,07	0,41± 0,15	0,66± 0,18	0,22± 0,07	0,23± 0,09	0,26± 0,07	0,18± 0,02	0,14± 0,08	0,31± 0,09	0,23± 0,08
	range	0,50 – 1,65	0,31 – 0,82	0,65 – 1,11	1,18 – 2,94	0,51 – 0,79	0,21 – 0,64	0,34 – 0,94	0,12 – 0,35	0,11 – 0,38	0,19 – 0,42	0,16 – 0,24	0,08 – 0,34	0,21 – 0,51	0,12 – 0,38
GLY	X±SE	4,10± 0,42	6,95± 1,26	4,41± 0,36	4,18± 0,84	2,51± 0,38	0,82± 0,12	2,25± 0,28	0,76± 0,13	0,33± 0,04	0,79± 0,20	0,79± 0,05	0,24± 0,02	1,04± 0,24	0,31± 0,02
	range	3,66 – 4,95	4,96 – 8,50	3,77 – 4,82	2,19 – 5,45	2,13 – 3,47	0,61 – 1,02	1,69 – 2,72	0,64 – 1,10	0,23 – 0,42	0,64 – 1,24	0,72 – 0,89	0,21 – 0,27	0,85 – 1,76	0,27 – 0,34
ALA	X±SE	7,86± 0,72	4,45± 0,88	4,30± 0,51	2,84± 0,57	1,73± 0,28	2,38± 0,40	1,73± 0,23	0,91± 0,25	0,63± 0,09	0,66± 0,02	0,75± 0,04	0,67± 0,09	1,09± 0,13	0,59± 0,02
	range	6,99 – 9,33	2,89 – 5,69	3,22 – 4,79	1,55 – 3,71	1,42 – 2,36	1,80 – 3,20	1,25 – 2,13	0,76 – 1,60	0,55 – 0,86	0,61 – 0,68	0,70 – 0,83	0,51 – 0,86	0,90 – 1,35	0,56 – 0,65
VAL	X±SE	8,07± 0,92	3,51± 0,88	3,38± 0,65	4,14± 0,90	2,13± 0,48	1,67± 0,21	2,07± 0,47	0,99± 0,27	0,46± 0,07	0,73± 0,13	0,96± 0,11	0,43± 0,08	1,08± 0,12	0,52± 0,06
	range	6,77 – 10,07	2,10 – 4,89	2,13 – 4,42	2,21 – 5,70	1,27 – 2,93	1,30 – 1,98	1,06 – 2,68	0,70 – 1,71	0,33 – 0,67	0,53 – 0,89	0,70 – 1,08	0,33 – 0,61	0,91 – 1,33	0,43 – 0,60
MET	X±SE	1,18± 0,35	0,98± 0,29	1,64± 0,28	0,49± 0,14	0,35± 0,09	0,43± 0,08	0,73± 0,20	0,11± 0,04	0,16± 0,02	0,15± 0,01	0,18± 0,02	0,10± 0,00	0,25± 0,07	0,14± 0,01
	range	0,23 – 1,53	0,59 – 0,52	1,26 – 2,08	0,27 – 0,84	0,18 – 0,48	0,34 – 0,59	0,55 – 1,12	0,06 – 0,23	0,12 – 0,23	0,13 – 0,17	0,15 – 0,23	0,09 – 0,11	0,09 – 0,36	0,11 – 0,17
ILE	X±SE	0,72± 0,08	1,97± 0,60	2,57± 0,47	2,65± 0,53	1,34± 0,22	1,03± 0,16	1,48± 0,32	0,60± 0,04	0,26± 0,03	0,38± 0,02	0,45± 0,03	0,26± 0,04	0,56± 0,07	0,26± 0,02
	range	0,63 – 0,88	1,16 – 2,79	1,66 – 3,06	1,38 – 3,42	0,97 – 1,85	0,75 – 1,29	0,74 – 1,93	0,53 – 0,67	0,23 – 0,33	0,33 – 0,41	0,39 – 0,50	0,19 – 0,34	0,46 – 0,76	0,23 – 0,28
LEU	X±SE	12,08± 1,26	4,37± 0,98	4,75± 0,67	4,55± 0,88	2,59± 0,33	3,81± 0,55	2,47± 0,37	1,20± 0,40	1,03± 0,13	0,77± 0,03	0,91± 0,06	0,93± 0,13	0,20± 0,12	0,99± 0,05
	range	10,57 – 14,67	2,83 – 6,09	3,35 – 5,50	2,38 – 5,81	2,20 – 3,36	3,01 – 4,98	1,80 – 3,07	0,96 – 2,32	0,86 – 1,34	0,71 – 0,81	0,78 – 0,99	0,70 – 1,20	1,03 – 1,48	0,91 – 1,06
TYR	X±SE	2,50± 0,42	1,55± 0,41	1,83± 0,29	1,54± 0,38	1,31± 0,31	0,98± 0,16	0,84± 0,17	0,31± 0,09	0,29± 0,04	0,26± 0,06	0,29± 0,08	0,22± 0,02	0,41± 0,12	0,27± 0,02
	range	2,06 – 3,30	0,86 – 2,15	1,33 – 2,39	0,74 – 2,29	0,71 – 1,74	0,71 – 1,24	0,51 – 1,11	0,19± 0,53	0,21 – 0,36	0,15 – 0,35	0,17 – 0,42	0,17 – 0,26	0,23 – 0,64	0,23 – 0,27
PHE	X±SE	6,93± 0,78	2,31± 0,54	2,45± 0,34	2,66± 0,52	2,07± 0,34	1,34± 0,21	1,70± 0,29	0,79± 0,27	0,39± 0,05	0,48± 0,04	0,54± 0,09	0,35± 0,04	0,76± 0,07	0,33± 0,06
	range	6,01 – 8,28	1,65 – 3,22	1,65 – 2,74	1,44 – 3,44	1,64 – 2,82	1,04 – 1,79	1,24 – 2,15	0,39 – 1,46	0,33 – 0,51	0,40 – 0,56	0,35 – 0,68	0,29 – 0,42	0,67 – 0,87	0,24 – 0,39
HIS	X±SE	5,49± 0,60	1,23± 0,19	1,62± 0,24	0,69± 0,24	0,87± 0,16	0,59± 0,10	0,86± 0,13	0,32± 0,18	0,24± 0,02	0,29± 0,05	0,36± 0,03	0,15± 0,03	0,47± 0,05	0,23± 0,01
	range	4,78 – 6,68	0,84 – 1,46	1,23 – 2,11	0,21 – 1,11	0,58 – 1,24	0,37 – 0,78	0,64 – 1,13	0,15 – 0,84	0,21 – 0,30	0,18 – 0,33	0,33 – 0,45	0,07 – 0,18	0,38 – 0,58	0,20 – 0,24
LYS	X±SE	8,58± 0,79	3,62± 0,75	4,86± 0,69	1,88± 0,38	1,48± 0,21	0,46± 0,11	1,35± 0,22	0,85± 0,23	0,22± 0,03	0,53± 0,01	0,64± 0,04	0,16± 0,02	0,81± 0,10	0,22± 0,02
	range	7,52 – 10,26	2,21 – 4,49	3,42 – 5,79	1,08 – 2,52	1,18 – 1,98	0,26 – 0,58	1,06 – 1,84	0,68 – 1,51	0,14 – 0,27	0,50 – 0,55	0,55 – 0,72	0,11 – 0,20	0,64 – 0,99	0,18 – 0,26
NH	X±SE	0,88± 0,07	0,73± 0,20	0,98± 0,15	0,83± 0,19	0,87± 0,13	0,78± 0,13	0,96± 0,13	0,31± 0,02	0,22± 0,03	0,30± 0,02	0,36± 0,07	0,22± 0,02	0,52± 0,77	0,24± 0,06
	range	0,79 – 1,05	0,38 – 1,04	0,69 – 1,24	0,40 – 1,15	0,72 – 1,14	0,60 – 1,04	0,76 – 1,23	0,27 – 0,37	0,18 – 0,29	0,28 – 0,34	0,27 – 0,54	0,20 – 0,26	0,21 – 2,95	0,20 – 0,38
ARG	X±SE	3,60± 0,40	4,06± 1,20	3,41± 0,31	3,74± 1,05	4,30± 0,63	0,71± 0,19	3,13± 0,50	0,51± 0,16	0,30± 0,03	0,72± 0,08	0,81± 0,19	0,18± 0,03	1,40± 0,17	0,27± 0,03
	range	2,96 – 4,47	2,44 – 6,29	2,69 – 3,81	1,71 – 5,98	3,45 – 5,45	0,33 – 0,98	2,40 – 3,86	0,36 – 0,91	0,24 – 0,35	0,55 – 0,83	0,37 – 1,04	0,12 – 0,24	1,12 – 1,67	0,22 – 0,32
TSAA	X±SE	2,11± 0,40	1,53± 1,20	2,48± 0,41	2,42± 1,05	1,04± 0,63	0,85± 0,19	1,39± 0,50	0,33± 0,16	0,39± 0,03	0,41± 0,08	0,37± 0,19	0,24± 0,03	0,56± 0,17	0,37± 0,03
	range	0,74 – 2,90	0,90 – 2,01	1,94 – 3,05	1,54 – 3,54	0,81 – 1,18	0,57 – 1,15	0,79 – 1,90	0,23 – 0,52	0,26 – 0,61	0,33 – 0,57	0,32 – 0,45	0,19 – 0,44	0,37 – 0,78	0,32 – 0,53
NX6,25	X±SE	77,99± 3,54	56,02± 4,88	60,66± 2,02	50,58± 9,31	36,50± 2,59	23,3± 2,40	35,84± 3,95	14,49± 2,34	7,94± 0,73	12,23± 0,97	13,75± 0,55	7,21± 0,66	15,17± 0,90	7,87± 0,00
	range	73,39 – 83,04	48,60 – 61,75	56,08 – 63,12	38,05 – 73,00	31,29 – 40,75	20,36 – 26,68	28,2 – 41,25	10,88 – 18,69	7,23 – 10,27	10,15 – 13,13	12,36 – 14,21	6,51 – 8,57	14,50 – 17,90	7,88
RESD*	X±SE	82,12± 7,82	50,50± 10,07	51,40± 6,24	48,52± 9,78	34,63± 4,80	23,30± 3,56	31,53± 4,42	11,59± 2,49	7,32± 0,93	9,78± 0,51	11,08± 0,82	6,26± 0,82	13,78± 1,69	6,95± 0,35
	range	73,38 – 97,82	32,53 – 65,59	37,84 – 58,86	25,68 – 62,79	28,95 – 46,15	18,19 – 30,57	23,87 – 39,63	9,54 – 18,34	6,33 – 9,34	8,79 – 10,45	9,95 – 1,25	4,82 – 7,83	10,86 – 16,89	6,42 – 7,26

*RESD = Sum of amino acid residues

Table 3

Summary of essential amino acid composition of feed ingredients (g amino acid per 100 g air-dry sample)

Ingredient \ Amino acid	THR	SER	CYS	GLY	VAL	MET	ILE	LEU	TYR	PHE	HIS	LYS	ARG	TSAA
Bloodmeal	4,21	4,38	0,92	3,49	6,86	1,04	0,61	10,27	2,13	5,89	4,67	7,29	3,06	1,96
Carcass meal	2,35	2,63	0,55	6,95	3,51	0,98	1,97	4,37	1,55	2,31	1,23	3,62	4,06	1,53
Fishmeal	2,81	2,71	0,83	4,41	3,38	1,64	2,57	4,75	1,83	2,45	1,62	4,86	3,41	2,48
P B P M	2,93	5,88	1,93	4,18	4,14	0,49	2,65	4,55	1,54	2,66	0,69	1,88	3,74	2,42
Groundnut oilcake	1,23	2,18	0,68	2,51	2,13	0,35	1,34	2,59	1,31	2,07	0,87	1,48	4,30	1,04
Brewers grain	0,96	1,28	0,41	0,82	1,67	0,43	1,03	3,81	0,98	1,34	0,59	0,46	0,71	0,85
Sunflower oilcake	1,45	1,79	0,66	2,25	2,08	0,73	1,48	2,47	0,84	1,70	0,86	1,38	3,13	1,39
Lucerne	0,69	0,75	0,22	0,76	0,99	0,11	0,60	1,20	0,31	0,79	0,32	0,85	0,51	0,33
Maize	0,32	0,44	0,23	0,33	0,46	0,16	0,26	1,03	0,29	0,39	0,24	0,22	0,30	0,39
De-germed maize	0,29	0,42	0,15	0,29	0,53	0,13	0,27	1,04	0,27	0,37	0,23	0,20	0,24	0,29
Wheat bran	0,44	0,60	0,26	0,79	0,73	0,15	0,38	0,77	0,26	0,48	0,29	0,53	0,72	0,41
Pollard	0,51	0,66	0,18	0,79	0,96	0,18	0,45	0,91	0,29	0,54	0,38	0,64	0,81	0,37
Sorghum	0,25	0,36	0,14	0,24	0,43	0,10	0,26	0,93	0,22	0,35	0,15	0,16	0,18	0,24
Rice bran	0,66	0,85	0,31	1,04	1,08	0,25	0,56	1,20	0,41	0,76	0,47	0,81	1,40	0,56

TSAA = Total sulphur amino acids

Table 4

The essential amino acid composition of feed ingredients expressed as a percentage of the requirement of broilers 0–3 weeks of age (Thomas, et al. *1978)*

Ingredient \ Amino acid	THR	SER	CYS	GLY	VAL	MET	ILE	LEU	TYR	PHE	HIS	LYS	ARG	TSAA
Bloodmeal	585	645	251	513	739	224	76	672	314	737	1 061	663	256	219
Carcass meal	328	388	149	1 022	378	219	241	286	228	289	281	329	339	188
Fishmeal	390	399	226	649	364	366	314	311	270	307	369	442	285	303
P B P M	407	865	523	616	445	110	323	297	227	333	157	171	312	296
Groundnut	172	321	186	369	229	79	164	170	193	259	199	135	359	127
Brewers grain	126	189	113	122	180	96	127	249	144	168	135	42	59	104
Sunflower	202	265	179	331	223	163	181	161	125	213	197	126	262	170
Lucerne	96	111	61	112	107	25	73	79	46	100	75	78	43	41
Maize	45	66	64	49	50	36	33	68	43	49	55	21	26	49
Wheat bran	61	89	72	117	79	34	47	51	39	61	68	48	61	51
Pollard	71	98	51	117	104	42	56	60	43	69	87	59	68	46
Sorghum	36	53	40	37	46	23	33	61	32	44	35	15	16	30
Rice bran	93	126	84	154	117	56	69	79	62	95	108	74	117	69

Table 5

The coefficients of variation of the amino acids in feed ingredients

Ingredient \ Amino acid	ASP	THR	SER	GLU	PRO	CYS	GLY	ALA	VAL	MET	ILE	LEU	TYR	PHE	HIS	LYS	NH_3	ARG
Bloodmeal	9,65	9,90	9,32	9,55	12,57	39,13	10,24	9,16	11,40	29,66	11,11	10,43	16,80	11,26	10,93	10,48	7,95	11,11
Carcass meal	21,12	20,00	17,49	20,81	18,72	27,27	18,42	19,78	25,07	29,59	30,46	22,43	26,45	23,38	15,45	20,72	27,40	29,56
Fishmeal	14,44	13,88	15,50	15,12	12,31	20,48	8,16	11,86	19,23	17,07	18,29	14,11	15,85	13,88	14,82	14,20	15,31	9,09
P B P M	20,73	19,80	20,58	19,75	22,27	23,83	20,10	20,07	21,74	28,57	20,00	19,34	24,68	19,55	34,78	20,21	22,89	28,08
Groundnut oilcake	19,92	13,01	13,76	15,40	16,87	10,29	15,14	16,19	22,54	25,71	16,42	12,74	23,66	16,43	18,39	14,19	14,94	14,65
Brewers grain	15,52	16,48	15,63	17,86	18,38	36,59	14,63	16,81	12,58	18,60	15,53	14,44	16,33	15,67	16,95	23,91	16,67	26,76
Sunflower oilcake	16,17	14,48	13,41	14,14	13,73	27,27	12,44	13,30	22,71	27,40	21,62	14,98	20,24	17,06	15,12	15,94	13,54	15,97
Lucerne	13,74	20,29	17,33	19,61	23,38	31,82	17,11	27,47	27,27	36,36	6,67	33,33	29,03	36,18	56,25	27,06	6,45	31,37
Maize	15,79	12,50	15,91	14,38	13,51	39,13	12,12	14,29	15,22	12,50	11,54	12,62	13,79	12,82	8,33	13,64	13,64	10,00
De-germed maize	7,84	6,90	7,14	10,46	6,67	33,33	13,79	8,07	16,98	30,77	11,11	8,65	25,93	8,11	13,04	20,00	58,62	37,50
Wheatbran	7,07	6,82	3,33	4,91	12,68	26,92	25,32	3,03	17,81	6,67	5,26	3,90	23,08	8,33	17,24	1,89	6,67	11,11
Pollard	6,42	3,92	6,06	6,00	8,64	11,11	6,33	5,33	11,46	11,11	6,67	6,59	27,59	16,67	7,90	6,25	19,44	23,46
Sorghum	11,32	12,00	13,89	14,29	16,36	57,14	8,33	13,43	18,61	...	15,39	13,98	9,09	11,43	20,00	12,50	9,09	16,67
Ricebran	17,95	12,12	14,12	15,28	11,59	29,03	23,08	11,93	11,11	28,00	12,50	10,00	29,27	9,21	10,64	12,35	148,08	12,14
Control maize	9,43	3,33	2,44	8,72	5,88	34,78	6,45	3,39	11,54	7,14	7,69	5,05	7,41	18,18	4,35	9,09	25,00	11,00

Table 6

Comparison of amino acid values obtained in present study with equivalent American values (all on air-dry basis)

		THR	SER	CYS	GLY	VAL	MET	ILE	LEU	TYR	PHE	HIS	LYS	ARG	TSAA
BLOODMEAL	A	4,21	4,38	0,92	3,49	6,86	1,04	0,61	10,27	2,13	5,89	4,67	7,29	3,06	1,96
	B	3,7		1,4	3,4	6,5	0,9	1,0	10,3	1,8	6,1	4,2	6,9	3,5	2,3
	C	2,47	3,0	1,00	2,95	5,20	0,65	0,62	7,60	1,17	3,90	3,05	4,50	2,35	1,65
	D	3,9	7,0	1,3	4,4	6,9	0,9	1,0	10,5	2,1	5,7	4,1	6,9	3,2	2,20
FISHMEAL	A	2,81		0,83	4,41	3,38	1,64	2,57	4,75	1,83	2,45	1,62	4,86	3,41	2,48
	B	2,6		1,0	4.5	3,4	1,8	3,5	5,0	2,0	2,7	1,5	5,1	3,4	2,8
	C	2,39		0,53	3,21	3,02	2,11	2,68	4,35	2,06	2,46	1,32	4,41	3,29	2,64
	D	2,8		0,56	3,5	1,88	3,0	5,0	2,26	2,4	1,5	4,7	3,6	2,44	
P B P M	A	2,93	5,88	1,93	4,18	4,14	0,49	2,65	4,55	1,54	2,66	0,69	1,88	3,74	2,42
	B	2,0		1,0	2,9	2,9	1,1	2,3	4,2	0,5	1,8	0,78	2,6	3,8	2,1
	C	2,06	2,75	1,0	6,80	2,43	1,28	1,88	3,68	1,58	2,03	0,93	2,44*	4,20	2,29
	D	2,0	2,5	1,0	5,9	2,6	1,28	1,9	3,7	1,6	2,1	0,93	2,7	4,2	2,28
GROUNDNUT OILCAKE	A[1]	1,23	2,18	0,68	2,51	2,13	0,35	1,34	2,59	1,31	2,07	0,87	1,48	4,30	1,04
	B[1]	1,4		0,8	2,6	2,2	0,5	2,2	3,2	1,9	2,5	1,1	1,8	5,2	1,3
	C[2]	1,05	1,40	0,72	2,70	1,97	0,44	1,62	2,90	1,40	2,42	1,00	1,56*	5,97	1,16
	D	1,1		0,68	2,3	1,75	0,42	1,7	2,6	1,5	2,0	0,85	1,6	4,6	1,10
BREWERS GRAIN	A	0,91	1,28	0,41	0,82	1,67	0,43	1,03	3,81	0,98	1,34	0,59	0,46	0,71	0,85
	B	0,9		0,3	1,0	1,6	0,6	1,5	2,3	1,2	1,3	0,5	0,9	1,3	0,9
	C	0,63	0,7	0,14	0,7	0,91	0,35	0,7	2,1	0,56	0,84	0,42	0,42	0,77	0,49
	D	0,9	1,0	0,3	1,0	1,5	0,5	1,4	2,3	0,7	1,5	0,6	0,72	1,0	0,8
SUNFLOWER OILCAKE	A	1,45	1,79	0,66	2,25	2,07	0,73	1,48	2,47	0,84	1,70	0,86	1,38	3,13	1,39
	B	1,50		0,4	2,7	2,3	0,65	2,1	2,6	0,8	2,2	1,0	1,4	3,5	1,05
	C	1,52	1,88	0,71	2,50	2,02	0,72	1,64	2,57	0,67	1,77	0,93	1,52	2,99	1,43
	D	0,7		0,5	2,0	1,6	0,5	1,0	1,6	0,6	1,15	0,55	1,0	2,3	1,0
LUCERNE	A	0,69	0,75	0,22	0,76	0,99	0,11	0,60	1,20	0,31	0,79	0,32	0,85	0,51	0,33
	B	0,6		0,3	0,8	0,7	0,25	0,75	1,1	0,5	0,7	0,3	0,53	0,0	0,55
	C	0,58	0,59	0,14	0,68	0,81	0,22	0,65	1,02	0,42	0,71	0,27	0,57	0,58	0,36
	D	0,70	0,80	0,18	0,88	0,85	0,28	0,80	1,25	0,55	0,8	0,32	0,73	0,75	0,46
MAIZE	A	0,32	0,44	0,23	0,33	0,46	0,16	0,26	1,03	0,29	0,39	0,24	0,22	0,30	0,39
	B	0,4		0,18	0,4	0,40	0,18	0,4	1,1	0,41	0,5	0,2	0,2	0,5	0,36
	C	0,35	0,47	0,15	0,34	0,50	0,20*	0,36	1,03	0,18	0,44	0,25	0,24*	0,36	0,35
	D	0,26	0,4	0,16	0,35	0,4	0,18	0,36	1,2	0,4	0,4	0,2	0,24	0,4	0,34
RICEBRAN	A	0,64	0,82	0,29	1,00	1,03	0,25	0,55	1,19	0,42	0,74	0,45	0,77	1,33	0,54
	B	0,62		0,4	0,8	0,91	0,29	0,61	1,2	0,68	0,76	0,56	0,77	1,4	0,69
	C[3]	0,30		0,10	0,70	0,60	0,30	0,30	0,50	0,20	0,30	0,10	0,50	0,50	0,40
	D	0,47	0,77	0,10	1,0	0,75	0,2	0,5	0,9	0,7	0,6	0,32	0,5	1,0	0,3
WHEATBRAN	A	0,44	0,60	0,26	0,79	0,73	0,15	0,38	0,77	0,26	0,48	0,29	0,53	0,72	0,41
	B	0,37		0,20	0,90	0,70	0,17	0,60	0,90	0,40	0,45	0,30	0,50	0,80	0,37
	C	0,23	0,43	0,15	0,54	0,45	0,11	0,37	0,57	0,28	0,29	0,19	0,37	0,62	0,26
	D	0,5	0,7	0,35	0,8	0,7	0,23	0,5	0,9	0,4	0,57	0,4	0,58	1,0	0,58

A = Results from present study
B = Values of Scott, Nesheim & Young (1976)
C = Values of Thomas (1978)
D = Values of Hubbell (1979)

* = Available, not total
1 = Solvent extracted
2 = Expeller extracted
3 = Rice "polishings"

Table 7

Correlation coefficients – comparison of Amino acid values obtained in present study with equivalent American values for ten ingredients

THREONINE

	A	B	C	D
A	1,0			
B	0,979	1,0		
C	0,952	0,949	1,0	
D	0,967	0,969	0,899	1,0

CYSTINE

	A	B	C	D
A	1,0			
B	0,713	1,0		
C	0,834	0,849	1,0	
D	0,768	0,907	0,932	1,0

GLYCINE

	A	B	C	D
A	1,0			
B	0,955	1,0		
C	0,875	0,722	1,0	
D	0,927	0,795	0,949	1,0

VALINE

	A	B	C	D
A	1,0			
B	0,979	1,0		
C	0,969	0,990	1,0	
D	0,971	0,988	0,975	1,0

METHIONINE

	A	B	C	D
A	1,0			
B	0,899	1,0		
C	0,830	0,972	1,0	
D	0,850	0,986	0,971	1,0

ISOLEUCINE

	A	B	C	D
A	1,0			
B	0,925	1,0		
C	0,935	0,980	1,0	
D	0,890	0,947	0,912	1,0

LEUCINE

	A	B	C	D
A	1,0			
B	0,981	1,0		
C	0,969	0,987	1,0	
D	0,979	0,991	0,969	1,0

TYROSINE

	A	B	C	D
A	1,0			
B	0,785	1,0		
C	0,869	0,707	1,0	
D	0,950	0,792	0,916	1,0

PHENYLALANINE

	A	B	C	D
A	1,0			
B	0,975	1,0		
C	0,939	0,948	1,0	
D	0,989	0,972	0,917	1,0

HISTIDINE

	A	B	C	D
A	1,0			
A	0,995	1,0		
C	0,968	0,978	1,0	
D	0,993	0,987	0,971	1,0

LYSINE

	A	B	C	D
A	1,0			
B	0,989	1,0		
C	0,947	0,974	1,0	
D	0,988	0,995	0,962	1,0

ARGININE

	A	B	C	D
A	1,0			
B	0,980	1,0		
C	0,946	0,947	1,0	
D	0,970	0,949	0,954	1,0

A = Present study
B = Scott, Nesheim & Young (1976)
C = Thomas (1978)
D = Hubbell (1979)

An interesting aspect of the results of Du Toit & Boyazoglu lies in their use of an analytical system designed for the separation of amino acids found in physiological fluids and their consequent reporting of hydroxyproline values. In the present study we have used a more rapid single-column procedure designed specifically for protein hydrolysates. In this system hydroxyproline is co-eluted with aspartic acid and, in consequence, if hydroxyproline is present our aspartic acid values will be erroneously elevated. However, as neither aspartic acid nor hydroxyproline is an essential amino acid, this potential error is of little practical moment.

A feature of the results expressed as a percentage of the requirement (Table 4) is the marked shortfall of amino acids in certain ingredients and the great surpluses of certain amino acids in other ingredients. However, more important than the balance of amino acids in individual ingredients is the balance in practical least-cost rations. We have used the values presented in Table 3 in the formulation of a number of such rations and from these studies three points of interest have emerged, namely that in practical rations surpluses of individual amino acids generally do not occur to any significant extent, that many practical rations are deficient in isoleucine and that in least cost rations small changes in the amino acid values of certain ingredients or small changes in the amino acid requirement values can have substantial economic impact. This latter fact imposes an imperative requirement for accurate amino acid values. The results obtained in the present study are presented as a step towards the realisation of this goal.

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