Acta Scientific NUTRITIONAL HEALTH (ISSN:2582-1423)

Volume 6 Issue 2 February 2022

Research Article

Amino Acids Analyses of Four Varieties of Raw and Cooked African Bitter Yam

Emmanuel Ilesanmi Adeyeye[1]*, Gbolagade Ayinde Yusuff[2], Ayodele Olajide[3], Idowu Olajumoke Tolulope[4], Popoola Olugbenga Kayode[1] and Idowu Kolade[1]

[1]Department of Chemistry, Faculty of Science, Ekiti State University, Ado-Ekiti, Nigeria

[2]Central Laboratory, Ekiti State University, Ado-Ekiti, Nigeria

[3]Department of Industrial Chemistry, Faculty of Science, Ekiti State University, Ado-Ekiti, Nigeria

[4]Chemistry Department, Afe Babalola University, Ado Ekiti, Ekiti State, Nigeria

***Corresponding Author:** Emmanuel Ilesanmi Adeyeye, Department of Chemistry, Faculty of Science, Ekiti State University, Ado-Ekiti, Nigeria.

Received: December 10, 2021

Published: January 25, 2022

Abstract

Background: *Dioscorea dumetorum* is a tuber that shows great variation in colour, form and quality.

Objective: The major purpose of this work is to report and compare the amino acid composition of both raw and cooked bitter yam.

Method: The *D. dumetorum* samples were the four edible different types available in Nigeria. For this work, the varieties were labelled as A_6, B_6, C_6 and D_6 (all raw samples), whereas A_{13}, B_{13}, C_{13} and D_{13} were the cooked equivalents. The method of amino acid analysis was by ion - exchange chromatography using the Technicon Sequential Multisample Amino Acid Analyser (TSM) (Technicon Instruments Corporation, New York, USA).

Results: For comparison, the raw and corresponding cooked samples had these total amino acid levels (in g $100g^{-1}$), A_6/A_{13} (61.1/54.7), B_6/B_{13} (65.1/54.7), C_6/C_{13} (52.6/54.6) and D_6/D_{13} (56.6/60.0). The amino acid values in the cooked samples showed both enhancement and leaching of the amino acids. EAA levels ranged from 25.5- 31.6g$100g^{-1}$ in raw and 24.1- 26.0g$100\ g^{-1}$ in cooked samples. P-PER range was 1.63 - 2.88 (raw) and 1.59 - 2.43 (cooked). EAAI was 99.1 - 100 (raw) and 99.3 - 100 (cooked) whereas the BV values were 96.3 - 97.3 (raw) and 96.5 - 97.3 (cooked). The limiting amino acids were Ser, Met + Cys and Lys depending on the amino acid scoring standards compared to. Statistical comparisons among the pairs at $r_{=0.01}$ showed that significantly different: A_6/A_{13}, B_6/B_{13}, C_6/C_{13} and D_6/D_{13}; A_6/D_6, A_6/B_6, A_6/C_6 and D_6/C_6; A_{13}/B_{13}, A_{13}/C_{13}, A_{13}/D_{13}, B_{13}/C_{13} and D_{13}/C_{13}.

Conclusion: The EAAI, BV and P-PER showed the samples to be highly bioavailable. Samples A_6 and B_6 had generally similar chemical characteristics and slightly better food qualities than C_6 and D_6 which also showed similar chemical characteristics. The A_{13}, B_{13}, C_{13} and D_{13} were appendages of their corresponding A_6, B_6, C_6 and D_6 respectively.

Keywords: *Dioscorea dumetorum*; Bitter yam; Raw and Cooked compared, Amino acids, High biological value

Introduction

With the exception of cereals, yams are known to be the most important food crops in West Africa [1,2]. Yams also serve as important food source in East Africa, the Caribbean, South America, India and Southeast Asia [3]. Yams are also good sources of pharmaceutical compounds like saponins and sapogenins which are precursors of cortisone and steroidal hormones [1].

Yam plants are classified under the genius *Dioscorea,* family Dioscoreaceae and order Dioscoreales [4]. Dioscoreales order is regarded as a member of the monocotyledonous group. The genius is further divided into sections within which the species are grouped. The section Enantiophyllum are distinguished by the fact that their vines twine in a clockwise direction (i.e., as one faces the plant, the vine passes upwards to the right). The section Lasiophyton consists of *D. dumetorum*, etc., have vines which twine anticlockwise [3]. According to Ozo [5], only about 10 species out of about 600 of *Dioscorea* are consumed as food; they are: *D. alata L.*, *D. bulbifera L.*, *D. cayenensis* Lam., *D. dumetorum* Pax., *D. esculenta* (Lour) Burk, *D. hispida* Dennst, *D. japonica* Thunb, *D. opposita* Thunb, *D. rotundata* Poir, *D. trifida* Thunb L.f. Yams are prepared for consumption in many ways such as boiling, roasting, fried as chips after boiling or parboiling and as *fufu*. Usually, yam prepared in any of these ways is eaten with stew vegetable oil or soup which provides a rich source of proteins, minerals and vitamins [5].

Dioscorea dumetorum (Kunth) Pax. has common names: three-leaved yam, bitter yam, cluster yam; trifoliate yam; *vernacular names*: Hausa: k'osain rogo, Igbo: ona, Yoruba: esiri or esuru [3]. *D. dumetorum* is not regarded as a proper yam in Southern Nigeria since its taste is different from that of the other yam varieties [6]. The plant can easily be identified by its trifoliate compound leaf. The stem twines anticlockwise. The tuber is large and coarse; a plant usually produces a cluster of tubers which are bitter due to the presence of alkaloids including dioscorine [3]. The tuber may be yellow, white or pale yellow in colour and it is regarded as of a poorer quality than yam. Although bitter yam is used as a vegetable, it is not pounded into fufu; this is owing to its soft texture and its bitter taste. Bitter yam soft texture is favoured by old people with poor teeth.

It is noted that information on the nutrient composition of bitter yam had been scanty. The major purpose of this work is to report the amino acid composition of both raw and cooked bitter yam, compare their analytical results, highlight the effect of cooking in terms of the amino acids composition and find out the quality of the amino acid composition across the bitter yam samples.

Materials and Methods

Materials

The *Dioscorea dumetorum* samples were the four edible different types available in Nigeria. The major basis of their varietal separation is the colour. The varieties were white (Yoruba: *Gbedu*), brownish white (Yoruba: *Eparoko*), yellow (Yoruba: *Epon agbo*) and light yellow (Yoruba: *Abeta*); these descriptions came from the colour of the tuber. The general Yoruba name for them is *Esuru*. Figure 1: a, b, c, d depict the various varieties. For the purpose of this work, the varieties were labelled as follows: A_6 (*Gbedu*), B_6 (*Eparoko*), C_6 (*Epon agbo*) and D_6 (*Abeta*) representing the raw samples whereas A_{13}, B_{13}, C_{13} and D_{13} were the cooked equivalents of A_6, B_6, C_6 and D_6 respectively. The samples do showcase different levels of bitterness.

Figure 1: *Dioscorea dumetorum* raw samples.

Collection of samples

The *D. dumetorum* samples were harvested at farm of Mr. A. A. Alonge located at Ekiti State University, Faculty of Agricultural Sciences experimental farm. The samples were authenticated at the Faculty of Agricultural Sciences, Ekiti State University, Ado-Ekiti.

Preparation of samples

The sample tubers, which were twelve (12) in number in each case, divided into two groups based on the colour. One set was used as the raw set whilst one set was set aside for the cooked.

The raw was sliced and dried in the oven until constant weight was achieved and peel removed. The moisture content to achieve dry weight went thus: moisture content in $g100g^{-1}$ for A_6 = 6.55, for B_6 = 7.39, C_6 = 5.87 and D_6 = 4.40. The second set (cooked) was cut into slightly bigger sizes and cooked differently in the laboratory using cooking gas. The samples were cooked with the peel. After cooking, the peel was removed, samples were sliced and oven dried to constant weight. Samples moisture content were ($g100g^{-1}$); A_{13} = 7.91, B_{13} = 6.56, C_{13} = 7.49 and D_{13} = 6.82. The dried samples were ground, sieved and kept in the refrigerator (2.8°C) in McCartney bottles pending analyses.

Analyses of samples

About 2.0g of each sample was weighed into an extraction thimble and the fat was extracted with chloroform/methanol mixture using Soxhlet extraction apparatus [7]. The extraction lasted 5-6h.

Between 30 and 35 mg of defatted samples were weighed into the glass ampoule. Seven millilitres of 6M HCl was added and oxygen was expelled by passing nitrogen gas into the ampoule (i.e., to avoid possible oxidation of some amino acids during hydrolysis). The glass ampoule was then sealed with a Bunsen flame and put in an oven at 105 ± 5°C for 22h. The ampoule was allowed to cool before breaking open at the tip, and the content was filtered to remove the humins.

The filtrate was then evaporated to dryness at 40°C under vacuum in a rotary evaporator. The residue was dissolved with 5ml acetate buffer and stored in plastic specimen bottles that were kept in the deep freezer.

The method of amino acid analysis was ion-exchange chromatography [8]. The amount loaded for the samples were between 5 and 10µl each. This was dispensed into the cartridge of the analyser, the Technicon Sequential Multisample Amino Acid Analyser (TSM) (Technicon Instruments Corporation, New York, USA), that was used for the analysis. The TSM was designed to separate and analyse free acidic, neutral and basic acids of the hydrolysate. The period of an analysis lasted for 76min for each sample. The column flow rate was $0.50mlmin^{-1}$ at 60°C with reproducibility consistent within ± 3%. The net height of each peak produced by the chart record of the TSM (each representing an amino acid) was measured and calculated. The internal standard used was nor leucine. Tryptophan was not determined due to cost. The values reported were averages of two determinations. All the amino acid values were reported as milligrams per gram of crude protein on a dry weight basis. Triplicate determinations were made for each sample.

Calculations made from analytical data results

Estimation of Isoelectric Point (pI)

The estimation of isoelectric point (*pI*) for a mixture of amino acid was carried out by the use of the equation of the form [9,10].

$$IP_m = \sum_i^n = I_iP_iX_i \text{---------- (1)}$$

Where IP_m is the isoelectric point of the mixture of amino acids, I_iP_i is the isoelectric point of the i^{th} amino acid in the mixture and X_i is the mass or mole fraction of the i^{th} amino acid in the mixture.

Estimation of predicted protein efficiency ratio (P - PER)

Computation of protein efficiency ratio (C-PER or P-PER) was carried out using the equations suggested by Alsmeyer., *et al.* [11]:

$$P\text{-}PER_1 = -0.468 + 0.454\ (Leu) - 0.105\ (Tyr) \text{--------(2)}$$

$$P\text{-}PER_2 = -0.684 + 0.456\ (Leu) - 0.047\ (Pro) \text{----------(3)}$$

$$P\text{-}PER_3 = -1.816 + 0.435 \times Met + 0.78 \times Leu + 0.211 \times His - 0.944 \times Tyr \text{----------(4)}$$

Leucine/Isoleucine ratio

The leucine/isoleucine ratio, their differences and percentage differences were calculated.

Determination of essential amino acid index (EAAI1)

The essential amino acid index was calculated by using the ratio of test protein to the reference protein for each eight essential amino acids plus histidine in the equation (5) [12]:

$$\text{Essential amino acid index} = \sqrt[8]{\frac{mgLysine\ in\ 1g\ test\ protein}{mgLysine\ in\ 1g\ reference\ protein}} \times \text{etc. for all 8 essential amino acids + His} \quad \text{---------(5)}$$

Determination of essential amino acid index (EAAI2)

The method of EAAI calculation was due to Oser [12] using the egg amino acids as the standard.

Calculation of biological value (BV)

Computation of biological value (BV) was calculated following the equation of Oser [13]:

$$\text{Biological value} = 1.09\ (EAAI) - 11.73 \text{---------(6)}$$

Computation of amino acid scores

The amino acid scores were computed using three different procedures:

- Scores based on amino acid values compared with whole hen's egg amino acid profile [14].
- Scores based on essential amino acid scoring pattern [15].
- Scores based on essential amino acid suggested pattern of requirements for pre-school children [16].

Other determinations

Other determinations such as total amino acid (TAA), total essential amino acid (TEAA), total non-essential amino acid (TNEAA), total acidic amino acid (TAAA), total basic amino acid (TBAA), total essential aliphatic amino acid (TEAlAA), etc. and their percentages were made as appropriate. Total sulphur amino acid (TSAA), percentage of cystine in TSAA (% cys in TSAA) were also calculated. The various amino acid groups into classes [17] were also calculated.

Statistical analysis

The data obtained in the amino acid analyses were subjected to two types of statistical analysis. The first was the descriptive analysis which involved the calculations for mean, standard deviation (SD) and coefficient of variation percent (CV%). The second form of statistical analysis dealt with inferential analysis. Here, correlation coefficient (r_{xy}), regression coefficient (R_{xy}), coefficient of determination or variance (r_{xy}^2), the coefficient of alienation (C_A) and the index of forecasting efficiency (IFE) were determined. Furthermore, the r_{xy} was subjected to critical table value (r_T) to see if significant differences existed among the various sample pair comparisons made in the tables among those generated from the data at $r_{=0.01}$ [18, 19].

Results and Discussion

Amino acids encountered in this report are:

Lysine (Lys) [PubChem C6H14N202, CID: 5962]; Glutamic acid (Glu) [PubChem C5H9N04, CID: 33032]; Methionine (Met) [PubChem C5H11N02S, CID: 6137]; Alanine (Ala) [PubChem C3H7N02, CID: 5950]; Arginine (Arg) [PubChem C6H14N402, CID: 6322]; Valine (Val) [PubChem C5H11N02, CID: 6287]; Leucine (Leu) [PubChem C6H13N02, CID: 6106]; Aspartic acid (Asp) [PubChem C4H7N04, CID: 5960]; Threonine (Thr) [PubChem C4H9N03, CID: 6288]; Isoleucine (Ile) [PubChem C6H13N02, CID: 791]; Phenylalanine (Phe) [PubChem C9H11N02, CID: 6925665]; Histidine (His) [PubChem C6H9N302, CID: 6274]; Tyrosine (Tyr) [PubChem C9H11N03, CID: 6057]; Cystine (Cys) [PubChem C6H12N204S2, CID: 67678]; Serine (Ser) [PubChem C3H7N03, CID: 5951]; Glycine (Gly) [PubChem C2H5N02, CID: 750]; Proline (Pro) [PubChem C51H9N02, CID: 145742].

PubChem CID

PubChem is a database of chemical molecules and their activities against biological assays. The system is maintained by the National Centre for Biotechnology Information (NCBI), a component of the National Library of Medicine, which is part of the United States National Institute of Health (NIH). Hence, we can talk of PubChem Compound ID (CID) [20].

Total amino acid profiles

The total amino acids profiles for both raw and cooked varieties of *Dioscorea dumetorum* were depicted in figure 2. Whereas the raw samples were labelled A_6, B_6, C_6 and D_6, their corresponding cooked samples were labelled A_{13}, B_{13}, C_{13} and D_{13} respectively.

On comparison basis, the values of the amino acids from the raw samples (mgg^{-1}) ranged from 52.6 - 65.1 (C_6 - B_6) whilst the cooked set ranged from 54.6 - 60.0 (C_{13} - D_{13}). Values of the cooked samples were mostly close as shown: $A_{13} \equiv B_{13} \equiv 54.7$ mgg^{-1} and C_{13} was 54.6mgg^{-1}. Whereas raw cooked samples had lower total amino acids than cooked raw samples in D_6/D_{13} (56.6/60.0) and C_6/C_{13} (52.6/54.6), it was the reverse in A_6/A_{13} (61.1/54.7) and B_6/B_{13} (65.1/54.7); this meant leaching of the amino acids could have happened in $A_6 \rightarrow A_{13}$ and $B_6 \rightarrow B_{13}$, it was enhancement in $D_6 \rightarrow D_{13}$ and $C_6 \rightarrow$ C13. The level of antinutrients could also had played some part in the reduction/enhancement.

In the EAA, the scenario observed in the TAA was different from that of the EAA. The observation followed this trend; for raw we have (mgg^{-1}): 25.5 - 31.6 (C_6 - A_6) and for cooked: 24.0 - 26.0 (B_{13} -D_{13}). Hence, in raw the trend was $A_6 > B_6 > D_6 > C_6$ and cooked had $A_{13} > D_{13} > C_{13} > B_{13}$; both trends being different from the trend among the total amino acid levels.

Amino acids of high concentrations in the samples were Arg, Asp, Glu, Pro, Gly, Ala, Leu and Phe; those with low levels were Lys, His, Thr, Cys, Val, Ile and Tyr, those with very low levels were Ser and Met. Lys was higher in raw than cooked in A_6, B_6 and D_6 but C_6 was lower than C_{13}. The three mostly consistently highest amino acid concentration in the samples were Glu > Leu > Asp.

Amino acids are highly necessary in the diet of man as their deficiencies would lead to deleterious diseases. Amino acid functions are now highlighted. Glu takes part in the synthesis of gluthathione. In transamination reactions Glu is converted to α-ketoglutaric acid [21]. Gamma amino butyric acid (GABA) is also formed from Glu and it is a neurotransmitter. Tyr is the precursor of the catecholamines and thyroid hormone [22]. Quantitatively, the amount needed for catecholamine and thyroid hormone syntheses is low [22], hence, dietary requirements are primarily to meet the needs for protein synthesis. Phe is irreversibly converted to Tyr in the liver and kidney [23]. Normally, Phe is converted to Tyr but if there is deficiency of Phe hydroxylase, Phe is not converted to Tyr, hence, alternative catabolites are produced. These catabolites are phenyl acetate and phenyl lactate. Phenyl acetate is conjugated with glutamine and excreted as phenyl acetyl glutamine in urine producing mouse odour in urine. Accumulation of phenyl alanine leads to defective serotonin formation, impaired melanin formation, children that are affected with this disease have fair hair and fair skin and they are also mentally retarded. Other features include seizure, psychosis and eczema [21]. Albinism is an inherited disorder that occurs due to deficiency of tyrosinase. Tyrosinase is involved in the synthesis of melanin. Due to deficiency of melanin, patient becomes white [21]. Proline is an AA which is hydroxylated to hydroxyproline in the presence of vitamin C but if vitamin C deficiency occurs, it leads to a disease condition called scurvy. Glycine is useful in the formation of bile acids; it also combines with colic acid to form glycocholate. It converts benzoic acid to hippuric acid in the liver. Furthermore, it is a component of glutathione; it is used in the biosynthesis of creatine, heme and purines. Ornithine which is a component of urea cycle (like citrulline) is formed from arginine by the action of arginase. During this reaction, urea synthesis occurs and carbon dioxide is produced [21]. Literature had shown that measurement of AA contents in the brains of patients with dominantly inherited cerebellar disorders revealed that moderate reduction of aspartate and glutamate contents in cerebellar cortex was observed. The studies concluded that reduction of AA content probably imply loss of specific cerebellar neurons [24].

Amino acid profile differences

table 1 had the amino acid differences in the *D. dumetorum* samples as A_6 - A_{13}, B_6 - B_{13}, D_6 - D_{13} and C_6 - C_{13} and the percentage differences. The table 1 showed the differences between the raw and the corresponding cooked samples. In the A_6 - A_{13}, A_6 was more positive than A_{13} in 12/17 (70.6%) amino acids, Pro had 0.00 mgg^{-1} and this also applied to Tyr, that is 0.00 = 2/17 (11.8%) whereas only three AAs were more positive towards A_{13}, i.e. 3/17 (17.6%). The percentage for A_6 > A_{13} ranged from + 2.54 (Thr) to + 64.6 (Met) showing the most likely leached AA was Met and least was Thr. In AAs where A_{13} > A_6, percentage range was -4.65 (Ser) to -24.3 (Asp) showing that cooking enhanced Asp highest and lowest enhanced was Ser. Generally, leaching was higher in EAA than the NEAA in the white variety; for such EAA we had Met, Phe, Leu, Val, His and Lys; but for NEAA, we had Glu, Ser and Gly.

Amino acid	Samples							
	A_6	A_{13}	B_6	B_{13}	D_6	D_{13}	C_6	C_{13}
Lys	31.6	26.2	31.6	20.3	27.0	25.1	26.5	32.1
His	19.5	16.4	19.0	13.2	15.0	16.4	20.3	18.3
Arg	38.0	36.2	40.5	44.0	33.0	39.7	31.9	35.0
Asp	57.1	71.0	69.5	59.2	57.4	69.5	62.3	56.5
Thr	23.6	23.0	22.6	21.0	2.20	23.0	21.5	21.5
Ser	30.1	31.5	25.0	30.1	30.1	31.5	19.0	25.5
Glu	81.8	69.0	106	79.0	76.5	111	75.7	83.3
Pro	23.4	23.4	24.4	23.4	21.4	23.4	22.4	26.5
Gly	28.3	30.2	37.5	30.3	31.2	38.4	25.5	21.9
Ala	36.0	35.0	37.6	41.7	37.2	25.4	34.2	35.3

Cys	9.30	5.60	9.20	6.60	7.90	4.00	12.5	8.00
Val	40.2	34.1	39.3	34.4	38.4	35.2	31.8	32.4
Met	13.0	4.60	8.80	7.30	13.5	7.20	7.20	7.30
Ile	34.0	33.0	26.6	32.6	32.3	33.3	26.3	28.8
Leu	78.1	51.3	81.0	51.3	53.5	57.3	53.5	59.0
Tyr	25.4	25.4	31.7	22.2	31.7	25.4	22.2	23.8
Phe	41.1	31.0	40.3	30.8	37.7	33.4	33.4	31.0

Table 1: Amino acid profiles (mgg^{-1}) of African bitter yam (*Dioscorea dumetorum).*

A_6 = Raw white variety; A_{13} = Cooked white variety; B_6 = Raw dull white variety; B_{13} = Cooked dull white variety; D_6 = Raw yellow variety; D_{13} = Cooked yellow variety; C_6 = Raw light-yellow variety; C_{13} = Cooked light-yellow variety.

In B_6 - B_{13} (%), $B_6 > B_{13}$ in 12/17 (70.6%) and $B_{13} > B_6$, we had 5/17 (29.4%). Among the EAA, $B_6 > B_{13}$ percentage changes ranged from + 7.08 (Thr) to + 36.7 (Leu). Some EAA with high percentages in $B_6 > B_{13}$ were Lys (+ 35.8%), His (+ 30.5%) and Leu (+ 36.7%) meaning leaching was high in these AAs. In AAs where $B_{13} > B_6$, the percentage change ranged from -8.64 (Arg) to -22.6 (Ile). Amino acids that were enhanced from $B_6 \rightarrow B_{13}$ were Arg, Ser, Ala, Ile and Phe.

For D_6 - D_{13} (%), $D_6 > D_{13}$ in only 7/17 (41.2%) whereas $D_{13} > D_6$ in 10/17 (58.8%). In D_6 - D_{13}, mostly the EAA were reduced in cooking, they included Lys, Val, Met and Phe whereas Cys, Ala and Tyr were the NEAA that reduced in their content on cooking. The percentage enhancement values ranged from -3.10 (Ile) to -45.5 (Glu) whereas those reduced had percentage values of 1.85 (Lys) to 49.4 (Cys). The C_6 - C_{13} (%) has similar pattern as we have in $B_{13} > B_6$ as $C_6 > C_{13}$ (although in reverse order) to the tune of 4/17 (29.4%), $C_{13} > C_6$ in 11/17 (64.7%) whereas Thr = 0, i.e., 1/17 (5.88%). Where $C_6 > C_{13}$, percentage range was + 7.19(Phe) to + 36.0 (Cys) and for $C_{13} > C_6$, it was -1.39 (Met) to -34.2 (Ser). Summarily in table 1, we have the following: Sample amino acid enhancement occurred thus, C_{13} (11a.a.) > D_{13} (10a.a.) > B_{13} (5a.a.) > A_{13} (3a.a.) (where a.a. = amino acids); from reduction from raw → cooked, we have, B_6 (12a.a.) ≡ A_6 (12a.a.) > D_6 (7a.a.) > C_6 (5a.a.) and 0.00 percentage change occurred as shown: A_6/A_{13} (2a.a.) > C_6/C_{13} (1a.a.). Whereas reduction could have been due to leaching of amino acids, cooking enhancement could be to antinutrient reduction.

Statistics in A6/A13, B6/B13, D6/D13 and C6/C13

The descriptive and inferential statistics between raw and cooked samples concerning the amino acid profile of *D. dumetorum* as A_6/A_{13}, B_6/B_{13}, D_6/D_{13} and C_6/C_{13} were compared in table 2. The inferential statistics involved correlation coefficient (r_{xy}), variance (r_{xy}^2) and regression coefficient (R_{xy}). It is interesting to note this trend: $A_6/A_{13} < B_6/B_{13} < D_6/D_{13} < C_6/C_{13}$ in the r_{xy} values. All the r_{xy} were positive, high and significant since all $r_{xyc} > r_{xyT}$ at the critical level of $r_{=0.01}$ and critical value of 0.590. The r_{xy}^2 values were high and followed the trend of r_{xy}. The R_{xy} ranged from 0.7058 to 1.39. The implication of R_{xy} was that as each raw sample value amino acid increased by 1.00 mg g^{-1}, the corresponding cooked value increased in amino acid composition by the R_{xy} value indicated in the table 2; this had further confirmed the observation discussed in table 1. The descriptive statistics had values for mean, standard deviation (SD) and coefficient of variation percent (CV%). Whereas the mean ± SD ranged from 3.03 ± 1.74 - 3.74 ± 2.49 mgg $100g^{-1}$ with CV% range of 53.7 - 66.7 in the raw samples of A_6, B_6, D_6 and C_6; the mean ± SD in the cooked (A_{13}, B_{13}, D_{13} and C_{13}) ranged between 3.10 ± 1.83 - 3.40 ± 2.51 mgg^{-1} with CV% levels of 59.9 - 73.9. For both raw and cooked samples, both their values for mean and SD were low and close among both raw and cooked. For CV%, the cooked values were slightly higher than the CV% values of the raw samples. The last part of the table 2 contained the coefficient of alienation (C_A) and index of forecasting efficiency (IFE). The C_A was calculated from the r_{xy} and IFE was calculated from the C_A. Whereas the C_A normally gives value for the error of prediction of relationship between two compared entities, IFE normally gives the reduction in the error of prediction between two compared entities. It should be noted however that C_A + IFE = 1.00 or 100%. In table 2, C_A range was 0.2029 - 0.4060 (20.3 - 40.6%) which were low; the trend was C_A: $A_6/A_{13} > B_6/B_{13} > D_6/D_{13} > C_6/C_{13}$; meaning the error of prediction between each pair ranged from 20.3 - 40.6%. There was a reverse of C_A in IFE as $A_6/A_{13} < B_6/B_{13} < D_6/D_{13} < C_6/C_{13}$. The

implication of IFE > C_A in each pair was that any member of a particular pair can function biochemically like its other pair since C_A < IFE for each pair and meant that prediction of relationship would also be easy.

Amino acid	Samples			
	A_6 -A_{13}(%)	B_6 - B_{13}(%)	D_6 - D_{13}(%)	C_6 - C_{13}(%)
Lys	+5.40(+17.1)	+11.3(+35.8)	+0.50(+1.85)	-5.60(-21.1)
His	+3.10(+15.9)	+5.30(+30.5)	-1.40(-9.33)	+2.00(+9.85)
Arg	+1.80(+4.74)	-3.50(-8.64)	-6.70(-20.3)	-3.10(-9.72)
Asp	-13.9(-24.3)	+10.3(+14.8)	-12.1(-21.1)	+5.80(+9.31)
Thr	+0.60(+2.54)	+1.60(+7.08)	-1.00(-4.55)	0.00
Ser	-1.40(-4.65)	-5.10(-20.4)	-1.40(-4.65)	-6.50(-34.2)
Glu	+12.8(+15.6)	+27.0(+25.5)	-34.8(-45.5)	-7.60(-10.0)
Pro	0.00	+1.00(+4.10)	-2.00(-9.35)	-4.10(-18.3)
Gly	-1.90(-6.71)	+7.20(+19.2)	-7.20(-23.1)	+3.60(+14.1)
Ala	+1.00(+2.78)	-4.10(-10.9)	+11.8(+31.7)	-1.10(-3.22)
Cys	+3.70(+39.8)	+2.60(+28.3)	+3.90(+49.4)	+4.50(+36.0)
Val	+6.10(+15.2)	+4.90(+12.5)	+3.20(+8.33)	-0.60(-1.89)
Met	+8.40(+64.6)	+1.50(+17.0)	+6.30(+46.7)	-0.10(-1.39)
Ile	+1.00(+2.94)	-6.00(-22.6)	-1.00(-3.10)	-2.50(-9.51)
Leu	+26.8(+34.3)	+29.7(+36.7)	-3.80(-7.10)	-5.50(-10.3)
Tyr	0.00	+9.50(+30.0)	+6.30(+19.9)	-1.60(-7.21)
Phe	+10.1(+24.6)	-6.90(-18.3)	+4.30(+11.4)	+2.40(+7.19)

Table 2: Amino acid profiles differences in the *D. dumetorum* samples as A6 - A13, B6 - B13, D6 - D13 and C6 - C13.
+ = in the two compared values when sample in the left hand is higher than right hand, the sign is positive and vice versa.

Statistics in A6/D6, A6/B6, A6/C6, B6/D6, B6/C6 and D6/C6 compared

table 3 profiled the statistical information on the above comparisons. Here, six pairs of raw samples were compared. All the paired samples had high, positive and significant r_{xy} values at $r_{0.01}$; this trend was followed by the r_{xy}^2 values. The R_{xy} values ranged between 0.6627 to 1.21 in which the left-hand sample represented 1.00 $g100g^{-1}$ and the right-hand sample values were the ones shown in the table 3 respectively. The mean values were low and close at 3.21 ± 1.72 to 3.74 ± 2.49 and the CV% values ranged between 53.7 to 66.7. The mean, SD and CV% were for A6, B6 and D6. The mean, SD and CV% values for D_6, C_6, B_6 (for right hand sides in the pair group) were 3.03 ± 1.74 to 3.74 ± 2.49 and CV% of 57.3 - 66.7. The C_A ranged from 0.2204 to 0.3234 leading to high levels of IFE that ranged between 0.6766 to 0.7796. The high levels of IFE would make the prediction of relationship easy and meant that interconversion of biochemical functions would be possible and easy between each member of a pair.

Statistics	A_6/A_{13}	B_6/B_{13}	D_6/D_{13}	C_6/C_{13}
r_{xy}	0.9138	0.9387	0.9572	0.9792
r_{xy}^2	0.8352	0.8811	0.9163	0.9588
R_{xy}	0.8359	0.7058	1.39	1.05
$Mean_1$	3.48	3.74	3.21	3.03
SD_1	2.00	2.49	1.72	1.74
$CV\%_1$	57.3	66.7	53.7	57.3
$Mean_2$	3.10	3.11	3.40	3.15
SD_2	1.83	1.87	2.51	1.85
$CV\%_2$	59.0	60.2	73.9	58.9

C_A	0.4060	0.3448	0.2894	0.2029
IFE	0.5940	0.6552	0.7106	0.7971
Remark	*	*	*	*

Table 3: Descriptive and inferential statistics between raw and cooked samples concerning the amino acid profiles of *D. dumetorum* as A_6/A_{13}, B_6/B_{13}, D_6/D_{13} and C_6/C_{13} compared.

r_{xy} = Correlation coefficient; r_{xy}^2 = Variance; R_{xy} = Regression coefficient; SD = Standard deviation; CV% = Coefficient o variation percent; C_A = Coefficient of alienation; IFE = Index of forecasting efficiency; Even numbers = Raw samples; Odd numbers = Cooked samples; Numbers 1,2 Correspond to even/odd number in each pair; * = Results significantly different at n-2 and $r_{=0.01}$ (critical value = 0.590).

Statistical comparisons among the cooked samples

In table 4, the cooked samples of the various varieties were compared as follows: A_{13}/D_{13}, A_{13}/C_{13}, A_{13}/B_{13}, B_{13}/D_{13}, B_{13}/C_{13} and D_{13}/C_{13}. All the r_{xy} values were positive, high and significant at $r_{=0.01}$; these were also followed intimately with the r_{xy}^2 values that were also high. The R_{xy} values were high but each less than 1.00 except A_{13}/D_{13} and B_{13}/D_{13} with a value of 1.28 each showing the ratio of A_{13}: D_{13} and B_{13}: D_{13} as 1.00: 1.28. Mean, SD and CV% for all A_{13}, B_{13} and D_{13} ranged from 3.10 ± 1.83 to 3.40 ± 2.51 and CV% of 59.0 to 73.9. For C_{13}, its descriptive statistical information was mean ± SD (3.15 ± 1.85) and CV% of 58.9. As observed earlier, all the C_A values were low at 0.2647 to 0.3630 leading to correspondingly high values for IFE at 0.6370 to 0.7353 thereby making prediction of relationship easy and each pair member could function biochemically like the other member in the pair.

Statistics	A_6/D_6	A_6/B_6	A_6/C_6	B_6/D_6	B_6/C_6	D_6/C_6
r_{xy}	0.9541	0.9717	0.9463	0.9587	0.9754	0.9549
r_{xy}^2	0.9105	0.9441	0.8954	0.9191	0.9514	0.9117
R_{xy}	0.8238	1.21	0.8228	0.6627	0.6791	0.9618
$Mean_1$	3.48	3.48	3.48	3.74	3.74	3.21
SD_1	2.00	2.00	2.00	2.49	2.49	1.72
$CV\%_1$	57.3	57.3	57.3	66.7	66.7	53.7
$Mean_2$	3.21	3.74	3.03	3.21	3.03	3.03
SD_2	1.72	2.49	1.74	1.72	1.74	1.74
$CV\%_2$	53.7	66.7	57.3	53.7	57.3	57.3
C_A	0.2992	0.2363	0.3234	0.2844	0.2204	0.2991
IFE	0.7008	0.7637	0.6766	0.7156	0.7796	0.7029
Remark	*	*	*	*	*	*

Table 4: Descriptive and inferential statistics between raw samples concerning the amino acid profiles of *D. dumetorum* as A_6/D_6, A_6/B_6, A_6/C_6, B_6/D_6, B_6/C_6 and D_6/C_6 compared.

Various quality parameters in the samples

The nutritional quality parameters in raw and cooked *D. dumetorum* samples were depicted in table 5. The TAA range was 52.6 - 65.1 $g100g^{-1}$ which was lower than the value in *Triticum durum* (70.3 $g100g^{-1}$) [25] and slightly above the half value of soybean (100 $g100g^{-1}$). The TNEAA values had values of 27.1 to 34.1 $g100g^{-1}$ with corresponding percentage values of 48.3 to 56.6. The TEAA range was 24.0 to 31.6 and percentage levels of 43.4 to 51.7. The values of TEAA/TNEAA ranged from 0.767 to 1.07, this ratio is important in protein body balance. While amino acid score is determined only from indispensable amino acid content, the metabolic demand is for both indispensable amino acids and non-essential nitrogen. Due to this, when any or all indispensable amino acids are present in excess of the demand, the absorbed mixture is unbalanced and limited by dispensable amino acids. If conversion of indispensable to dispensable amino acids occurs, then all of the absorbed nitrogen will be utilised in the same way as that of an absorbed mixture which exactly matches the demand (the reference pattern) [26].

The percentage ratio of TEAA to TAA that ranged between 44.1 to 51.7 were above the values 39% considered adequate as ideal food for infants, 26% for children and 11% for adults [16]; whereas the TEAA/TAA in egg is 50% [27] and in soybean it is 35.6%.

The total aromatic amino acid (TArAA) ranged from 6.62 to 9.10 $g100g^{-1}$ and the TEArAA range was 4.40 to 6.06 $g100g^{-1}$; these values were within the range of values suggested for ideal protein (6.8 - 11.8 $g100g^{-1}$ protein) for children [16]. The TArAA values in *Moringa oleifera* were (g100g-1 protein): leaves (7.00), stem (6.54) and root (6.59) [28]; in *T. durum* flour, TArAA value was 7.94 $g100g^{-1}$ protein [25]. Soybean flour had TArAA value of 12.2 $g100g^{-1}$ with corresponding TEArAA value of 7.5 $g100g^{-1}$; both values being higher than the TArAA and TEArAA under discussion.

The total sulphur amino acid (TSAA) values ranged from 1.02 to 2.23 $g100g^{-1}$ protein in the samples; these values were low. The percentage TSAA/TAA range was 1.87 to 3.78. The TSAA recommended for infants is 5.8 $g100g^{-1}$ protein [16] which is much higher than the values of 1.02 to 2.33 $g100g^{-1}$ protein. The %Cys/TSAA range was 35.7 to 63.5. The %Cys/TSAA in the diet of rat, chick and pigs is 50% in each case [8] but the standard value of %Cys/TSAA in man is unknown [16]. It is usual for AA in animal proteins to have low %Cys/TSAA [29-32]; such values ranged between 21.0% to 38.8%. Values of 36.9 and 35.7%Cys/TSAA fell within this category. On the other hand, vegetable protein %Cys/TSAA had higher values usually greater than 40%. Such literature values of %Cys/TSAA were in *Anacardium occidentale* (50.51%) [33]; coconut endosperm (62.8%) [34]; *M. oleifera*: leaves (51.6%), stem (48.6%) and root (48.5%) [28] and in *T. durum* (40.7%) [25]. Cystine and cysteine in the diet would reduce the need for Met and because all the sulphur in the diet is derived from these three AAs the sulphur can sometimes be used as an approximate assessment of the adequacy of protein [35]. The predicted isoelectric point (pI) values in table 5 ranged from 3.02 to 3.71, these were in the acid region of the pH. The *pI* value is an important function in the functionality of food. The predicted *pI* would assist in the preliminary prediction of *pI* for any organic compound whose isoelectric point is to be determined without going through the process of determining the minimum pH value in sample protein solubility determination. The plant *pI* values were lower than literature values of *T. durum* (4.05) [25] and *M. oleifera*: leaves (5.8), stem (5.5), root (5.4) [28].

Two forms of essential amino acid index (EAAI) were calculated and reported as $EAAI_1$ and $EAAI_2$. Whilst $EAAI_1$ was compared to soybean EAAI, $EAAI_2$ was compared with the whole egg protein EAAI. In table 5, $EAAI_1$, had values of 0.707 to 0.939 which were all lower than the value in soybean of 1.26 [36] and that of whole hen's egg (1.55). In *M. oleifera* $EAAI_1$ values were leaves (0.93) stem (0.86) and root (0.91) [28] which were highly comparable with the *D. dumetorum* samples. For the $EAAI_2$, values were 99.1 - 100. It should be noted that all the cooked samples had values of 100 except D_{13} and all raw samples had values <100 except C_6 that had 100. The biological values (BV) of 96.3 to 97.3 were observed as reported in table 5. These were all BV values that were favourable nutritionally. The $EAAI_2$ and BV values in *T. durum* were 96.8 and 93.8 respectively [28]. In soybean flour, the $EAAI_2$ was 86.7 and BV was 82.8. Both the $EAAI_2$ and BV in the samples were all correspondingly higher than the literature values as published by Oser [13] for leafy vegetables. The EAAI is useful as a rapid tool in the evaluation of food formulation for protein quality.

In the predicted (calculated) protein efficiency ratios, calculated for were $P\text{-}PER_1$, $P\text{-}PER_2$ and $P\text{-}PER_3$. The *in vivo* P-PER as suggested by Muller and Tobin [37] is of the order of 2.2. According to Friedman's [38] classification, P-PER is poor (< 1.5), moderate (1.5 - 2.0) and superior (> 2.0). For $P\text{-}PER_1$, values for C_{13}, A_6 and B_6 were in the superior group whilst others were in the moderate group. For $P\text{-}PER_2$, samples A_6 and B_6 were in superior group and others were in moderate group. In $P\text{-}PER_3$, samples A_6 and B_6 were in superior group, all other samples were in the poor group. The $P\text{-}PER_1$ and $P\text{-}PER_2$ values in *T. durum* flour were 2.37 and 2.26 respectively [25]. In the report of Sridhar., *et al.* [39], all the $P\text{-}PERs_{(1',2,3)}$ had values that ranged between moderate to superior groups in ripened split beans of three *Canavalia landraces*. It has been observed that the better the protein, the lower the level in the diet required to produce the highest protein efficiency ratio. This underscores the need for proper nutritive balance of all the amino acids to produce optimum metabolic efficiency.

The information on Leu/Ile as depicted in table 5 ran thus: Leu/Ile ratio (1.55 - 3.05), Leu-Ile (difference) (1.83-4.41), % Leu - Ile/Leu (35.7 - 67.2). From literature, the most ideal Leu/Ile is 2.36 [8]. Whereas samples A_6, A_{13}, B_{13}, D_6, D_{13}, C_6 and C_{13} might not lead to concentration antagonism in the samples when consumed as protein source in food, sample B_6 had Leu/Ile ratio value of 3.05 which was more than the ideal (2.36), this meant that B6 could be used to complement Leu deficiency in protein food sources. It had been suggested that an AA imbalance from excess Leu might be a

factor in the development of pellagra [40]. A high Leu imbalance in the diet impairs the metabolism of Trp and niacin, this is responsible for the niacin deficiency in sorghum eaters [41]. Experiments in dogs had shown that animals fed sorghum proteins with <11g100g^{-1} protein Leu did not suffer nicotinic acid deficiency [42]. Leu levels in the samples ranged between 5.12 to 8.10 g100g^{-1} protein, all being less than 11.0 g100g^{-1} protein; therefore about 87.5% of the samples could be beneficially exploited to prevent pellagra in endemic areas [43].

Phenylalanine can be irreversibly converted to Tyr in the liver and kidney [23]. When there is no limitation in the conversion, dietary aromatic amino acid needs can all be provided as Phe (this being termed "maximum phenylalanine requirement"). Excess dietary Tyr will limit the need for dietary Phe to meet the needs for protein synthesis. The concept of a maximum and minimum Phe requirement is analogous to the concept of the maximum and minimum excess of cysteine requirements for methionine [44]. The Phe: Tyr in the samples ranged from 1.19 to 1.62 showing that Tyr was not in excess of Phe. The mean minimum Phe requirement estimate in the presence of an excess Tyr is 9.1 mgkg^{-1}day^{-1}. Hence Tyr can spare 78% of dietary Phe need. The optimal proportions of dietary Phe and Tyr have been shown to be 60:40 respectively [45]. Both Phe and Tyr values were low in the present samples (table 5) and did not meet the optimal proportion of dietary Phe and Tyr of 60:40 respectively.

Included in table 5 were the various class groupings. The class groups were classes I - VII [17]. The concentration trend of the classes had been shown in table 5 (g100g^{-1}) as shown: class I (17.1 - 22.2) > class IV (13.4 - 18.1) > class V (7.50 - 9.11) > class VI (6.62 - 9.10) > class II (4.05 - 5.45) > class VII (2.14 - 2.44) > class III (1.02 - 2.23). A close look at the percentages would show that they were close to their individual values with little differences; they ran thus: value (percentage): class I, 17.1 - 22.2(31.6 - 35.5); class II, 4.05 - 5.45 (7.32 - 9.97); class III, 1.02 - 2.23(1.87 - 3.78); class IV, 13.4 -18.1(22.8 - 30.2); class V, 7.50 - 9.11(13.3 - 15.6); class VI, 6.62 - 9.10(12.1 14.9); class VII, 2.14 - 2.44(2.83 - 4.26). The crude protein contents reflected the amino acid profiles of the samples; this could be demonstrated as follows: protein (g100g^{-1}) and paired raw/cooked samples amino acids: 10.4, A_6(6.11) and 6.26, A_{13}(5.47); 14.6, B_6(6.51) and 7.88, B_{13}(5.47); 7.44, D_6(5.66) and 7.56, D_{13}(6.00); 11.8, C_6(5.26) and 12.8, C_{13}(5.46); i.e. higher protein content led to higher amino acid contents.

Statistics	A_{13}/B_{13}	A_{13}/C_{13}	A_{13}/D_{13}	B_{13}/C_{13}	B_{13}/D_{13}	D_{13}/C_{13}
r_{xy}	0.9643	0.9339	0.9319	0.9529	0.9499	0.9539
r_{xy}^2	0.9300	0.8722	0.8685	0.9081	0.9022	0.9099
R_{xy}	0.9901	0.9486	1.28	0.9428	1.28	0.7048
$Mean_1$	3.10	3.10	3.10	3.11	3.11	3.40
SD_1	1.83	1.83	1.83	1.87	1.87	2.51
$CV\%_1$	59.0	59.0	59.0	60.2	60.2	73.9
$Mean_2$	3.11	3.15	3.40	3.15	3.40	3.15
SD_2	1.87	1.85	2.51	1.85	2.51	1.85
$CV\%_2$	60.2	58.9	73.9	58.9	73.9	58.9
C_A	0.2647	0.3575	0.3630	0.3032	0.3127	0.3002
IFE	0.7353	0.6425	0.6370	0.6968	0.6973	0.6998
Remark	*	*	*	*	*	*

Table 5: Descriptive and inferential statistics between cooked samples concerning the amino acid profiles of *D. dumetorum* as A_{13}/D_{13}, A_{13}/C_{13}, A_{13}/B_{13}, B_{13}/D_{13}, B_{13}/C_{13} and D_{13}/C_{13} compared.

Amino acid scores based on whole hen's egg

Figure 2 depicted the amino acid scores of *D. dumetorum* samples based on whole hen's egg amino acid profile. Glycine stood out as the only AA that has scores greater than 1.00 in five out of eight samples. For the EAAs, Lys scores ranged as 0.327 - 0.518; His ranged from 0.550 - 0.846; Thr was 0.422 - 0.463; Val was 0.424 -

0.536; Met has scores of 0.144 - 0.422; Ile had 0.470 - 0.607; Leu was 0.618 - 0.976 and Phe was 0.604 - 0.806. Limiting amino acid of each sample was: Ser (0.81) in A_6; Met (0.144) in A_{13}; Met (0.275) in B_6; Met (0.228) in B_{13}; Ser (0.381) in D_6; Cys (0.222) in D_{13}; Ser (0.241) in C_6 and Met (0.228) in C_{13}. To correct the limiting AAs in order to fulfil the day's needs for all the AAs in the samples, we have 100/38.1 or 2.62 x A_6 protein; 100/14.4 or 6.94 x A_{13} protein; 100/27.5 or 3.64 x B_6 protein; 100/22.8 or 4.39 x B_{13} protein; 100/38.1 or 2.62 x D_6 protein (as we have in A_6); 100/22.2 or 4.50 x D_{13} protein; 100/24.1 or 4.15 x C_6 protein and 100/22.8 or 4.39 x C_{13} protein have to be consumed when they serve as the sole protein sources in the diet.

Figure 2: Amino acid scores of *D. dumetorum* samples based on whole hen's egg amino acid.

Essential amino acid scores based on fao/who [15] standards

In figure 3, the amino acid scores depicted were based on the comparison with the FAO/WHO [15] standards. Whereas scores were greater than 1.00 in A_6 and B_6 in Leu, three samples (A_6, B_6 and D_6) had scores in Phe + Tyr greater than 1.00. It has been said earlier that the metabolic demand is for both indispensable amino acids and non-essential nitrogen. As a result of this, when any or all the indispensable AAs are present in excess of the demand (Leu, Phe + Tyr in figure 3), the absorbed mixture is unbalanced and limited by dispensable amino acids.

In the absence of this conversion/absorption, it might be concluded that there can be no benefit from an amino acid score > 1.00 with the theoretical possibility of a disadvantage if interconversion were incomplete [26]. In figure 3, the limiting AA(LAA) in the samples were Lys (0.575) in A_6, Met + Cys (0.291) in A_{13}, Met + Cys (0.514) in B_6, Lys (0.369) in B_{13}, Lys (0.491) in D_6, Met + Cys (0.320) in D_{13}, Lys (0.481) in C_6 and Met + Cys (0.437) in C_{13}. It is good that all the LAAs were within the first two members of the acids that make up the essentiality of an amino acid. For corrections, we have 100/57.5 or 1.74 x A_6 proteins; 100/29.1 or 3.44 x A_{13} protein; 100/51.4 or 1.95 x B_6 protein; 100/36.9 or 2.71 x B_{13} protein; 100/49.1 or 2.04 x D_6 protein; 100/32.0 or 3.13 x D_{13} protein; 100/48.1 or 2.08 x C_6 protein and 100/43.7 or 2.29 x C_{13} protein. The issue of scores > 1.00 had been discussed under tables 6 and figure 2.

Amino acid	Class	A_6	A_{13}	B_6	B_{13}	D_6	D_{13}	C_6	C_{13}
TAA		61.1	54.7	65.1	54.7	56.6	60.0	52.6	54.6
TNEAA		29.5	29.6	34.1	30.8	28.7	33.9	27.1	28.4
%TNEAA		48.3	54.2	52.3	56.2	50.7	56.6	51.5	52.0
TEAA/TNEAA		1.07	0.848	0.909	0.779	0.972	0.767	0.941	0.849
TEAA with His without His		 31.6 29.6	 25.1 23.4	 31.0 29.1	 24.0 22.7	 27.9 26.4	 26.0 24.4	 25.5 23.5	 24.1 22.2
%TEAA with His without His		 51.7 48.5	 45.8 42.8	 47.7 44.7	 43.8 41.4	 49.3 46.7	 43.4 40.7	 48.5 44.6	 44.1 40.7
TAIAA	I	21.7	18.4	22.2	19.0	19.3	19.0	17.1	17.4
%TAIAA		35.5	33.6	34.1	34.8	34.0	31.6	32.6	32.5
TArAA	VI	8.60	7.28	9.10	6.62	8.44	7.52	7.59	7.31
%TArAA		14.1	13.3	14.0	12.1	14.9	12.5	14.4	13.4
TEArAA		6.06	4.74	5.93	4.40	5.27	4.98	5.37	5.48
%TEArAA		9.93	8.67	9.11	8.04	9.31	8.31	10.2	10.0
TAAA	IV	13.9	14.0	17.6	13.8	13.4	18.1	13.8	14.0
%TAAA		22.8	25.6	27.0	25.2	23.7	30.2	26.2	25.6

TBAA	V	8.91	7.88	9.11	7.75	7.50	8.12	7.87	8.54
%TBAA		14.6	14.4	14.0	14.2	13.3	13.5	15.0	15.6
TNAA		38.3	32.8	38.4	33.2	35.7	33.8	27.8	32.1
%TNAA		62.7	60.0	59.0	60.6	63.1	56.3	52.8	58.8
THAA	II	5.37	5.45	4.76	5.10	5.21	5.45	4.05	4.70
%THAA		8.80	9.97	7.32	9.34	9.21	9.09	7.70	8.60
CAA(Pro)	VII	2.34	2.34	2.44	2.34	2.14	2.34	2.24	2.65
%CAA		2.83	2.83	3.75	3.83	3.78	3.83	4.26	4.85
TSAA	III	2.23	1.02	1.80	1.39	2.14	1.12	1.97	1.53
%TSAA		3.65	1.87	2.77	2.54	3.78	1.87	3.74	2.80
%Cys in TSAA		41.7	54.9	51.1	47.5	36.9	35.7	63.5	52.3
Leu/Ile ratio		2.30	1.55	3.05	1.57	1.66	1.72	2.03	2.05
(Leu-Ile) diff		4.41	1.83	5.44	1.87	2.12	2.40	2.73	3.02
%(Leu-Ile)/Leu		56.5	35.7	67.2	36.5	39.6	41.9	50.8	51.2
Phe : Tyr		1.62	1.22	1.27	1.39	1.19	1.31	1.50	1.30
P-PER$_1$		2.81	1.59	2.88	1.63	1.63	1.87	1.73	2.43
P-PER$_2$		2.77	1.55	2.89	1.55	1.66	1.82	1.65	1.88
P-PER$_3$		2.85	0.334	2.29	0.686	0.268	0.915	1.00	1.24
pI		3.56	3.15	3.71	3.17	3.26	3.36	3.02	3.17
EAAI$_1$		0.939	0.736	0.889	0.707	0.832	0.759	0.788	0.791
EAAI$_2$		99.8	100	99.1	100	100	99.3	100	100
BV		97.0	97.3	96.3	97.3	97.3	96.5	97.3	97.3
Crude protein		10.4	6.26	14.6	7.88	7.44	7.56	11.8	12.8

Table 6: Various quality parameters as they concern the concentrations of aromatic, non-essential, neutral, etc. amino acids (g100g^{-1} protein) of *D. dumetorum* samples.

TAA = Total Amino Acid; TNEA = Total Non-Essential Amino Acid; TEAA = Total Essential Amino Acid; TAIAA = Total Aliphatic Amino Acid; TEAIAA = Total Essential Aliphatic Amino Acid; TArAA = Total Aromatic Amino Acid; TEArAA = Total Essential Aromatic Amino Acid; TAAA = Total Acidic Amino Acid; TBAA = Total Basic Amino Acid; TNAA = Total Neutral Amino Acid; THAA = Total Hydroxylic Amino Acid; CAA = Cyclic Amino Acid; TSAA = Total Sulphur Amino Acid; *pI* = Isoelectric Point; EAAI = Essential Amino Acid Index; BV = Biological Value and P - PER = Predicted Protein Efficiency Ratio.

Figure 3: Essential amino acid scores of *D. dumetorum* based on FAO/WHO [15] standards.

Essential amino acid scores based on pre-school child requirements

Essential amino acid scores of the bitter yam samples based on requirements of pre-school child (2-5years) could be seen in figure 4. Many AAs showed > 1.00 scores in many of the samples, they were: Val in A_6, B_6, D_6 and D_{13}; Leu in A_6 and B_6, Phe + Tyr in A_6, B_6 and D_6 and His in A_6, B_6 and C_6. For LAAs, we have Lys (0.545) in A_6; Met + Cys (0.408) in A_{13}; Lys (0.545) in B_6; Lys (0.350) in B_{13}; Lys (0.466) in D_6; Lys (0.433) in D_{13}; Lys (0.457) in C_6 and Lys (0.553) in C_{13}. Whereas Lys (first LAA) was limiting in seven samples, the second LAA (Met + Cys) was limiting in only one sample. The concern on interconversion (dispensable AA) and indispensable AA

became very prominent here more than in figures 2 and 3. The correction values were A_6 x 1.83; A_{13} x 2.45; B_6 x 1.83; B_{13} x 2.86; D_6 x 2.15; D_{13} x 2.31; C_6 x 2.19 and C_{13} x 1.81 protein where they serve as the only protein source in the diet.

Figure 4: Essential amino acid scores of *D. dumetorum* based on requirements of pre-school child (2 - 5 years).

Summary of the amino acid profiles into factors A and B means

The summary of the amino acid profiles into Factors A and B means are shown in figure 5. Factor A means constituted amino acids of the eight samples along the vertical axis whilst Factor B means constituted the amino acids along the horizontal axis: both containing the EAA and NEAA. Both Factors A and B means gave similar value of 28.5 $g100g^{-1}$ protein.

Figure 5: Summary of the amino acid profiles into Factors A and B means.

Conclusions

The work reported in this article was based on amino acid composition of *Dioscorea dumetorum* which were in two groups of raw (A_6, B_6, C_6 and D_6) and cooked (A_{13}, B_{13}, C_{13} and D_{13}). The work discussed the quality of the amino acids in the samples and some consumption consequences. Although bitter yam is regarded as of a poorer quality than yam, this notion is hardly supported by the amino acid composition of these varieties which are richer in crude protein than many other yam varieties. Amino acid values of cooked samples were very close as shown: $A_{13} \equiv B_{13} \equiv 54.7$ $g100g^{-1}$ > C_{13} of 54.6 $g100g^{-1}$. For the EAA trend: $A_6 > B_6 > D_6 > C_6$ (all raw) and in cooked: $A_{13} > D_{13} > C_{13} > B_{13}$; both trends being different from the trend observed among the total amino acid levels. The three most consistently highest amino acids concentration in the samples were Glu > Leu > Asp. The Leu/Ile range was 1.55 to 3.05 but the ideal is 2.36 meaning that sample B6 could complement diets with protein of low Leu. For P-$PER_{(1,2,3)}$ A6 and B6 were in the superior group (> 2.0); other samples in both P-$PER_{(1,2)}$ were in the moderate group (1.5 - 2.0) whereas others in P-PER_3 were in the poor group (<1.5). In EAAI soybean comparison ($EAAI_1$) values in raw (0.788 - 0.939) > cooked (0.707 - 0.791); for egg comparison ($EAAI_2$) values were virtually similar: raw (99.1 - 100) and cooked (99.3 - 100) and same for the BV values: raw (96.3 - 97.3) and cooked (96.5 - 97.3).

In this conclusion, there is the need to demonstrate the similarities of samples or group of samples. In the TAA, similarities existed between A_6/A_{13} (61.1/54.7) and B_6/B_{13} (65.1/54.7) $g100g^{-1}$ first group and second group being C_6/C_{13} (52.6/54.6) and D_6/D_{13} (56.6/60.0). Both A_6 and B_6 had higher TAA values than their A_{13} and B_{13} analogues but C_{13} and D_{13} had higher TAA levels than their C_6 and D_6 respectively. In the percentage amino acid (a.a.) concentration contribution in the sample pairs we have: A_6/A_{13}, A_6 (70.6%), A_{13} (17.6%); B_6/B_{13}, B_6 (70.6%), B_{13} (29.4%); in C_6/C_{13}, C_6 (29.4%), C_{13} (64.7%); D_6/D_{13}, D_6 (41.2%), D_{13} (58.8%) showing that similarities existed between A and B groups; also, in C and D groups. Amino acids in the cooked samples demonstrated both enhancement and reduction in amino acid (a.a.) concentration. Hence, for enhancement: C_{13} (11a.a.) > D_{13} (10a.a.) (both similar) > B_{13} (5a.a.) > A_{13} (3a.a.) (both similar); for reduction from raw to cooked: B_6 (12a.a.) ≡ A_6 (12a.a.) (similar) > D_6 (7a.a.) > C_6 (5a.a.) (similar) and 0.00% change in A_6/A_{13}(2a.a.) > C_6/C_{13}(1a.a.).

Summarily, samples A_6 and B_6 had generally similar chemical characteristics and slightly better food qualities than C_6 and D_6 which also showed similar chemical characteristics. The A_{13}, B_{13}, C_{13} and D_{13} were appendages of their corresponding A_6, B_6, C_6 and D_6 respectively.

Acknowledgment

We acknowledge the support of Mr. A. A. Alonge from whose farm we harvested the bitter yam samples.

Funding

This research did not receive any grant from funding agencies in the public, commercial, or not-for-profit sectors.

Bibliography

1. Coursey DG. "Yams". London: Longmans (1967).
2. Onwueme IC. "The tropical tuber crops: yams, cassava, sweet potato and cocoyams". Chicheser. John Wiley and Sons (1978).
3. Okonkwo SNC. "The botany of the yam plant and its exploitation in the enhanced productivity of the crop". In Advances in yam research (The biochemistry and technology of the yam tuber) (1985): 1-28. Nsukka, Nigeria: Biochemical Society of Nigeria in collaboration with Anambra State University of Technology.
4. Ayensu ES. "Anatomy of monocotyledons, VI Dioscoreales". Oxford: Oxford University Press (1972).
5. Ozo ON. "Analytical procedures for polyphenols and polyphenoloxide of yam tubers". In Advances in yam research (The biochemistry and technology of the yam tuber) (1985): 163-212. Nsukka, Nigeria: Biochemical Society of Nigeria in collaboration with Anambra State University of Technology.
6. Oyenuga VA. "Nigeria's foods and feed-stuffs" (3rd revised edn.). Ibadan, Nigeria: IUP (1968).
7. AOAC. "Official methods of analysis" (18th edition). Washington DC, USA: Association of Official Analytical Chemists (2006).
8. FAO/WHO. "Protein quality evaluation. Report of joint FAO/WHO expert consultation, Food and nutrition paper 51". Rome, Italy: FAO (1991).
9. Olaofe O and Akintayo ET. "Prediction of isoelectric points of legume and oilseed proteins from their amino acid composition". *The Journal of Technoscience* 4 (2000): 49-53.
10. Finar IL. "Organic Chemistry" (5th edition). London: ELBS and Longman Group Ltd 2 (1975).
11. Alsmeyer RH. *et al.* "Equations to predict PER from amino acid analysis". *Food Technology* 2 (1974): 24-38.
12. Steinke FH. "Nutritional evaluation (PER) of isolated soybean protein and combinations of food proteins". Journal of Food Science 45 (1980): 323-327.
13. Oser BL. "An integrated essential amino acid index for predicting biological value of proteins". In A.A. Albanese (Ed.), Protein and amino acid nutrition. New York, USA: Academic Press (1959): 281-295.
14. Paul AA. *et al.* "First supplement to McCance and Widdowson's the composition of foods". London: HMSO (1978).
15. FAO/WHO. "Energy and protein requirements". Technical report series number 522. Geneva, Switzerland: WHO (1973).
16. FAO/WHO/UNU. "Energy and protein requirements". Technical report series 724. Geneva, Switzerland: WHO (1985).
17. Nieman DC. "Nutrition". Dubuque, USA: Wc Publishers (1992).
18. Oloyo RA. "Fundamentals of research methodology and applied sciences". Ilaro, Nigeria: ROA Educational Press (2001).
19. Chase CI. "Elementary statistical procedures" (2nd edition). Tokyo, Japan: McGraw-Hill Kogakusha Ltd (1976).
20. PubChem and the American Chemical Society. Reshaping scholarly communication. California, USA: University of California (2005).
21. Akram M. *et al.* "Amino acids: a review article". *Journal of Medicinal Plant Research* 5.17 (2011): 3997-4000.
22. Matthews DE. "Proteins and amino acids". In M.E. Shike, A.C. Rose, B. Caballero and R.J. Cousins (Eds.), Modern nutrition in health and disease (10th ed.) Philadelphia: Lippincott, Williams and Wilkins (2006): 23-61.
23. Tessari P. *et al.* "Phenylalanine hydroxylation across the kidney in humans, rapid communication". *Kidney International* 56 (1999): 2168-2172.
24. Thomas L.*et al.* "Neurotransmitter amino acids in dominantly inherited cerebella disorders". *Neurology* 31.3 (1981): 237.
25. Adeyeye EI and Olaleye AA. "Composition of amino acids and evaluation of protein quality in Triticum durum grown in Nigeria". *American Journal of Chemistry and Applications* 5.1 (2018): 10-14.
26. WHO/FAO/UNU. "Protein and amino acid requirements in human nutrition". Report of a joint WHO/FAO/UNU expert consultation. WHO technical report series 935. Switzerland: WHO (2007).

27. FAO/WHO. "Protein quality evaluation". Report of joint FAO/WHO consultation held in Bethesda, USA. December 1989. Rome, Italy: FAO (1990): 4-8.

28. Olaofe O. *et al.* "Comparative study of proximate, amino acids and fatty acids of Moringa oleifera tree". *Elixir International Journal* 51 (2013): 12543-12554.

29. Adeyeye EI. "Amino acid composition of whole body, flesh and exoskeleton of female common West African freshwater crab Sudananautes africanus africanus". *Pakistan Journal of Nutrition* 7 (2008): 748-752.

30. Adeyeye EI. "The composition of the winged termites Macrotermites bellicosus". *Journal of Chemical Society of Nigeria* 30.2 (2005a): 145-149.

31. Adeyeye EI. "Amino acid composition of variegated grasshopper, Zonocerus variegatus". *Tropical Science* 45.4 (2005b): 141-143.

32. Adeyeye EI and Afolabi EO. "Amino acid composition of three different types of land snails consumed in Nigeria". *Food Chemistry* 85.4 (2004): 535-539.

33. Adeyeye EI. *et al.* "Amino acids composition of two masticatory nuts (Cola acuminata and Garcinia kola) and snack nut (Anacardium occidentale)". *International Journal of Food Sciences and Nutrition* 58.4 (2007): 241-249.

34. Adeyeye EI. "The chemical composition of liquid and solid endosperm of ripe coconut". *Oriental Journal of Chemistry* 20.3 (2004): 535-539.

35. Bingham S. "Dictionary of nutrition". London: Barrie and Jenkins (1977).

36. Cavins JC.*et al.* "Amino acid analysis of soybean meal: interlaboratory study". *Journal-Association of Official Analytical Chemists* 55 (1973): 686-694.

37. Muller HG and Tobin G. "Nutrition and food processing". Westport, CT, USA: Avi Publishing (1980).

38. Friedman M. "Nutritional value of proteins from different food sources - A review". *Journal of Agricultural and Food Chemistry* 44 (1996): 6-29.

39. Sridhar KR. *et al.* "Nutraceutical attributes of ripened split beans of three Canavalia landraces". *International Journal of Agricultural Technology* 12.7 (2016): 1277-1297.

40. FAO. "Sorghum and millets in human nutrition". FAO food nutrition series number 27. Rome, Italy: FAO/UN (1995).

41. Belavady B.*et al.* "The effect of oral administration of leucine on the metabolism of tryptophan". *Biochemical Journal* 87 (1963): 652-655.

42. Belavady B and Rao PU. "Leucine and isoleucine content of jowar and its pellagragenicity". *Indian Journal of Experimental Biology* 17.7 (1979): 659-661.

43. Deosthale YG. "Nutritional dimension of high yielding and hybrid crop varieties: locational and varietal differences in nutritional value". In FAO, FAO food and nutrition series number 27, Sorghum and millets in human nutrition. Rome, Italy: FAO (1980): 82.

44. Ball RO. "The *in vivo* sparing effect of cystine on methionine requirements in animal models and adult humans". *Journal of Nutrition* 136 (2006): S1682- S1693.

45. Pencharz PB. "What are the essential amino acids for the preterm and term infants? In 10th Nutricia Symposium". Dordrecht (the Netherlands): Kluwer Academic Publishers 21 (1996): 278-296.