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Research article

AMINO ACID PROFILES OF RAW, PROTEIN CONCENTRATE, WASTE OF *CELOSIA ARGENTEA* AND *AMARANTHUS HYBRIDUS* VEGETABLES CONSUMED IN NIGERIA

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ABSTRACT

Two major samples that made up six sub-samples were analysed for their amino acids composition. The two major samples were *Celosia argentea* and *Amaranthus hybridus*. The sub-samples were *C. argentea* raw (CR), protein concentrate (CC), waste (CW) and for A. *hybridus* raw (AR), protein concentrate (AC), waste (AW). Determinations were on dry weight basis. The total amino acids (TAA) was a reflection of the protein values in the samples seen a follows (protein/TAA) (g/100g): CR (22.7/79.5) <CC (28.8/80.6)> CW (21.0/69.9) and AR (21.8/73.8) <AC (24.2/80.6) >AW (20.2/66.2). But digestibility had a different trend as follows (%): CR (86.8) > CC (84.2)> CW (82.9) and AR (88.1) > AC (85.6)> AW (83.4). On intra-sample comparisons, the followings were observed: CR<CC (except in Cys, Pro, digestibility), CR > CW (in all determined parameters), CC> CW (in all parameters) and AR< AC (except in Glu, digestibility), AR >AW (in all parameters), AC > AW (in all parameters). In the inter-sample comparisons, observations were CR>AR (except in Ala, Phe, Glu, Ser, Tyr, digestibility), CC > AC (except in Phe, Ala, Val, Glu, Pro, Ser, Tyr, digestibility) and CW > AW (except in Met, Phe, Ala, Glu, Pro, Tyr, digestibility); results showed that Ala, Phe, Glu, Tyr and digestibility were constantly more concentrated in *A. hybridus* than *C argentea*. In the six samples, P-PER values were: $P\text{-}PER_1$ [2.15 to 2.22 (*C. argentea*; C.a.), 1.52 to 1.87 (*A. hybridus*: *A.h.*]; $P\text{-}PER_2$ [2.08 to 2.24 (*C.a.*), 1.57 to 2.00 (*A.h.*)]; $P\text{-}PER_3$ [1.27 to 1.34 (*C.a.*),-0.335 to -0.591 (*A.h.*)] showing *C. argentea* to be consistently better than *A. hybridus* in all the P-PER. EAAI. (soy stand.) values were 1.03 to 1.17 (*C.argentea*) and 0.801 to 0.986 (*A.hybridus*); soy is 1.26. $EAAI_2$ (egg stand.) values were 93.0 to 93.5 (*C.argentea*) and 96.1 to 97.2 (*A.hybridus*), i.e. better in *A hybridius*; egg is 100. Pattern of $EAAI_2$ was followed by BV: 89.6 to 90.2(*C.argentea*) and 93.0 to 94.2 (*A.hybridus*). Limiting amino acid score (LAAS) in egg/PDCAAS in CR (Ala, 0.27/0.24), CC (Met, 0.36/0.31), CW(Ala,0.24/0.20); AR(Cys, 0.29/0.26), AC(Cys, 0.37/0.32) and AW(Cys, 0.23/0.19). EAA scoring pattern: CR(Thr, 0.76/0.66), CC(Met+ Cys, 0.67/0.56), CW(Met + Cys, 0.55/0.45); AR (Met + Cys, 0.47/0.42, AC(Met + Cys, 0.55/0.47) and AW (Met + Cys, 0.38/032). In pre-school EAA requirement scores/PDAAS (LAAS), CR (Thr, 0.89/ 0.78), CC (Thr, 0.91/0.77), CW(Met + Cys, 0.76/0.63); AR (Met + Cys, 0.66/0.59), AC (Met + Cys, 0.76/0.65) and AW (Met + Cys, 0.54/0.45). More than required values of EAA requirements at ages 10 – 12 years (mg/kg/day) were observed in the samples. Statistical analysis were carried out for CR/CC, CC/CW,CR/CW; AR/AC, AC/AW, AR/AW, CR/AR, CC/AC and CW/AW; they all showed significant differences at $r_{xy = 0.01}$ at n-2 (df) since all $r_{xy(C)} > r_{xy(T)}$.

1.Introduction

Vegetables are the cheapest and most available sources of important protein, vitamins, minerals and essential amino acids. They are included in meals mainly for their nutritional value, although, some are reserved for the sick because of their medicinal properties (Mensah *et al.,* 2008). The dependence of most developing countries on starch-based foods as the main staple foods for the supply of both energy and protein accounts in part for protein deficiency which prevails among the populace as recognized by FAO (Akubugwo et al., 2007). In

Nigeria, the daily diet is dominated by starch staple food, vegetables are the cheapest and most readily sources of important proteins, vitamins minerals and essential amino acids (Akubugwo et al., 2007).

Many of the local vegetable materials are under-exploited because of inadequate scientific knowledge of their nutritional potentials. Adequate intake of dietary vegetable can lower the serum cholesterol level, risk of coronary heart diseases, hypertension, constipation, diabetes, colon and breast cancer (Ishida *et al*. 2000; Rao and (Newmark, 1998). The Recommended Dietary Allowance (RDA) of fibre for children, adults, pregnant and lactating mother are 19-25g, 21 – 38g, 28 and 30g respectively. Plant is capable of contributing 34-45, 23-41, 31 and 30% of their respective daily requirements when 100g dried leaves are consumed and as such could be valuable sources of dietary fibre in human nutrition (Akubugwo et al., 2007). The nutrient contents of different types of vegetable vary considerably and they are not major sources of carbohydrates compared to the starchy food which form the bulk of food eaten, but contain vitamins, essential amino acids, as well as mineral and antioxidants (Fasuyi, 2006). They are important protective food and useful for the maintenance of health and the prevention and treatment of various diseases (Sobukola et al., 2010). A healthy heart and circulation system could benefit from a balanced diet with adequate fruits and vegetable (Zheng et al., 2017). Also epidemiological evidences support a significantly positive correlation between eating fruits and vegetable as well as cardiovascular health (Sikand et al., 2005; Trude et al., 2015).

The etymology of vegetables shows that the meaning of vegetables as a plant grown for food was not established until the 18th century (Ayto, 1993). In 1767, the word was specifically used to mean a plant cultivated for food and edible herb or root (Rachie, 1972).

The use of extracted leaf protein (LP) as a food for people and other non-ruminants has been suggested at various times during the past 100 + years, and at various times during the past 50 + years, samples have been made with which quality and acceptability could be tested (Pirie, 1971). Sustained work started over 30 years ago. The year 1973 marked the bicentenary of the discovery by G.F. and H.M. Rouelle that the coagulum which was separated from a heated leaf extract was nutritionally similar to the curd obtained from milk (Rouelle, 1773). Slade (1937) and Pirie (1942) described the procedure suggested for extracting protein from herbage for human consumption. From the massive number of papers dealing with various aspects of protein extraction from different crops it could be concluded that: there is sufficient evidence available to indicate that the nutritional value of protein concentrates extracted from green vegetation is comparable to that of protein isolates of animal origin and superior or similar to protein isolates of seeds (Morris, 1977).

The *Amaranthus hybridus* (Table 1) belongs to the family of Amaranthaceae consisting of about 60-70 species, cultivated in many parts of the world. It is a grain native to Mexico and Central America. *Amaranthus* was grown for centuries in pre-Columbia America as a staple crop along with corn, several of which are cultivated to leafy vegetables or forage, others are for grain production and some are planted as ornamental plants. Grain amaranth's balanced amino acid composition is close to the optimum protein reference pattern in the human diet according to FAO/WHO requirement (Ojo, 2001). It is grown as more of intercropped with other staple food crops in traditional farming system for family consumption and market (Ojo, 2001). *Celosia argentea* (Table 1) belongs to the family of Malvaceae and is one of the important leafy vegetables commonly found in traditional intercropping system of the tropics. It is commonly known as `Sokoyokoto` or `Ajefawo` amongst the Yorubas (Schippers, 2000) and is a vegetable of high economic value for most rural vegetable farmers (Akinfasoye et al., 2008). The leaves have also been found to suppress elevation of post prandial blood glucose level in humans and are rich sources of vitamins A and C, also the seeds possess broad antibacterial properties (Innami et al., 2005).

Table 1. Major vegetable samples used

Botanical names	Family	English	Local names
Amaranthus hybridus	Amaranthaceae	Bush green	Tete-arowojeja(Yoruba
Celosia argentea	Malvaceae	Garden herb	Ajefowo (Yoruba)

Some literature works are available generally on vegetables, *Celosia argentea* and *Amaranthus hybridus* in particular. Adesina and Adeyeye (2013) reported on the amino acid profile of three non-conventional leafy vegetables: *Cucurbita maxima, Amaranthus viridis* and *Basella alba*, consumed in Ekiti State, Nigeria. Comparative study of proximate, chemical and physicochemical properties of less explored tropical leafy vegetables (Babarinde *et al*., 2018). Elemental composition, mineral safety index, mineral bioavailability, phytochemical and non-starch polysaccharides content of fourteen leafy vegetables consumed in Ekiti State, Nigeria had been reported (Adesina et al., 2022). Ojo (2001) studied the density and cutting height as they affect the production of *Celosia argentea.* Akinfasoye *et al*. (2008) studied the effect of organic fertilizer and spacing on growth and yield of Lagos

spinach (*Celosia argentea*). Innami et al. (2005) reported on how jews mellow leaves (*Corchorus litorius*) suppress elevation of post prandial blood glucose levels in rat and humans. There are also some works on leaf protein concentrate (LPC) from various leafy vegetable sources. Protein extraction from grasslands: Ostrowski – Meissner (1979, 1980), Pirie (1942, 1971), Saunders et al. (1973). Chemical composition and functional properties of leaf protein concentrates of *Amaranthus hybridus* and *Telfairia occidentalis* (Adeyeye and Omolayo, 2007).

Lack of protein may lead to high mortality and lowered resistance to disease, especially in childhood. In view of the economic situation in the rural area and because kwashiorkor is rife in Nigeria, it is essential to look for inexpensive sources of good quality protein that can be used as alternatives to expensive animal protein. Since the high cost of animal protein is due mainly to the price of feeds, it was felt that a local substitute such as leaf protein concentrate (LPC) might decrease the cost of animal protein.

The major objective of this presentation is to present and discuss the amino acid profiles of raw, leaf protein concentrate and 'waste' of *Celosia argentea* and *Amaranthus hybridus* simultaneously. The novelty of this study is the comparative analysis and discussion of the sub-samples from the same stock: *C. argentea* (raw, concentrate, 'waste') and *A. hybridus* (raw, concentrate, 'waste'). Whereas most of the raw vegetables are always analysed without further treatment, production of LPC had become common but the 'waste' from the LPC preparation had always been thrown off or used as animal feed. This comparative study (raw, concentrate, 'waste') would show whether any 'waste' actually existed when LPCs were prepared from leafy vegetables. From the above, some null hypotheses were generated as follows:

There is no significant difference between the statistical analysis of the intra-sample amino acids of *Celosia argentea* represented as, CR/CC, CC/CW, CR/CW where C represented *Celosia argentea*. CR(raw), CC (concentrate), CW"waste"; and AR/AC, AC/AW, AR/AW where A represented *Amaranthus hybridus*, AR(raw), AC(concentrate), AW('waste').

There is no significant difference between the statistical analysis of the inter-sample amino acids of *Celosia argentea* and *Amarathus hybridus*: CR/AR, CC/AC, CW/AW. Level of significance for each of the hypotheses was α=0.01 at n-2 (df).

2. Material and methods

2.1. Collection of samples

The leafy vegetables used for the studies were harvested from a farm land located in Ikere-Ekiti, Ekiti State, Nigeria. The samples were planted about three metres from each other on the same plot of farm land. The vegetable samples were authenticated at the Herbarium unit of the Department of Plant Science and Bio-technology, Ekiti State University, Ado-Ekiti, Nigeria.

2.2. Treatment of samples

The vegetable leaves were destalked, thoroughly washed under running tap water, drained and each specie was divided into three equal parts. Two of the parts were combined in each of the two vegetables to prepare the protein concentrate and the 'waste' samples, whilst the other one-third was used as raw sample.

2.3. Preparation of raw samples

The one-third of the vegetable leaves of each of the vegetables was air-dried at room temperature to a constant weight. The dried samples were then pulverized to powder using an electric stainless steel Excella- Mixer grinder (3 S.S. Jars Model, India). The powdered samples were stored in airtight plastic containers and refrigerated (2.8^{o}C) pending further chemical analysis.

2.4. Preparation of leaf protein concentrate (LPC) and 'waste'

The leaves were washed and weighed prior to pulping using the Posho mill, followed by pressing with screw press to separate the juice. The Posho mill has sharp blades which can be adjusted to carry out the pulping. The leaves were fed in from a tray above the pulper. The mill is available in every community in Nigeria and is used mainly for grinding corn and beans. Since there is no electricity in the communities, the mill is designed to run on a diesel engine (Oke, 1983). The separated leaf juice were heated in batches to 80 - 90^{o}C for about 10 min to coagulate the leaf protein. The protein coagulum was separated from the fraction by filtering through cloth filter followed by pressing with screw-press as described for *garri* making (Aletor, 1993). The LPCs were then washed with distilled water and repressed. The products were pulverized and spread in the sum to dry prior to analysis. The flow chart for the low cost fractionation scheme as adapted from Fellows (1987) is shown in Fig.1. After sundrying the LPCs, they were subjected to the various analyses after they have been ground into flour and preserved in polyethylene bottles.

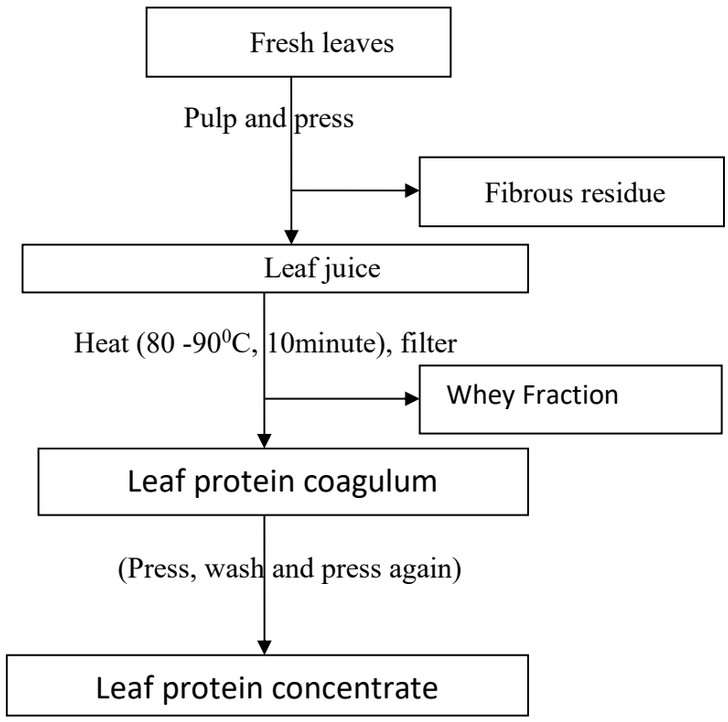


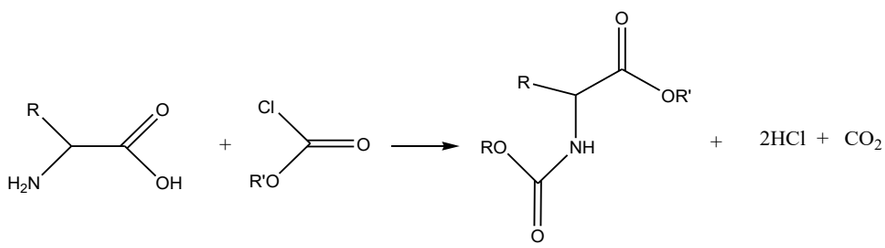
Figure 1. Flow-chart of leaf protein concentrate (LPC) production (adapted from Fellows, 1987)

2.5. Extraction and analysis

Extraction and instrumental analysis were carried out by following AOAC method (2006) and Danka et al. (2012).

The dried pulverized sample was made to be free of water by ensuring constant weight for a period of time in the laboratory. The sample of 10.0g was weighed into 250ml conical flask capacity. The sample was defatted by extracting the fat content of the sample with 30ml of petroleum spirit three times with Soxhlet extractor that was equipped with thimble. The sample was hydrolyzed three times for complete hydrolysis to be achieved for the totality of amino acids recovery.

The pulverized and defatted sample was soaked with 30ml of 1M potassium hydroxide solution and was incubated for 48 hours at 110^{o}C in hermetically closed borosilicate glass container. After the alkaline hydrolysis, the hydrolysis was neutralized to get pH in the range of 2.5 to 5.0. The solution was purified by cation-exchange solid-phase extraction. The amino acids in purified solutions were derivatised with ethylchloroformate by the established mechanism:



R' = C_2H_5

Derivatization process of amino acid (1)

The derivatizing reagent was removed by scavenging with nitrogen. The derivatized amino acid was made up to 1ml in a vial for gas chromatography analysis. The gas chromatographic conditions for the amino acids analysis were as follows: GC: HP6890 powered with HP ChemStation rev. A09.01 (1206) software; injection temperature: split injection; split ratio: 20:1; carrier gas: hydrogen; flow rate: 1.0ml/min; inlet temperature: 250^{o}C; column type: EZ; column dimensions: 10m x 0.2mm x 0.25 µm; oven programme: initial @ 110^{o}C, first ramp @ 27^{o}C/min to 320^{o}C; second, constant for 5 min. at 320^{o}C; detector : PFPD; detector temperature: 320^{o}C; hydrogen pressure: 20 psi; compressed air: 35 psi.

Some calculations were made from the analytical data results.

(i) Estimation of isoelectric point *(PI)*: The estimation of isoelectric point *(PI)* for a mixture of amino acids was carried out using the

(ii) equation of the form (Olaofe and Akintayo, 2000):

(iii) $IP_m = \sum_{i=1}^{n} IiPiXi$ (2)

where IPm is the isoelectric point of the mixture of amino acids. Iipi is the isoelectric point of the ith amino acid in the mixture and

Xi is the mass or mole fraction of the ith amino acid in the mixture.

(iv) Estimation of predicted protein efficiency ratio (P-PER): Computation of protein efficiency ratio (C-PER or P-PER) was done using the equations by Alsmeyer et al. (1974):

$$P\text{-}PER_1 = -0.468 + 0.454\ (Leu) - 0.105\ (Tyr) \quad (3)$$

$$P\text{-}PER_2 = -0.684 + 0.456\ (Leu) - 0.047\ (Pro) \quad (4)$$

$$P\text{-}PER_3 = -1.816 + 0.435 \times Met + 0.78 \times Leu + 0.211 \times His - 0.944 \times Tyr \quad (5)$$

(v) Estimation of the differences between intra- and inter-samples and the percentage differences.

(vi) Calculations into the amino acid groups of the samples and classifications into classes I - VII *(Nieman* et al*.* (1992) occurred.

(vii) Amino acids composition of the samples grouped into their quality parameters.

(viii) Leucine/isoleucine ratio: The leucine/isoleucine ratio, their differences and their percentage differences were calculated.

(ix) Determination of essential amino acid index (EAAI): 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 (Steinke et al., 1980):

$$\text{Whey Fraction} = \sqrt[9]{\frac{mg\ Lys\ in\ 1g\ test\ protein}{mg\ Lys\ in\ 1g\ reference\ protein}} \times \textit{Essential amino acid index} \quad (6)$$

Determination of essential aminoacid index ($EAAI_2$)

The method of EAAI calculation based on Oser (1959) method using the egg protein amino acids as the standard.

(x) Estimation of essential amino acid index ($EAAI_2$): The method of EAAI calculation was due to Oser (1959) using the egg protein amino acids as the standard.

(xi) Computation of biological value (BV): Computation of biological value (BV) was calculated following the equation of Oser (1959):

$$\text{Biological value (BV)} = 1.09\ (EAAI) - 11.73 \quad (7)$$

(xii) Computation of Lys/Trp and Met/Trp: The ratios of Lys/Trp (L/T) and Met/Trp (M/T) were computed.

(xiii) Computation of amino acid scores: The amino acid scores were computed using four different procedures:

-Scores based on amino acid values compared with whole hen's egg amino acid profile (Paul et al*.,* 1978).

-Scores based on essential amino acid scoring pattern (FAO/WHO, 1973).

-Scores based on essential amino acid suggested pattern of requirements for pre-school children (FAO/WHO/UNU, 1985).

-Conversion of the three amino acid scores stated above to give corrected scores based on the determined protein digestibility, protein digestibility-corrected amino acid scores (PDCAAS) (FAO/WHO, 1991).

(xiv) Estimates of amino acid requirements at different ages (mg/kg/day): These estimates were based on the essential amino requirements in mg/kg/day body weight of 10 to 12 years school boys (FAO/WHO/UNU, 1985).

(xv) Other calculations: Other determinations such as total amino acid (TAA), total essential amino acid (TEAA), total non-essential amino acid (TNAA), total acidic

(xvi) amino acid (TAAA), total basic amino acid (TBAA), total essential aliphatic amino acid (TEAIAA) and their percentages were made. Total sulphur amino acid (TSAA), percentage of cystine on TSAA (% Cys in TSAA) were also calculated.

2.6. Determination of Protein digestibility

The *in-vitro* protein digestibility was determined by the modified method of Akeson and Stahmant (1964) and AOAC (2006). The sample containing the exact amount of 100mg of protein was incubated with 1.5mg of pepsin in 15ml of 0.1M hydrochloric acid at a temperature of 38^0C for 3h. The solution was neutralised with 0.2M sodium hydroxide. Four mg (4 mg) of pancreas in 7.5ml phosphate buffer of pH 8.0 was added with the addition of 1ml of toluence for the prevention of microbial growth and the solution was incubated for another 24h at 38^0C. The protein content in the solution after 24h of digestion was taken as a measure of the digested product. Following the 24h incubation, the enzyme was inactivated by the addition of 10ml of 10% trichloroacetic acid (TCA) to precipitate undigested protein that was later filtered off. The volume of the filtrate was made up to 100ml and centrifuged at 5000 rpm for 30 minutes; the supernant was collected for protein determination. Blank was digested following the same procedure and employed 1g of each source

of enzyme to make protein measurement carried out effectively (Abimorad et al., 2008). The digestibility of the protein was calculated by the equation shown below:

$$\text{Digestibility} = \frac{\text{Protein in supernant}}{\text{Total protein of the sample}} \times 100 \quad (8)$$

2.7. Determination of protein digestibility-corrected amino acid score (PDCAAS)

To calculate for protein digestibility-corrected amino acid score for individual foods requires some steps to be taken. These steps are enumerated as follows. Proximate composition must be determined; protein can be calculated by using a nitrogen-to-protein conversion factor of 6.25. In amino acid profile, protein hydrolysate should be prepared and analysed for amino acid using standard method. Amino acid scores would then be calculated (to give uncorrected amino acid scores). Based on the determined protein digestibility, protein digestibility-corrected amino acid score (PDCAAS) of the test food was then calculated by multiplying the amino acid score x true protein digestibility (or each amino acid score might also be corrected using this similar approach as the case may be). In this report, the score was expressed as a decimal, but it can be expressed in percentage terms (FAO/WHO, 1991).

2.8. Statistical evaluation

The intra-samples (CR/CC, CC/CW, CR/CW); (AR/AC, AC/AW, AR/AW) and inter-samples (CR/AR, CC/AC, CW/AW) results were subjected to statistical analyses of correlation coefficient (r_{xy}), regression coefficient (R_{xy}), coefficient of determination or variance (r_{xy}^2),the coefficient of alienation (C_A) and index of forecasting efficiency (IFE). Other calculations were grand mean, standard deviation (SD) and coefficient of variation (CV%). The r_{xy} value was converted to critical Table value (r_T) to see if significant differences existed among the various comparisons made in the pairs enumerated at $r_{=0.01}$ (Oloyo, 2001; Chase, 1976).

3. Results and Discussion

Amino acids encountered in this work were: Lysine (Lys) [PubChem C6H14N202, CID: 5962]; Glutamic acid (Glu) (PubChem C5H9NO4, CID: 33032]; Methionine (Met) [PubChem C5H11NO2S, CID: 6137]; Alanine (Ala) [PubChem C3H7NO2, CID: 5950]; Arginine (Arg) [PubChem C6H14NO4O2, CID: 6322]; Valine (Val) [PubChem C5H11NO2, CID: 6287]; Leucine (Leu) [PubChem C6H13NO2, CID: 6106]; Aspartic acid (Asp) [PubChem C4H7NO4, CID: 5960]; Threonine (Thr) [PubChem C4H9NO3, CID: 6288]; Tryptophan (Trp) [PubChem C11H12N2O2, CID: 6305]; Isoleucine (Ile) [PubChem C6H13NO2, CID: 791]; Phenylalanine (Phe) [PubChem C9H11NO2, CID: 6925665]; Histidine (His) [PubChem C6H9NO3O2, CID: 6274]; Tyrosine (Tyr) [PubChem C9H11NO3, CID: 6057]; Cystine (Cys) [pubchem PubChem C6H12N2O4S2, CID: 67678]; Serine (Ser) [PubChem C3H7NO3, CID: 5951]; Glycine (Gly) [PubChem C2H5NO2, CID: 750]; Proline (Pro) [PubChem C5H9NO2, CID: 145742].

3.1. 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 Institutes of Health (NIH). Hence we can talk of PubChem Compound ID (CID) (PubChem, 2018).

Table 2. Amino acids composition of *Celosia argentea* [CR (raw), CC (protein concentrate), CW (waste)] and *Amarnthus hybridus* [AR (raw), AC(protein concentrate), AW (waste)] (g/100g, dry weight)

Amino acid	CR	CC	CW	AR	AC	AW	Mean	SD	CV%
Leu	6.62	6.69	6.47	5.71	6.24	5.24	6.16	0.573	9.31
Ile	2.72	3.74	3.55	2.55	3.64	2.35	3.09	0.618	20.0
His	2.70	2.75	2.50	2.32	2.38	2.21	2.48	0.215	8.65
Lys	5.21	5.37	4.95	4.26	4.81	3.28	4.65	0.772	16.6
Met	1.15	1.16	0.80	1.13	1.24	0.920	1.07	0.169	15.8
Thr	3.04	3.10	2.92	2.69	2.94	2.64	2.89	0.186	6.43
Phe	4.31	4.68	3.82	4.94	5.15	4.81	4.62	0.481	10.4
Trp	1.68	1.71	1.42	1.13	1.14	0.950	1.34	0.315	23.5
Val	4.11	4.27	3.71	3.79	4.57	3.29	3.96	0.454	11.5
Arg	6.26	6.34	5.70	4.98	5.58	4.28	5.52	0.786	14.2

Ala	1.48	3.15	1.28	3.32	3.74	2.77	2.62	1.01	38.7
Asp	7.65	8.07	7.28	6.64	7.04	6.13	7.14	0.696	9.75
Cys	1.68	1.18	1.11	0.530	0.671	0.420	0.932	0.478	51.3
Glu	13.3	14.0	12.2	14.9	14.4	14.2	13.8	0.956	6.91
Pro	5.52	2.64	2.34	3.36	3.48	2.87	3.37	1.14	33.8
Gly	4.59	4.98	3.99	3.59	4.40	3.39	4.16	0.610	14.7
Ser	3.19	3.41	2.80	3.20	4.48	2.70	3.30	0.638	19.3
Tyr	3.26	3.37	3.01	4.46	4.69	3.72	3.75	0.681	18.2
Total	79.5	80.6	69.9	73.5	80.6	66.2	75.1	6.14	8.18
Protein	22.7	28.8	21.0	21.8	24.2	20.2	23.1	3.11	13.5
Digestibility	86.8	84.2	82.9	88.1	85.6	83.4	85.2	2.03	2.39

3.2. Amino acid profiles

The concentration of the amino acids (dry weight) reported in g/100g crude protein (CP) for the six samples had been depicted in Table 2. The most concentrated amino acid in all the samples was Glu that ranged from 12.2 to 14.0 (CR to CW) and 14.2 to 14.9 (AR to AW) showing *Amaranths hybridus* to be more concentrated in Glu than in *Celosia argentea*; however, the values were still close since the variation [coefficient of variation (CV%] value was 6.91. This was followed by the second acidic amino acid (AAA), Asp with values of 7.28 to 8.07 (CR to CW) and 6.13 to 7.04 in AR to AW; however here, Asp in *C. argentea* > *A. hybridus* with slightly higher CV% of 9.75. The two most concentrated essential amino acids were Leu (6.47 to 6.69) (CR to CW), 5.24 to 6.24 (AR to AW) and Lys (4.95 to 5.37) (CR to CW), 3.28 to 4.81 (AR to AW) respectively. Whereas CV% was 9.31 (Leu) but 16.6 (Lys). Other amino acids of good concentrations (g/100g cp) in the samples were Ile, His, Thr, Phe, Val, Arg, Pro, Ser and Tyr whereas the following amino acids were relatively low: Met, Trp, Ala and Cys all across board. The least concentrated amino acid in *C. argentea* was Met (0.80 to 1.16) but Cys (0.420 to 0.671) was the least concentrated in *A. hybridus*. The highest variation of the amino acid values was in Cys (51.3%) but least variation occurred in Thr (6.43%). Most variations were below 50%. In *C. argentea,* the CC amino acids were higher than CR except in Cys (CR/CC = 1.68/1.18) and Pro (CR/CC=5.52/2.64); also all the CC values were greater than all CW values. CR values were greater than CW values except in Ile (CR/CW = 2.72/3.55). The observations in *A. hybridus* showed that AC had greater values of amino acids than in AR except in Glu (AR/AC = 14.9/14.4); also all the AC values were greater than all AW values. AR values were greater than all AW values. The summary of these observations was that the protein concentrate samples contained highest concentrated amino acids in their groups, that is, CC>CR> CW; and AC>AR>AW. The total amino acids (TAA) showed these trends (g/100g cp): CC (80.6) > CR (79.5) > CW (69.9) as also seen in AC (80.6) > AR (73.5) > AW (66.2). The protein followed similar trends (g/100g): CC (28.8) > CR (22.7) > CW (21.0); and AC (24.2)> AR (21.8), AW (20.2). The values of the crude protein versus the corresponding TAA showed that the true protein present in the crude protein exhibited predictable levels of true protein in each of the crude protein value of the samples. However, there was a reverse trend between raw and leaf protein concentrate in both *C. argentea* and *A. hybridus* as follows (%): CR (86.8)>CC (84.2)> CW (82.9); and AR (88.1) > AC (85.6) > AW (83.4). Inter-sample comparisons showed that trends varied between the samples in total amino acids, protein and digestibility. In TAA, CR (79.5)> AR (73.5), CC (80.6) ≡ AC (80.6) CW (69.9) > AW (66.2); in protein, CR (22.7)> AR (21.8), CC (28.8) >AC (24.2), CW (21.0) > AW (20.2); in digestibility, CR (86.8) < AR (88.1), CC (84.2) < AC (85.6), CW (82.9) < AW (83.4). The digestibility values variation was low at 2.39%.

3.2.1. Amino acid individual percentage levels

The percentage levels of the individual amino acids composition in the samples were shown in Table 3. In CR, percentage levels varied between 1.45% (Met) to 16.7% (Glu), this position was held in both CC and CW; in AR, percentage range was 0.721% (Cys) to 20.3% (Glu); in AC and AW, similar observation as in AR was depicted. No CV% was up to 50.0% (unlike the observation in Table 2). The CV% values ranged between 4.45(Val) to 48.2 (Cys). The intra-sample amino acid differences and their percentage differences were shown in Table 4. In CR-CC (%) values ranged as -0.02 (-0.54) to -1.67 (-113) for the negative differences and +2.60 (+3.00) to +2.88 (+52.2); all the negative differences (18 parameters) had CR<CC whereas all the positive differences (3 parameters) had CR>CC. In CR-CW (%) values it was observed that all CR>CW; and in CC-CWC %), all values were positive, that is, CC>CW in all parameters. In AR-AC (%), AR>AC (%) only in Glu, +0.50 (+3.36) and

+2.50(+2.84) in digestibility but AR<AC in all other amino acids; in AR-AW (%), AR>AW (%) in all parameters and in AC-AW (%), all values showed that AC>AW (%) in all parameters. The inter-sample differences (and percentage differences) of the amino acid parameters were shown in Table 5.

In CR-AR (%), CR>AR (%) in 15 parameters except the followings: Phe, -0.58 (-13.3%), Ala,-1.84(-124%), Glu,-1.60(-12.0%), Ser, -0.01(-31.3%), Tyr, -1.20 (-36.8) and digestibility, -1.30 (-1.50%). In CC-AC (%), CC>AC (%) in Leu, Ile, His, Lys, Met, Thr, Trp, Arg, Asp, Cys, Gly, TAAs and protein (this is 13/21 or 61.9%) whereas CC<AC (%) in 8 parameters or 8/21 (38.1%). In CW-AW (%), CW>AW (%) in 14 parameters (14/21 or 66.7%) but CW<AW (%) in seven parameters (7/21 or 33.3%).

3.2.2. Amino acid correlates

The inter-correlation of the amino acids composition within group (intra-samples) of C. argentea and A. hybridus was shown in Table 6. Determined were the correlation coefficient (rxy), variance, (rxy2) regression coefficient (Rxy), mean, standard deviation (SD), coefficient of variation (CV%), coefficient of alienation (C_A) and index of forecasting efficiency (IFE). The r_{xy} was subjected to statistical comparison to see if different significances occurred in the compared samples at $r_{xy\ =0.01}$ at n-2 degrees of freedom (df). The compared pairs were CR, CC, CW (for *C. argentea* intra-samples) and AR, AC, AW (for *A. hybridus* intra-samples). In CR/CC, CC/CW, CR/CW, AR/AC, AC/AW and AR/AW had their r_{xy} (samples) values greater than $r_{xy\ (Table)}$ at r_{xy} =0.01 and critical level of 0.590 and n-2(df). Since all $r_{xy(C)} >> r_{xy(T)}$, then the pair samples were significantly different between themselves. All the r_{xy} values were high and positive with values range of 0.9556 to 0.9883 in *C. argentea* (CR/CC, CC/CW, CR/CW) and 0.9854 to 0.9970 in *A. hybridus* (AR/AC, AC/AW, AR/AW) showing that r_{xy}(*C. argentea)* < r_{xy} (*A. hybridus)*. All the corresponding r_{xy}^2 values were high at range of 0.9152 to 0.9941. All the values of R_{xy} were each <1.0 but still regarded high as at ranges of 0.9007 to 0.9929 in the six samples. The R_{xy} would need further explanation. Taking the pair CR/CC, the explanation goes thus: CR= x and CC= y, hence we could have $CR_{(x)}/CC_{(y)}$. When x increases by 1.00g/100g cp of amino acid, y would increase by 0.9929. If this is taken as a ratio form it becomes $CR_{(xy)}(1)$: $CC_{(y)}$ (0.9929), measured in g/100g cp. This explanation goes for the other five sample pairs. Table 6 had two values for each sample pair as $mean_1$, SD_1, $CV\%_1$, and $mean_2$, SD_2, $CV\%_2$. In each of the samples, the first member from the left would have the values for $mean_1$, SD_1, $CV\%_1$, whereas the second member would have values of $mean_2$, SD_2, $CV\%_2$. Both the $mean_1/mean_2$ and SD_1/SD_2 were low across board as they ranged from 4.07 to 4.48/3.68 to 4.48 and 2.91 to 3.14/2.76 to 3.02 respectively. It is interesting to observe the mean values as shown: CR(4.36)>AR(4.07); 66.7 to 77.1 and $CV\%_2$ series had values of CC(4.48) ≡ AC(4.48); CW(3.88)>AW(3.68). The $CV\%_1$ series had values of 67.1 to 81.8.

Table 3. Percentage levels of the individual amino acids composition of *Celosia argentea* (CR,CC,CW) and *Amaranthus hybridus* (AR,AC,AW) based on the data in Table 1

Amino acid	CR	CC	CW	AR	AC	AW	Mean	SD	CV%
Leu	8.33	8.30	9.26	7.77	7.74	7.92	8.22	0.570	6.93
Ile	4.68	4.64	5.08	3.47	4.52	3.55	4.32	0.658	15.2
His	3.40	3.41	3.58	3.16	2.95	3.34	3.31	0.221	6.67
Lys	6.55	6.66	7.08	5.80	5.97	4.95	6.17	0.759	12.3
Met	1.45	1.44	1.14	1.54	1.54	1.39	1.42	0.148	10.4
Thr	3.82	3.85	4.18	3.66	3.65	3.99	3.86	0.203	5.25
Phe	5.48	5.81	5.46	6.72	6.39	7.27	6.19	0.731	11.8
Trp	2.11	2.12	2.03	1.54	1.41	1.44	1.78	0.346	19.5
Val	5.17	5.30	5.31	5.16	5.67	4.97	5.26	0.234	4.45
Arg	7.87	7.87	8.15	6.78	6.92	6.47	7.34	0.702	9.56
Ala	1.86	3.91	1.83	4.52	4.64	4.18	3.49	1.30	37.2
Asp	9.62	10.0	10.4	9.03	8.73	9.26	9.51	0.624	6.56
Cys	2.11	1.46	1.59	0.721	0.833	0.634	1.22	0.588	48.2
Glu	16.7	17.4	17.5	20.3	17.9	21.5	18.6	1.90	10.2
Pro	6.94	3.28	3.35	4.57	4.32	4.34	4.47	1.33	29.7
Gly	5.77	6.18	5.71	4.88	5.46	5.12	5.52	0.471	8.53

Ser	4.01	4.23	4.01	4.35	5.56	4.08	4.37	0.597	13.6
Tyr	4.10	4.18	4.31	6.07	5.82	5.62	5.02	0.912	18.2

Table 5. Intersample differences (and percentage differences) of amino acid composition of *C. argentea* and *A. hybridus*: [CR-AR,(%); CC-AC,(%); CW-AW(%)]

Amino acid	**CR-AR**	**(%)**	**CC-AC**	**(%)**	**CW-AW**	**(%)**
Leu	+0.91	+13.7	+0.45	+6.73	+1.23	+19.0
Ile	+1.17	+31.5	+0.10	+2.67	+1.20	+33.9
His	+0.38	+14.1	+0.37	+13.5	+0.29	+11.6
Lys	+0.95	+18.2	+0.56	+10.4	+1.67	+33.7
Met	+0.02	+1.74	+0.08	+6.90	-0.12	-15.0
Thr	+0.35	+11.5	+0.16	+5.16	+0.28	+9.59
Phe	-0.58	-13.3	-0.47	-10.0	-0.99	-25.9
Trp	+0.55	+32.7	+0.57	+33.3	+0.47	+33.1
Val	+0.32	+7.79	-0.30	-7.03	+0.42	+11.3
Arg	+1.28	+20.4	+0.76	+12.0	+1.42	+24.9
Ala	-1.84	- 124	-0.59	-18.7	-1.49	-116
Asp	+1.01	+13.2	+1.03	+12.8	+1.15	+15.8
Cys	+1.15	+68.5	+0.51	+43.1	+0.69	+62.2
Glu	-1.60	- 12.0	-0.40	-2.86	-2.00	-16.4
Pro	+2.16	+39.1	-0.84	-31.8	-0.53	-22.6
Gly	+1.00	+21.8	+0.58	+11.6	+0.60	+15.0
Ser	-0.01	-31.3	-1.07	-31.4	+0.10	+3.57
Tyr	- 1.20	-36.8	-1.32	-39.2	-0.71	-23.6
Total	+6.00	+7.55	+0.02	+0.02	+3.70	+5.29
Protein	+0.90	+3.96	+4.60	+16.0	+0.80	+3.81
Digestibility	-1.30	-1.50	-1.40	-1.66	-0.50	-0.60

Table 6. Inter correlation of the amino acids composition within group (intra samples) of *C. argentea* [CR/CC, CC/CW, CR/CW] and *A. hybridus* [AR/AC, AC/AW, AR/AW] from the data in Table 1

Statistics	**CR/CC**	**CC/CW**	**CR/CW**	**AR/AC**	**AC/AW**	**AR/AW**
r_{xy}	0.9566*	0.9883*	0.9649*	0.9914*	0.9854*	0.9970*
r_{xy}^2	0.9152	0.9767	0.9310	0.9828	0.9710	0.9941
R_{xy}	0.9929	0.9007	0.9127	0.9541	0.9829	0.9567
$Mean_1$	4.36	4.48	4.36	4.07	4.48	4.08
SD_1	2.91	3.02	2.91	3.14	3.02	3.14
$CV\%_1$	66.7	67.4	66.7	77.1	67.4	77.0
$Mean_2$	4.48	3.88	3.88	4.48	3.68	3.68
SD_2	3.02	2.76	2.76	3.02	3.01	3.01
$CV\%_2$	67.4	71.1	71.1	67.4	81.8	81.8
C_A	0.2912	0.1526	0.2627	0.1311	0.1703	0.0768
IFE	0.7088	0.8474	0.7373	0.8689	0.8297	0.9232

r_{xy}= correlation coefficient ; r_{xy}^2=variance; R_{xy}=regression co-efficient; SD=standard deviation; CV%=coefficient of variation; C_A= coefficient of alienation; IFE=index of forecasting efficiency; $mean_1$, SD_1, $CV\%_1$, represent values for first member; of a and $mean_2$, SD_2, $CV\%_2$ represent values for second pair member; *= values significant at $r_T = 0.01$ at n-2 = 18 – 2 = 16 (df) at 0.590

Table 7. Intercorrelation of the amino acids composition between sample groups of *C. argentea* and *A. hybridus* as CR/AR, CC/AC, and CW/AW from the data in Table 1

Statistics +	CR/AR	CC/AC	CW/AW
r_{xy}	0.9433*	0.9753*	0.9411*
r_{xy}^2	0.8899	0.9513	0.8857
R_{xy}	1.02	0.9738	1.03
$Mean_1$	4.36	4.48	3.88
SD_1	2.91	3.02	2.76
$CV\%_1$	66.7	67.4	71.1
$Mean_2$	4.08	4.48	3.68
SD_2	3.14	3.02	3.01
$CV\%_2$	77.0	67.4	81.8
C_A	0.3318	0.2207	0.3381
IFE	0.6682	0.7793	0.6619

+, *=See Table 6

The C_A values were all low at 0.0768 to 0.2912 with corresponding high values of IFE at 0.7088 to 0.9232. Both C_A and IFE work together in this type of statistical evaluation as C_A+IFE=1.00 (when fraction is used) or C_A+IFE=100% (when percentage is used). Since C_A+IFE=1.00, it goes to show that when C_A is high, IFE is low and vice versa.

On the other hand, whilst C_A is the error involved in the prediction of relationship between two compared similar entities, IFE is the reduction in the error of prediction of relationship between the compared similar entities. Hence, taking CR/CC as an example, the error of prediction would be 29.12% and its reduction would be 70.88%, therefore it would be easier to use CR to characterise CC. In all the samples, C_A<<IFE; and since C_A<<IFE in each pair, the functions of a member in a pair could be used to predict the functions (food properties) of the other member of the pair. Table 7 contained inter-correlation statistics of the amino acids composition between the inter-sample groups of *C, argentea* and *A. hybridus.* All the statistical parameters reported in Table 6 were repeated in Table 7 for CR/AR, CC/AC, CW/AW. All the r_{xy} values were positive, high and significantly different at 0.9411 to 0.9753; the r_{xy}^2 were also high at 0.8857 to 0.9513. R_{xy} values showed the following relationships: CR(x): AR(y) = 1.00:1.02, CC(x): AC(y) = 1.00:0.9738, CW(x): AW(y) = 1.00:1.03 meaning CR<AR, CC >AC, CW<AW. Both mean and SD values were low but CV% values were all high being above 50.0% in each case. The C_A values were low (0.2207 to 0.3381) but higher than as seen in Table 6 (0.0768 to 0.2912). Also the IFE was high at 0.6619 to 0.7793 but lower than the values in Table 6 (0.7088 to 0.9232).

All other discussions as they pertain to C_A and IFE would be the same as in Table 6.

3.2.3. Amino acid groups

In Table 8 were the amino acid groups divided into classes (*Nieman* et al*.,* 1992). The concentration trend of the classes followed as shown in g/100g cp: class I (17.0 to 22.8) > class IV (19.5 to 22.1) > class V (9.77 to 14.5) > class VI (10.8 to 13.4) > class II (5.34 to 6.51) > class VII (2.34 to 5.52) > class III (1.34 to 2.83). In Nigerian (Beef Jerky Meat) (Adeyeye et. al., 2020), it was as arranged in the vegetable samples; in *Neopetrolisthes maculatus* the trend changed between classes VII and III (Adeyeye, 2019) as well as in *N. maculatus* (Adeyeye, 2017). Further observation would show that most of the percentage values were close to their individual values with very slight differences: class I (17.0/25.8 to 22.8/28.3), class II (5.34/8.07 to 6.51/8.08), class III (1.34/2.03 to 2.83/3.56), class IV (19.5/27.9 to 22.1/27.4), class V (9.77/14.8 to 14.5/17.9), class VI (10.8/15.4 to 13.4/16.6) and class VII (2.34/3.35 to 5.52/6.94). Amino acids that constituted neutral amino acids were listed and values enumerated in Table 8; same was done for non-neutral amino acids. The values (with percentages) range were 35.1/53.1 to 45.2/56.1 (NAA) and 31.1/46.9 to 38.2/47.4 (N-NAA).

Table 4. Intra sample differences (and percentage differences) of amino acid composition of *C. argentea* [CR-CC, (%); CR-CW, (%); CC-CW, (%)] and *A. hybridus* [AR-AC, (%); AR-AW, (%); AC-AW, (%)]

Amino acid	CR-CC	(%)	CR -CW	(%)	CC-CW	(%)	AR- AC	(%)	AR-AW	(%)	AC-AW	(%)
Leu	-0.07	-1.07	+0.15	+2.27	+0.22	+3.23	-0.53	-9.28	+0.47	+8.23	+1.00	+16.0
Ile	-0.02	-0.54	+0.17	+4.57	+0.19	+5.08	-1.09	-42.7	+0.20	+7.84	+1.29	+35.4
His	-0.05	-1.85	+0.20	+7.41	+0.25	+9.09	-0.06	-2.59	+0.11	+4.74	+0.17	+7.14
Lys	-0.16	-3.07	+0.26	+4.99	+0.42	+7.82	-0.55	-12.9	+0.98	+23.0	+1.53	+31.8
Met	-0.01	-0.87	+0.35	+30.3	+0.36	+31.0	-0.11	-9.73	+0.21	+18.6	+0.32	+25.8
Thr	-0.06	-1.97	+0.12	+3.95	+0.18	+5.81	-0.25	-9.29	+0.05	+1.86	+0.30	+10.2
Phe	-0.32	-7.34	+0.54	+12.4	+0.86	+18.4	-0.21	-4.25	+0.13	+2.63	+0.34	+6.60
Trp	-0.03	-1.79	+0.26	+15.5	+0.29	+17.0	-0.01	-0.88	+0.18	+15.9	+0.19	+16.7
Val	-0.16	-3.89	+0.40	+9.73	+0.56	+13.1	-0.78	-20.6	+0.50	+13.2	+1.28	+28.0
Arg	-0.08	-1.26	+0.56	+8.95	+0.64	+10.1	-0.60	-12.0	+0.70	+14.1	+1.30	+23.3
Ala	-1.67	-113	+0.20	+13.5	+1.87	+59.4	-0.42	-12.7	+0.55	+16.6	+0.97	+25.9
Asp	-0.42	-5.49	+0.37	+4.84	+0.79	+9.79	-0.40	-6.02	+0.51	+7.68	+0.91	+12.9
Cys	+0.50	+29.8	+0.57	+33.9	+0.07	+5.93	-0.14	-26.6	+0.11	+20.8	+0.25	+37.4
Glu	-0.70	-5.26	+1.10	+8.27	+1.80	+12.9	+0.50	-3.36	+0.70	+4.70	+0.20	+1.39
Pro	+2.88	+52.2	+3.18	+57.6	+0.30	+11.4	-0.12	-3.57	+0.49	+14.6	+0.61	+17.5
Gly	-0.39	-8.50	+0.60	+13.1	+0.99	+19.9	-0.81	-22.6	+0.20	+5.57	+1.01	+22.9
Ser	-0.22	-6.90	+0.39	+12.2	+0.61	+17.9	-1.28	-40.0	+0.50	+15.6	+1.78	+39.7
Tyr	-0.11	-3.37	+0.25	+7.67	+0.36	+10.7	-0.23	-5.16	+0.74	+16.6	+0.97	+20.7
Total	-1.10	-1.38	+6.60	+8.63	+9.60	+12.1	-7.10	-9.65	+7.30	+9.93	+14.4	+17.9
Protein	-6.10	-26.9	+1.70	+7.49	+7.80	+27.1	-2.40	-11.0	+1.60	+7.34	+4.00	+16.5
Digestibility	+2.60	+3.00	+3.90	+4.49	+1.30	+1.54	+2.50	+2.84	+4.70	+5.33	2.20	+2.57

Table 8. Amino acid groups of the vegetable samples of *C. argentea* and *A. hybridus*

	Class	CR		CC		CW		AR		AC		AW	
		g/100g	%	g/100g	%	g/100g	%	g/100g	%	g/100g	%	g/100g	%
1.	[with aliphatic side chains and carbon) = Gly, Ala, Val, Leu, Ile]	20.5	25.8	22.8	28.3	19.0	27.2	19.0	25.8	22.6	28.0	17.0	25.8
2.	[with side chains containing hydroxylic (OH) groups = Ser, Thr]	6.23	7.83	6.51	8.08	5.72	8.19	5.89	8.01	7.42	9.21	5.34	8.07
3.	[with side chains containing sulphur atoms = Cys,Met]	2.83	3.56	2.34	2.90	1.91	2.73	1.66	2.26	1.91	3.37	1.34	2.03
4.	[with side chains containing acidic groups or their amides = Asp,Glu]	21.0	26.3	22.1	27.4	19.5	27.9	21.5	29.3	21.4	26.6	20.3	30.7
5.	[with side chains containing basic groups = Arg, Lys, His]	14.2	17.8	14.5	17.9	13.2	18.8	11.6	15.7	12.8	15.8	9.77	14.8
6.	[containing aromatic rings=His, Phe, Tyr, Trp]	12.0	15.1	12.5	15.5	10.8	15.4	12.9	17.5	13.4	16.6	11.7	17.7
7.	[imino acids = Pro]	5.52	6.94	2.64	3.28	2.34	3.35	3.36	4.57	3.48	4.32	2.87	4.34
	Neutral aa: Gly, Ala, Val, Ile, Leu, Tyr, Phe, Ser, Cys, Thr, Met, Pro	42.7	53.7	42.4	52.6	35.8	51.3	39.3	53.4	45.2	56.1	35.1	53.1
	Non-neutral aa: Asp, Glu, Lys, Arg, Trp, His	36.8	46.3	38.2	47.4	34.1	48.7	34.2	46.6	35.4	43.9	31.1	46.9

aa= amino acid

Table 9. Amino acid composition of *Celosia argentea* [CR (raw), CC(protein concentrate), CW(waste)] and *Amaranthus hybridus* [AR (raw), AC(protein concentrate), AW (waste] grouped into their quality parameters

Parameter	*Celosia argentea*			*Amaranthus hybridus*			Grand mean	Standard deviation (SD)	Coefficient of variation (CV%)
	CR	CC	CW	AR	AC	AW			
TAA	79.5	80.6	69.9	73.5	80.6	66.2	75.1	6.14	8.18
TNEAA	42.0	42.6	35.6	35.6	43.1	36.3	39.9	3.27	8.18
% TNEAA	52.8	52.8	51.0	54.4	53.5	54.9	53.2	1.38	2.60
TEAA (with His)	37.5	38.0	34.3	33.5	37.5	29.8	35.1	3.20	9.12
TEAA (with His)%	47.2	47.2	49.0	45.6	46.5	45.1	46.7	1.38	2.96
TEAA (no His)	34.8	35.3	31.8	31.2	35.1	27.6	32.6	3.03	9.29
% TEAA (no His)	43.8	43.8	45.5	42.4	43.5	41.7	43.5	1.31	3.02
EAA/NEAA	0 .894	0.893	0.963	0.838	0.869	0.821	0.880	0.050	5.71
% EAA/NEAA	1.12	1.11	1.14	1.14	1.08	1.24	1.14	0.055	4.79
TALAA	20.5	22.8	19.0	19.0	22.6	17.0	20.2	2.27	11.3
% TALAA	25.8	28.3	27.2	25.8	28.0	25.8	26.8	1.17	4.36
TEALAA	14.5	14.7	13.7	12.1	14.5	10.9	13.4	1.56	11.6
% TEALAA	18.2	18.2	18.7	16.4	17.9	16.4	17.6	0.989	5.61
THAA	6.23	6.51	5.72	5.89	7.42	5.34	6.19	0.728	11.8
% THAA	7.83	8.08	8.19	8.01	9.21	8.07	8.23	0.494	6.00

TSAA	2.83	2.34	1.91	1.66	1.91	1.34	2.00	0.524	26.2
% TSAA	3.56	2.90	2.73	2.26	2.37	2.03	2.64	0.550	20.8
% Cys in TSAA	59.4	50.4	58.1	31.9	35.1	31.3	44.4	13.1	29.6
TAAA	21.0	22.1	19.5	21.5	21.4	20.3	21.0	0.933	4.44
%TAAA	26.3	27.4	27.9	29.3	26.6	30.7	28.0	1.68	6.01
TBAA	14.2	14.5	13.2	11.6	12.8	9.77	12.7	1.76	13.9
% TBAA	17.8	17.9	18.8	15.7	15.8	14.8	16.8	1.58	9.38
TArAA	12.0	12.5	10.8	12.9	13.4	11.7	12.2	0.924	7.56
% TArAA	15.1	15.5	15.4	17.5	16.6	17.7	16.3	1.13	6.93
TEArAA	8.74	9.14	7.74	8.39	8.67	7.97	8.44	0.519	6.15
% TEArAA	11.0	11.3	11.1	11.4	10.8	12.0	11.3	0.418	3.70
TCAA	5.52	2.64	2.34	3.36	3.48	2.87	3.37	1.14	33.8
% TCAA	6.94	3.28	3.35	4.57	4.32	4.34	4.47	1.33	29.7
TNAA	42.7	42.4	35.8	39.3	45.2	35.1	40.1	4.05	10.1
% TNAA	53.7	52.6	51.3	53.4	56.1	53.1	53.4	1.58	2.96
TN-NAA	36.8	38.2	34.1	34.2	35.4	31.1	45.0	4.53	10.1
%TN-NAA	46.3	47.4	48.7	46.6	43.9	46.9	46.6	1.58	3.39
TN-AA/TNAA	0.861	0.903	0.951	0.872	0.781	0.884	0.875	0.056	6.40
% TN-NAA/TNAA	1.08	1.12	1.36	1.19	0.969	1.34	1.18	0.152	12.9

pI	4.67	4.70	4.09	4.20	4.67	3.72	4.34	0.403	9.29
Leu/Ile	1.78	1.79	1.82	2.24	1.71	2.23	1.93	0.240	12.4
Leu/Ile (diff.)	2.90	2.95	2.92	3.16	2.60	2.89	2.90	0.179	6.17
%(Leu-Ile/Leu)	43.8	44.1	45.1	55.3	41.7	55,2	47.5	6.08	12.8
P-PER$_1$	2.20	2.22	2.15	1.66	1.87	1.52	1.94	0.300	15.5
P-PER$_2$	2.08	2.24	2.16	1.76	2.00	1.57	1.97	0.255	13.0
P-PER $_3$	1.34	1.31	1.27	-0.519	-0.335	-0.374	0.870	0.487	56.0
EAAI$_1$(soybean stand.)	1.15	1.17	1.03	0.947	0.986	0.801	1.01	0.137	13.5
EAAI$_2$(egg stand.)	93.5	93.0	93.0	97.2	96.1	97.2	95.0	2.06	2.16
Lys/Trp(L/T)	3.10	3.14	3.49	3.77	4.22	3.45	3.53	0.419	11.9
Met/Trp(M/T)	0.685	0.678	0.563	1.00	1.09	0.968	0.831	0.215	25.9
Phe/Tyr	1.34	1.39	1.27	1.11	1.10	1.29	1.25	0.120	9.59
Met/Cys	0.685	0.983	0.721	2.13	1.85	2.19	1.43	0.707	49.5
BV	90.2	89.6	89.6	94.2	93.0	94.2	91.8	2.24	2.45

Table 10. Amino acid scores of *Celosia argentea* based on whole hen's egg amino acid and the corresponding digestibility – corrected amino acid score (PDCAAS)

Amino acid	C. *argentea* raw sample (CR)				C. *argetea* protein concentrate sample (CC)				*C. argetea* waste sample (CW)			
	Egg sc.	PDCAAS	Diff.	%diff.	Egg sc.	PDCAAS	Diff.	%diff.	Egg sc.	PDCAAS	Diff.	%diff.
Leu	0.80	0.69	0.11	13.8	0.81	0.68	0.13	16.0	0.78	0.65	0.13	16.7
Ile	0.66	0.58	0.08	12.1	0.67	0.56	0.11	16.4	0.63	0.53	0.10	15.9
His	1.13	0.98	0.15	13.3	1.15	0.97	*0.*18	15.7	1.04	0.86	0.18	17.3
Lys	0.84	0.73	0.11	13.1	0.87	0.73	0.14	16.1	0.80	0.66	0.14	17.5
Met	0.36	0.31	0.05	13.9	0.36	0.31	0.05	13.9	0.25	0.21	0.04	16.0
Thr	0.60	0.52	0.08	13.3	0.61	0.51	0.10	16.4	0.52	0.43	0.09	17.3
Phe	0.85	0.74	0.11	12.9	0.92	0.77	0.15	16.3	0.75	0.62	0.13	17.3
Trp	0.93	0.81	0.12	12.9	0.95	0.80	0.15	15.8	0.79	0.65	0.14	17.7
Val	0.55	0.48	0.07	12.7	0.57	0.48	0.09	15.8	0.49	0.41	0.08	16.3
Arg	1.03	0.89	0.14	13.6	1.04	0.88	0.16	15.4	0.93	0.77	0.16	17.2
Ala	0.27	0.24	0.03	11.1	0.58	0.49	0.09	15.5	0.24	0.20	0.04	16.7
Asp	0.72	0.62	0.10	13.9	0.75	0.64	0.11	14.7	0.68	0.56	0.12	17.6
Cys	0.93	0.81	0.12	12.9	0.66	0.55	0.11	16.7	0.62	0.51	0.11	17.7
Glu	1.11	0.96	0.15	13.5	1.17	0.99	0.18	15.4	1.02	0.85	0.17	16.7
Pro	1.45	1.26	0.19	13.1	0.69	0.59	0.10	14.5	0.62	0.51	0.11	17.7
Gly	1.53	1.33	0.20	13.1	1.66	1.40	0.26	15.7	1.33	1.10	0.23	17.3
Ser	0.40	0.35	0.05	12.5	0.43	0.36	0.07	16.3	0.35	0.29	0.06	17.1
Tyr	0.82	0.71	0.11	13.4	0.84	0.71	0.13	15.5	0.75	0.62	0.13	17.3
Total	0.80	0.70	0.10	12.5	0.81	0.68	0.13	16.0	0.70	0.58	0.12	17.1

Egg sc. = egg score; Diff. = difference

Table 11. Amino acid scores of *Amaranthus hybridus* based on whole hen's egg amino acid and the corresponding protein digestibility- corrected amino acid score (PDCAAS)

Amino acid	*A. hybridus* raw sample (AR)				*A. hybridus* protein concentrate sample (AC)				*A. hybridus* waste sample (AW)			
	Egg sc.	PDCAAS	Diff.	%diff.	Egg sc.	PDCAAS	Diff.	%diff.	Egg sc.	PDCAAS	Diff.	%diff.
Leu	0.69	0.60	0.09	13.0	0.75	0.64	0.11	14.7	0.63	0.53	0.10	15.9
Ile	0.46	0.40	0.06	13.0	0.65	0.56	0.09	13.8	0.42	0.35	0.07	16.7
His	0.97	0.85	0.12	12.4	0.99	0.85	0.14	14.1	0.92	0.77	0.15	16.3
Lys	0.69	0.61	0.08	11.6	0.78	0.66	0.12	15.4	0.53	0.44	0.09	17.0
Met	0.35	0.31	0.04	11.4	0.39	0.33	0.06	15.4	0.29	0.24	0.05	17.2
Thr	0.53	0.46	0.07	13.2	0.58	0.49	0.09	15.5	0.52	0.43	0.09	17.3
Phe	0.97	0.85	0.12	12.4	1.01	0.87	0.14	13.9	0.94	0.79	0.15	16.0
Trp	0.63	0.55	0.08	12.7	0.63	0.54	0.09	14.3	0.53	0.44	0.09	17.0
Val	0.51	0.45	0.06	11.8	0.61	0.52	0.09	14.8	0.44	0.37	0.07	15.9
Arg	0.82	0.72	0.10	12.2	0.91	0.78	0.13	14.3	0.70	0.59	0.11	15.7
Ala	0.61	0.54	0.07	11.5	0.69	0.59	0.10	14.5	0.51	0.43	0.08	15.7
Asp	0.62	0.55	0.07	11.3	0.66	0.56	0.10	15.2	0.57	0.48	0.09	15.8
Cys	0.29	0.26	0.03	10.3	0.37	0.32	0.05	13.5	0.23	0.19	0.04	17.4
Glu	1.24	1.09	0.15	12.1	1.20	1.03	0.17	14.2	1.18	0.98	0.20	16.9
Pro	0.88	0.78	0.10	11.4	0.92	0.78	0.14	15.2	0.76	0.63	0.13	17.1
Gly	1.20	1.06	0.14	11.7	1.47	1.26	0.21	14.3	1.13	0.94	0.19	16.8
Ser	0.41	0.36	0.05	12.2	0.57	0.49	0.08	14.0	0.34	0.29	0.05	14.7
Tyr	1.12	0.99	0.13	11.6	1.17	1.00	0.17	14.5	0.93	0.78	0.15	16.1
Total	0.74	0.65	0.09	12.2	0.81	0.69	0.12	14.8	0.66	0.55	0.11	16.7

Egg sc. = egg score; Diff. = difference

Table 12. Amino acid scores of *Celosia argentea* based on essential amino acid scoring pattern and the corresponding protein digestibility-corrected amino acid score (PDCAAS)

Amino acid	*C. argentea* raw sample (CR)				*C. argentea* protein concentrate sample (CC)				*C. argentea* waste sample (CW)			
	Sc. pat.	PDCAAS	Diff.	%diff	Sc. pat.	PDCAAS	Diff.	%diff.	Sc. pat.	PDCAAS	Diff.	%diff.
Lys	0.95	0.82	0.13	13.7	0.98	0.82	0.16	16.3	0.90	0.75	0.15	16.7
Thr	0.76	0.66	0.10	13.2	0.78	0.65	0.13	16.7	0.73	0.61	0.12	16.4
Met + Cys	0.81	0.70	0.11	13.6	0.67	0.56	0.11	16.4	0.55	0.45	0.01	18.2
Val	0.82	0.71	0.11	13.4	0.85	0.72	0.13	15.3	0.74	0.62	0.12	16.2
Ile	0.93	0.81	0.12	12.9	0.94	0.79	0.15	16.0	0.89	0.74	0.15	16.9
Leu	0.95	0.82	0.13	13.7	0.96	0.81	0.15	15.6	0.92	0.77	0.15	16.3
Phe + Tyr	1.27	1.10	0.17	13.4	1.34	1.13	0.21	15.7	1.14	0.95	0.19	16.7
Trp	1.68	1.46	0.22	13.1	1.71	1.44	0.27	15.8	1.42	1.18	0.24	16.9
Total	0.97	0.84	0.13	13.4	0.98	0.83	0.15	15.3	0.88	0.73	0.15	17.0

Sc. pat.= scoring pattern

Table 13. Amino acid scores of *Amaranthus hybridus* based on essential amino acid scoring pattern and the corresponding protein digestibility-corrected amino acid score (PDCAAS)

Amino acid	*A. hybridus* raw sample (AR)				*A. hybridus* protein concentrate sample (AC)				*A. hybridus* waste sample (AW)			
	Sc. pat.	PDCAAS	Diff.	%diff.	Sc. pat.	PDCAAS	Diff.	%diff.	Sc. pat.	PDCAAS	Diff.	%diff.
Lys	0.77	0.68	0.09	11.7	0.87	0.75	0.12	13.8	0.60	0.50	0.10	16.7
Thr	0.67	0.59	0.08	11.9	0.74	0.63	0.11	14.9	0.66	0.55	0.11	16.7
Met +Cys	0.47	0.42	0.05	10.6	0.55	0.47	0.08	14.5	0.38	0.32	0.06	15.8
Val	0.76	0.67	0.09	11.8	0.91	0.78	0.13	14.3	0.66	0.55	0.11	16.7
Ile	0.64	0.56	0.08	12.5	0.91	0.78	0.13	14.3	0.59	0.49	0.10	16.9
Leu	0.82	0.72	0.10	12.2	0.89	0.76	0.13	14.6	0.75	0.63	0.12	16.0
Phe +Tyr	1.57	1.38	0.19	12.1	1.64	1.40	0.24	14.6	1.42	1.18	0.24	16.9
Trp	1.13	1.00	0.13	11.5	1.14	0.98	0.16	14.0	0.95	0.79	0.16	16.8
Total	0.83	0.76	0.07	8.43	0.97	0.83	0.14	14.4	0.77	0.64	0.13	16.9

Sc. pat. = scoring pattern

Table 14. Essential amino scores of *Celosia argentea* based on requirements of pre-school child (2-5 years) standards and the corresponding protein digestibility-corrected amino acid score (PDCAAS)

Amino acid	*C. argentea* raw sample (CR)				*C. argentea* protein concentrate sample(CC)				*C. argentea* waste sample (CW)			
	Pre-schl req.	PDCAAS	Diff.	%diff	Pre-schl req.	PDCAAS	Diff.	%diff.	Pre-schl req.	PDCAAS	Diff.	%diff.
Lys	0.90	0.78	0.12	13.3	0.93	0.78	0.15	16.1	0.85	0.71	0.14	16.5
Thr	0.89	0.78	0.11	12.4	0.91	0.77	0.14	15.4	0.86	0.71	0.15	17.4
Met+Cys	1.13	0.98	0.15	13.3	0.94	0.79	0.15	16.0	0.76	0.63	0.13	17.1
Val	1.17	1.02	0.15	12.8	1.22	1.03	0.19	15.6	1.06	0.88	0.18	17.0
Ile	1.33	1.15	0.18	13.5	1.34	1.13	0.21	15.7	1.27	1.05	0.22	17.3
Leu	1.00	0.87	0.13	13.0	1.01	0.85	0.16	15.8	0.98	0.81	0.17	17.3
Phe +Tyr	1.13	0.98	0.15	13.3	1.28	1.08	0.20	15.6	1.08	0.90	0.18	16.7
Trp	1.53	1.33	0.20	13.1	1.55	1.31	0.24	15.5	1.29	1.07	0.22	17.1
His	1.42	1.23	0.19	13.4	1.45	1.22	0.23	15.9	1.32	1.09	0.23	17.4
Total	1.11	0.96	0.15	13.5	1.12	0.94	0.18	16.1	1.01	0.84	0.17	16.8

Pre-schl req. = school child requirement

Table 15. Essential amino acid scores of *Amaranthus hybridus* based on requirement of pre-school child (2-5 years) standards and the corresponding protein digestibility – corrected amino acid score (PDCAAS)

Amino acid	*A. hybridus* raw sample (AR)				*A. hybridus* protein concentrate sample(AC)				*A. hybridus* waste sample (AW)			
	Pre-schl req.	PDCAAS	Diff.	%diff.	Pre-schl req.	PDCAAS	Diff.	%diff.	Pre-schl req.	PDCAAS	Diff.	%diff.
Lys	0.73	0.65	0.08	11.0	0.83	0.71	0.12	14.5	0.57	0.47	0.10	17.5
Thr	0.79	0.70	0.09	11.4	0.86	0.74	0.12	14.0	0.78	0.65	0.13	16.7
Met+Cys	0.66	0.59	0.07	10.6	0.76	0.65	0.11	14.5	0.54	0.45	0.09	16.7
Val	1.08	0.95	0.13	12.0	1.31	1.12	0.19	14.5	0.94	0.78	0.16	17.0
Ile	0.91	0.80	0.11	12.1	1.30	1.11	0.19	14.6	0.84	0.70	0.14	16.7
Leu	0.87	0.76	0.11	12.6	0.95	0.81	0.14	14.7	0.79	0.66	0.13	16.5
Phe+Tyr	1.49	1.31	0.18	12.1	1.56	1.34	0.22	14.1	1.35	1.13	0.22	16.3
Trp	1.03	0.91	0.12	11.7	1.04	0.89	0.15	14.4	0.86	0.72	0.14	16.3
His	1.22	1.07	0.15	12.3	1.25	1.07	0.18	14.4	1.16	0.97	0.19	16.4
Total	0.99	0.87	0.12	12.1	1.11	0.95	0.16	14.4	0.88	0.73	0.15	17.0

Pre-Schl req.= Pre-school child requirement

Table 16. Estimates of amino acid requirements at ages 10 – 12 years (mg/kg/day)

Sample	Ile	Leu	Lys	Met + Cys	Phe+Tyr	Thr	Trp	Val	Total
CR	844	1503	1183	642	1730	690	381	933	7906
CC	1077	1927	1547	674	2318	893	492	1230	10158
CW	746	1359	1040	401	1434	613	298	779	6670
AR	556	1245	929	362	2049	586	246	826	6799
AC	881	1510	1164	462	2381	711	276	1106	8216
AW	475	1058	663	271	1723	533	192	665	5579

Celosia argentea (CR = raw, CC = protein concentrate, CW = waste); *Amaranthus hybridus* (AR = raw, AC = protein concentrate, AW = waste

3.2.4. Amino acid quality parameters

Table 9 contained the amino acids as grouped into their quality parameters. The total amino acids (TAAs) ranged between (g/100gcp): 69.9 to 80.6 *(C. argentea)* and 66.2 to 80.6 *(A. hybridus)*. LPC in Adeyeye and Omolayo (2007) reported for *A. hyridus* and *Telfairia occidentalis* had respective values of 678.1mg/g and 455.3mg/g (both are lower than the present report). Total essential amino acid with histidine ranged from 29.8 to 38.0g/100g cp (45.1 to 49.0%) and no His, 27.6 to 35.3 g/100gcp (41.7 to 45.5%). In the LPC of *A. hybridus,* TEAA (with His) was 393.5 mg/g (or 58.0%) and no His, 360.3mg/g (or 53.1%) whilst TEAA with His in *T. occidentalis* was 256.1mg/g (or 56.3%) and no His, 244.9 (or 53.8%). Whereas LPC results under discussion had lower TEAA percentages of the TAA (CC=47.2/43.8, AC= 46.5/43.5), the literature values showed greater percentages of the TEAA for both samples. The total neutral amino acid (TNAA) had ranges of 35.8 to 42.7g/100g cp (*C. argentea*) and 35.1 to 45.2g/100gcp (*A. hybridus)*. LPC in *C. argentea* was 42.4g/100cp (52.6%) and in *A. hybridus* was 45.2 g/100gcp (56.1%); from literature: in *A. hybridus*, it was 441.8 (65.2%) and 264.4 (58.1%) in *T. occidentialis* (Adeyeye and Omolayo, 2007). Total acid amino acid (TAAA) ranged from 19.5 to 22.1g/100gcp (26.3 to 30.7%) whose LPC values were 22.1/27.4% (*C.argentea)* and 21.4/26.6% (*A. hybridus)* higher than 104.4 (15.4%) in *A. hybridus* and 94.9 (20.8%) in *T. occidentalis* in literature.

The TAAA values might be a reflection of the calculated isoelectric points (*PI*) of the samples. *PI* range was 3.72 to 4.70: for the LPC, they were 4.70 (*C. Argentea*) and 4.67 (*A. hybridus*). The samples TAAA were close at 22.1g/100g (27.4%) (*C. argentea*) and 21.4g/100g (26.6%) (*A.* hybridus) with the following further explanation: sample/AAA/percentage/*PI.C.argentea*/22.1g/100g cp/27.4%/4.70 and *A. hybridus* /21.4g/100gcp/26.6%/4.67 showing that the higher the AAA, the higher the *PI*. In the literature *A. hybridus* the *PI* was 4.2 with a lower TAAA% (15.4) while *PI* was 2.8 in *I. Occidentalis* with a higher TAA% (20.8); this contrasted the results under current discussion meaning that this relationship needs further evaluation. However the relationship might better be appreciated by limiting the relationship between *PI*/TAAA to **PI** TAAA concentration rather than *PI*/TAAA(%); in the current report, both TAAA/% TAAA in *C. argentea* (LPC) were higher than TAAA/% TAAA in *A. hybridus* but in the literature cited, TAAA in *A. hybridus* was higher but lower percentage whereas in *T. occidentalis,* TAAA was lower but percentage was higher. Calculated *PI* is useful to determine the pH of minimum solubility in the preparation of protein isolates of biological materials. For the % TEAA, recommendations were: 39% adequate for ideal protein food for infants; 26% adequate for children; 11% adequate for adults. TEAA is 50% in egg (FOA/WHO, 1990). Current results were all very good on this basis: %TEAA with His = 47.2 to 49.0 (*C. argentea)*, 45.1 to 46.5 (*A. hybridus)*. The TEAA for pre-school children (2.5y) is 33.9g/100g (with His) or 32.8g/100g cp (without His). All samples would satisfy this condition except AW which was marginally below this standard: 29.8 (with His) and 27.6 (no His). The amino acid requirement for infant is 460mg/g (with His) (FAO, 1970; DHSS, 1977). In the samples under discussion [with Arg (a marginal EAA for children)], the value of 460mg/g are favourably comparable with the present results ((mg/gcp); literature value/present result: 460/427.4 (CR), 460/443.6 (CC), 460/399.6 (CW); 460/384.9 (AR), 460/430.51 (AC) and 460/341.1 (AW).

The total sulphur amino acid (TSAA) of C. *argentea* ranged from 1.91 to 2.83g/100gcp and from 1.34 to 1.91g/100g cp in *A. hybridus.* Their LPC values were (g/100g cp): 2.34 (*C. argentea)* and 1.91 (*A. hyridus)*. However, CR (2.83) > CC (2.34) but AR (1.66) < AC (1.91). The %TSAA ranged between 2.03 to 3.56 (which were low) for the six samples; CV% were low at 26.2 (TSAA) and 20.8 (%TSAA). In the LPC of *A. hybridus* (literature), TSAA was 46.7mg/gcp and in *T. occidentalis* it was 16.4mg/gcp (Adeyeye and Omolayo, 2007. Both the present report and literature report had TSAA lower than 58mg/g cp recommended for infants (FAO/WHO/UNU, 1985). The % Cys in TSAA values were 50.4 – 59.4 in *C. argentea;* LPC being 50.4%. These values followed literature values in % Cys/TSAA in plants; see these literature examples: 62.9% in coconut meat (Adeyeye, 2004), its range was 58.9 to 72.0 in guinea corn (*Sorghum bicolor*) (Adeyeye, 2008), it is 50.5% in cashew nut (Adeyeye et at., 2007), in raw wheat (*Triticum durum*) %Cys/TSAA was 52.6 (raw wheat) and 51.4 in germinated wheat (Adeyeye, 2011). *Anacardium occidentale* has a value of 50.51% (Adeyeye et al., 2007). The %Cys/TSAA in *A. hybridus* had values of 31.3 to 35.1 which are close to typical values in most none conventional animal proteins like: 25.59% in *Zonocerus variegatus* (Adeyeye, 2005a), 36.3% in *Macrotermes bellicosus* (Adeyeye, 2005b), 35.3% in Archachatina marginata (Adeyeye and Afolabi, 2004), 38.8% in Archatina archatina (Adeyeye and Afolabi, 2004). The FAO/WHO/UNU (1985) did not give any indication of the proportion of TSAA which can be met by Cys in man; for the rat, chick and pig, the proportion is about 50% (FAO/WHO, 1991). Information on the agronomic advantages of increasing the Concentration of sulphur – containing amino acids in staple foods shows that Cys has positive effects on mineral

absorption, particularly Zn (Mendoza, 2002). Cysteine and cystine are two non-essential amino acids. They are interchangeable in the body: cystine is composed of two molecules of cysteine. Both are made from the EAA methionine in the body but are also present in food proteins. They are required, like other amino acids, for synthesis of new protein needed for growth and repair. Cystine and cysteine in the diet reduce the needs for Met, and since almost all the sulphur in the diet is derived from these three amino acids the sulphur content is sometimes used as an approximate assessment of the adequacy of a protein (Bingham, 1977). Cysteine is an additive used in new bread making process. The literature values of the %Cys/TSAA in *A. hybridus* (27.0) and *T. occidentale* (39.1) Adeyeye and Omolayo, 2007) were close to the values of 31.3 to 35.1 observed in the present *A. hybridus values. %*Cys/TSAA > 50.00 stands Cys in good chance in carrying out its functions effectively.

The TArAA range for infant protein is 68 to 118mg/g cp. TArAA are precursors of epinephrine (adrenaline) and thyroxine (the iodine-containing hormone secreted by the thyroid) gland (Robinson, 1987). The TArAA values in the samples were highly comparable to the standard TArAA in infants. Results were (g/100g), standard/result: 68 to 118m/g/12.0g/100g (CR)/12.5gl100g (CC)/ 10.8g/100g (CW)/12.9g/100g (AR)/13.4g/100g (AC)/11.7g/100g (AW). These sample results would make these samples to be good sources of ArAA and might also be qualified as a supplement to foods of lower ArAA values. Even the TEArAA (g/100g cp) were all within the range of the standard infant protein with results of 7.74 to 9.14g/100g. The TArAA of the LPCs of *A. hybridus* and *T. occidentale* were 61.2mg/g cp and 44.3mg/g cp respectively (Adeyeye and Omolayo, 2007) which were lower than the present report.

The Leu/Ile ratios were 1.71 to 2.24; being lower in CR to CW (1.78 to 1.82) than in AR to AW (1.71 to 2.24). The % (Leu-Ile/Leu) ranged from 41.7 to 55.3 showing that Leu > Ile. Leu/Ile imbalance from excess Leu might be a factor in the development of pellagra particularly in maize eaters (FAO, 1995). Clinical, biochemical and pathological observations in experiments conducted in humans and laboratory animals showed that high Leu in the diet impairs the metabolism of Trp and niacin and is responsible for niacin deficiency in sorghum eaters (FAO, 1995). High Leu is also a factor contributing to the pellagragenic properties of maize (Belavady and Gopalan, 1969). Dietary excess of Leu could be counteracted by increasing the intake of niacin or Trp or by supplementation with Ile (FAO, 1995). From literature, the most ideal Leu/Ile is 2.36 (FAO/WHO, 1991) The Leu/Ile ratios of 1.71 to 2.24 were all lower than 2.36, hence we might not experience concentration antagonism in the sample when consumed as food source. Experiments in dogs have shown that animals fed sorghum proteins with < 11g/100g cp Leu did not suffer from nicotinic acid deficiency (Belavady and Rao, 1979). The present values of Leu ranged between 5.24 to 6.69 g/100g cp which are much less than 11g/100g cp and therefore considered safe and could be beneficially exploited to prevent pellagra in endemic areas (Deosthale, 1995).

The predicted protein efficiency ratio (P-PER) was calculated in three forms P-PER 1,2 and 3 in all the samples. The predicted protein efficiency ratio is defined as the gain in weight per gram of ingested protein. The (PER) values obtained vary between 0.00 for a very poor protein to a maximum possible of just over 4 (Muller and Tobin, 1980). The *in-vivo* P-PER is of the order of 2.2 (Muller and Tobin, 1980). The values as calculated in the samples were (for Soybean comparison: $P\text{-}PER_1$ = 2.15 to 2.22 (CR to CW) and 1.52 to 1.87 (AR to AW); $P\text{-}PER_2$ = 2.08 to 2.24 (CR to CW) and 1.57 to 2.00 (AR to AW); $P\text{-}PER_3$ = 1.27 to 1.34 (CR to CW) and – 0.335 to – 0.591(AR to AW). In all the 3 P-PERs, *C. argentea* was consistently higher than *A. hybridus* on comparative basis. The P-PER 1 and 2 values in *C. argentea* were highly comparable to the *in-vivo* value (2.2). The $P\text{-}PER_1$ values in millet (*ogi*) is 1.62 and 0.27 in sorghum (*ogi*) (Oyarekua and Eleyinmi, 2004); this means the *C. argentea* results will be good complements of the *ogi* samples. According to Friedman's (1996) classification, the PER is poor (<1.5 to 2.0) and superior (>2.0). On this classification, P- PERs 1,2 were in the group of superior category in *C .argentea* whereas its' $P\text{-}PER_3$ was in the poor category; P-PER 1 and 2 were in moderate group category in *A. albidus* whereas it's $P\text{-}PER_3$ was in the poor group category. The P-PER 1,2,3 where 2.70, 2.62 and 2.56 in kilishi (Adeyeye et al*;* 2020) which were all comparable to P-PER l and 2 in *C . argentea.* In *Callinectes latimanus* (a lagoon crab), $P\text{-}PER_1$ was 1.21 and $P\text{-}PER_2$ was 1.39 (Adeyeye et al*;* 2014). The present P-PER values (particularly in *C. argentea*) indicated that it might be a more physiologically utilized protein source. In general, it has been discovered that the better the protein, the lower the level in the diet that is required to produce the highest protein efficiency ratio. This emphasizes a clear reflection of the importance of the proper nutritive balance of all amino acids to produce optimum metabolic efficiency.

The essential amino acid index (EAAI) calculated were recorded in two different forms of EAAI1 and $EAAI_2$. In the $EAAI_1$, the values were 1.03 to 1.17 (in *C. argentea*) and 0.801 to 0.989 (in *A. hybridus*). The $EAAI_1$ under this mode has soybean as its standard for comparison. The value of EAAI in defatted soybean flour is 1.26 (Schweigert and Payne,

1956) which is higher than the present sample; that for whole hen's egg on this comparison is 1.55. For the $EAAI_2$, values is from whole hen's egg standard. In $EAAI_2$, the comparison is from whole hen's egg standard. In $EAAI_2$ values of the samples were 93.0 to 93.5 (CR to CW) and 96.1 to 97.2 (AR to AW) which were all high values; their corresponding biological values (BV) were: 89.6 to 90.2 (in *C. argentea*) and 93.0 to 94.2 (in *A. hybridus*) depicting the quality of the vegetable samples. From animal comparisons, we have some protein values of EAAI and BV which are as follows (Oser, 1959): milk, cow (whole, nonfat, evaporated or dry), EAAI (88) and BV(84, predicted ; 90, observed); human, EAAI (87) and BV(83); eggs, chicken (whole, raw or dried) EAAI (100), BV(97, predicted; 96, observed); whites (raw or dried), EAAI(95), BV(92, predicted; 93, observed); yolks (raw or dried, EAAI (93), BV(89, predicted); shellfish (shrimp, including prawns, raw or canned), EAAI(67), BV(61, predicted); also 86.9 to 89.9 (EAAI) and 83.0 to 86.3 (BV) in meat of *N.maculatus* (Adeyeye, 2017) and 88.7 to 89.2 (EAAI) and 85.0 to 85.5 (BV) in innards of *N. maculatus* (Adeyeye, 2019). In kilishi, EAAI was 94.5 and BV was 91.3 (Adeyeye et al; 2020). In literature leafy vegetables (Oser, 1959) we have : Brussels sprouts (*Brassica oleracea* var. *gemmifera*), EAAI is 64 and BV(58); Cabbage (*Brassica oleracea* var. *capitata*), EAAI is 56 and BV(49); Kale (*Brassica oleracea* var. *acepahala*), EAAI is 61 and BV(54); Spinach (*Spinacia oleracea*), EAAI is 82 and BV(77) these and Trrnip greens (*Brassica rapa*), EAAI is 76 and BV(71). This literature result show the quality position of *C . argentea* and *A . hybridus* protein EAAI is useful as a rapid tool in the evolution of food formulation for protein quality.

Table 9 also contained the Lys/Trp (L/T), Met/Trp (M/T) and Phe/Tyr ratio of the samples. According to Albanese (1959), in infant's protein requirements, a growth pattern of amino acid requirement was obtained by assigning values of unity to the Trp need. Similar calculation of the amino acid content of mammalian tissue showed that there exists good agreement of growth needs and tissue amino acid patterns. This agreement is said to be good for the L/T and M/T ratios of muscle protein which constitute approximately 75% of the infant body protein. The present result had L/T levels of 3.10 to 4.22 and M/T levels of 0.563 to1.09. In the innards of *N. maculatus,* L/T was 3.00 to 5.01 (highly comparable to the present samples) and *N. maculatus* meat as 3.31 to 4.27 (also close); in M/T values, innards ranged from 1.78 to 3.50 and meat, 1.97 to 2.64 (Adeyeye, 2017; 2019), both being better than the present samples.

Mammalian tissue patterns have the following values; L/T: muscle (6.3), viscera (5.3), plasma proteins (6.2). M/T: muscle (2.5), viscera (2.0), plasma proteins (1.1)(Mitchell, 1959). Available evidence indicates that the utilization of dietary proteins increases as their Lys and Trp approaches that of muscle tissue. In the present study, the *C. argentea* L/T range was 3.10 to 3.49 meaning they are less than the muscle standard of 6.3 L/T by 50.8 down to 44.6%; in viscera, values were less than 5.3 by 41.5 down to 34.2%; in plasma, values were less than 6.2 by 50.0 down to 43.7%. *A . hybridus* range was 3.45 to 4.22 meaning they would be less than the muscle standard of 6.3 L/T by 45.2 down to 33.0%; in viscera, values were less than 5.3 by 34.9 down to 20.4%; in plasma, values were less than 6.2 by 44.4 down to 31.9%. Also the M/T values of the present work was 0.563 to 0.685 (*C . argentea*) and 0.968 to 1.09 (*A . hybridus*) which were much lower than the muscle standard M/T value of 2.5, viscera of 2.0 and close to 1.1 plasma proteins (particularly in *A. hybridus*). The L/T and M/T values were lower than the earlier observations for *N. maculatus* innards and meat (Adeyeye, 2017; 2019) and in kilishi (Adeyeye et al; 2020). The mean minimum Phe requirement estimate in the presence of an excess of Tyr is 9.1mg/kg/day. Hence, Tyr can spare 78% of the dietary Phe need. Also the optimal proportion of dietary Phe and Tyr has been shown to be 60:40 respectively (Pencharz et al; 2007). The Phe/Tyr ratios were close to the Phe standard whereas the Tyr values were higher than the standard shown as follows: CR=Phe/Tyr, 1.34 (56.9: 43.1); CC=Phe/Tyr, 1.39(58.1: 41.9); CW=Phe/Tyr, 1.27(55.9: 44.1); AR=Phe/Tyr, 1.11 (55.2: 49.8); AC= Phe/Tyr, 1.10(52.3: 47.7); and AW=Phe/Tyr, 1.29(56.4: 43.6). The Phe/Tyr values in these results were strictly low as shown in Table 9 which did not meet exactly the optimal proportion of dietary Phe/Tyr of 60:40 respectively. To rectify this slight imbalance, food low in Tyr would complement these vegetables to lower the Tyr values and enhance higher the Phe levels.

Lysine, an essential amino acid (EAA) has a reference egg protein of 63mg/g cp. Most of the present results are closer with values of 4.95 to 5.37 g/100g cp (*C . argentea*) and 3.28 to 4.81g/100g cp (*A . hybridus*). Arginine and histidine are good for children and they were high in the samples: Arg(g/100gcp) [5.70 to 6.34 (*C . argentea*) and 4.28 to 5.58 (*A . hybridus*)]; His(g/100cp [2.50 to 2.75(*C . argentea*) and 2.21 to 2.38 (*A . hybridus*)]; all are good for food fortification/ food complementation. Harper (1984) had listed His as being essential for children (perhaps for adults) and also Arg (perhaps for children). Total EAA for egg reference is 566mg/gcp; present results were above average and highly comparable to animal protein sources: in *C. argentea*, TEAA range was 34.3 to 38.0 and 29.8 to 37.5g/100gcp in *A. hybridus*. These values are highly comparable to these animal values: TEAA=300.2 to 317.4

mg/gcp in fin fishes (Adeyeye and Afolabi, 2004); in pink shrimp, range is 361.3 to 419.6mg/gcp (Adeyeye and Adubairo, 2004); in female crab, range is 349.8 to 387.3mg/gcp and male crab, range is 298.2 to 356.6mg/gcp (Adeyeye, 2002).

3.2.5. Amino acid scores

Table 10 depicted the amino acid scores of *C. argentea* based on whole hen's egg amino acid and the corresponding protein disgestibility-corrected amino acid score (PDCAAS), their differences and percentage differences. Egg comparison scores> 1.00 were observed for His(1.13), Arg (1.03), Glu(1.11), Pro (1.45) and Gly (1.53) *in C. argentea* (CR), although all the PDCAAS values were less than 1.00. The percentage differences ranged between 11.1 to 13.9 being Ala and Metc, respectively. The lowest amino acid score or limiting amino acid (LAAS) was Ala: 0.27 (egg score) and 0.24 (PDCASS). Amino acid scores>1.00 in CR were similar (except Pro) in CC, although with higher scores. LAAS was Met: 0.36 (egg) and 0.31(PDCAAS). Percentage differences range was 13.9 to 16.7. Amino acid scores >1.00 in CW were His(1.04), Glu(1.02) and Gly(1.33) whereas the percentage change range was 15.9 to 17.7. LAAS was 0.24 (egg) and 0.20 (PDCASS) in Ala. Egg correcting scores so that all the amino acids would be available for physiological usage go thus: Ala: 0.27/0.24= 3.70/4.17×protein content in C. *argentea* (CR); Met:0.36/0.31 2.78/3.23×protein content in C. *argentea* (CC); Ala :0.24/0.20=4.17/5.0×protein content in *C. argentea* (CW). The calculations reported in Table 10 were repeated in Table 11 replacing *C . argentea* with *A . hybridus*. In AR, only Glu, Gly and Tyr had egg scores >1.00; Cys was limiting at 0.29/0.26 and correction was Cys: 0.29/0.26=3.45/3.85×protein content. In AC, scores >1.00 were Phe, Glu,Gly and Tyr; Cys was limiting at 0.37/0.32 and correction was Cys: 0.37/0.32 = 2.70/3.13 x protein content. In AW, scores > 1.00 were in Glu and Gly; Cys was limiting at 0.23/0.19 and correction was Cys: 0.23/0.19=4.35/5.26×protein content. In AW, scores>1.00 was limiting at 0.23/0.19 and correction was Cys:0.23/0.19=4.35/5.26×protein content. Summary, we have LAAS as follows: CR(Ala), CC(Met), CW(Ala), AR(Cys), AC(Cys), AW(Cys).

In Table 12 amino acid scores of *C. argentea* based on EAA scoring pattern and the corresponding PDCAAS and percentage difference had been depicted. For *C. argentea* samples: in CR, both Phe+Tyr and Trp had their scores > 1.00 for both scoring pattern and PDCASS, Thr at 0.76/0.66 was the LAAS and the correction was Thr: 0.76/0.66=1.32/1.52×protein content ; in CC, scores > 1.00 were similar to observation in CR, Met/Cys at 0.67/0.56 was the LAAS and the correction would be Met+Cys: 0.67/0.56=1.49/1.79×protein contents; in CW, again Phe+Tyr and Trp had scores > 1.00, Met+Cys at 0.55/0.45 was the LAAS and the correction was Met+Cys: 0.55/0.45 = 1.82/2.22×protein content . Similar exercise in Table 12 was repeated in Table 13 for *A. hybridus*. In AR, scores of the Phe+Tyr and Trp were >1.00. LAAS was 0.47/0.42 in Met+Cys and corrected as, Met+Cys: 0.47/0.42= 2.13/2.38×protein content; in AC, similar amino acids with scores > 1.00 were as observed in Table 12, LAAS was Met+Cys at 0.55/0.47, therefore correction was Met+Cys: 0.55/0.47=1.82/2.13×protein content; and in AW, only Phe+Tyr had score> 1.00, again Met+Cys was limiting at 0.38/0.32 with correction of Met+Cys: 0.38/0.32=2.63/3.13×protein content. In summary we have LAAS as follows: CR(Thr), CC(Met+Cys), CW(Met+Cys), AR(Met+Cys), AC(Met+Cys), AW(Met+Cys).

Essential amino acid scores of *C. argentea* based on the requirement of pre-school child (2-5years) standards corresponding PDCAAS, differences and percentage differences were shown in Table 14. In CR, only Lys and Thr had score less than 1.00 and Thr was limiting at 0.89/0.78; correction was 0.89/0.78=1.12/1.28×protein content. In CC, only three amino acids had scores < 1.00, they were Lys, Thr, Met+Cys. Limiting AA was Thr with a score of 0.91/0.77, corrected as follows: 0.91/0.77=1.10/1.30×protein content. In CW, Lys, Thr, Met+Cys, and Leu were having scores < 1.00; Met+Cys was limiting at 0.76/0.63 and correction was; Met+Cys: 0.76/0.63=1.32/1.59×protein content. In Table 15, the exercise in Table 14 was repeated for *A. hybridus*. In AR, Val, Phe+Tyr, Trp and His had scores >1.00. LAA was Met+Cys at value of 0.66/0.59; then correction Met+Cys: 0.66/0.59=1.52/1.69×protein content. In AC, amino acid scores < 1.00 were in Lys, Thr, Met+Cys and Leu; Met+Cys was limiting at 0.76/0.65 correcting at Met+Cys: 0.76/0.65= 1.32/1.54 ×protein content. In AW, only Phe+Tyr and His had scores > 1.00. Again Met+Cys was limiting at a score of 0.54/0.45 and correcting as, Met+Cys: 0.54/0.45=1.85/2.22×protein content. Summary of LAAS from Tables 14 and 15, we have: CR(Thr), CC(Thr), CW(Met+Cys), AR(Met+Cys), AC (Mat+Cys), AW(Mat+Cys). LAAS from Tables 10 and 11; 12 and 13; 14 and 15 can now be put together to be observed at a glance: in Tables 10+11, we have CR=CW=Ala, CC=AR=AC=AW=Cys; in Tables 12+13, we have CR=Thr, CC=CW=AR=AC=AW=Met+Cys; in Tables 14+15, we have CR=CC=Thr, CW=AR=AC=AW=Met+Cys. EAA most often acting in a limiting capacity are (a) Lys; (b) Met+Cys; (c) Thr and (d) Trp (Bingham, 1977).

Looking at Tables 12+13 and 14+15, it meant that it is the second and third LAA that occurred in the two samples.

3.2.6. Amino acid requirements at ages 10-12 years

In Table 16, we have estimates of amino acid requirements at ages 10 to 12 years in mg/kg/day at the body weight of 30kg. Among the four principal of LAAs of Lys (first), Met+Lys (second), Thr(third) and Trp(fourth), their standard respective estimates are (mg/kg/day); Lys(1800), Met+Cys(810), Thr (1050), Trp(120). Lys values were lower than the standard in all the samples of 663 to 1547; in Met+Cys values less than the standard were all samples (271 to 674), in Thr, all values were less than the standard at 533 to 893 but all values were greater than Trp standard having values of 192 to 492 mg/kg/day. The total calculated standard essential amino acids requirements for 10-12years school boys is 7830 mg/kg/day at the age of 30years. From the present samples under discussion, only three samples will meet this total requirements with the LPC taking a pride of place. These are: CC (10158) > AC (8216) > CR (7906). Total comparison among the samples goes thus: CC > AC > CR > AR > CW > AW showing the quality concentration gradient of the samples.

Table 17. Summary of the amino acid profiles into Factors A and B means

Parameter	**Sample (Factor A)**				**Factor B means**
Amino acid composition	CR	CC	CW	AR	
		AC	AW		
Total essential amino acid	37.5	3.80	34.3	33.5	35.1
Total non-essential amino acid		37.5	29.8		39.2
	42.0	4.26	35.6	35.6	
		43.1	36.3		
Factor A means	39.8	40.3	35.0	34.6	37.2
		40.3	33.1		

Table 18. The leaf protein concentrates of *Celosia argentea, Amaranthus hybridus*, *Solanum aethiopicum* and *Solanum macrocarpon* compared

Amino acid	***Celosia argentea***	***Amaranthus hybridus***	***Solanum aethiopicum***	***Solanum macrocarpon***
Leu	6.69	6.24	6.96	7.56
Ile	3.74	3.64	4.67	5.83
His	2.75	2.38	3.11	2.86
Lys	5.37	4.81	6.64	5.70
Met	1.16	1.24	1.71	1.39
Thr	3.10	2.94	4.16	4.32
Phe	4.68	5.15	5.35	6.30
Trp	1.71	1.14	a	a
Val	4.27	4.57	4.67	3.72
Arg	6.34	5.58	5.08	6.64
Ala	3.15	3.74	4.47	5.58
Asp	8.07	7.04	8.54	13.3
Cys	1.18	0.671	1.89	1.35
Glu	14.0	14.4	15.0	14.0
Pro	2.64	3.48	6.27	6.49
Gly	4.98	4.40	3.86	4.32
Ser	3.41	4.48	3.64	4.62
Tyr	3.37	4.69	4.62	6.30

[a] = Not available

3.2.7. Amino acid profiles into Factors A and B means

The summary of the amino acid profiles into Factors A and B means was shown in Table17. Factor A means constituted amino acids value of the six samples along the vertical axis, whilst Factor B means constituted the amino acid values along the horizontal axis as shown in the Table17.

Both Factors contained the values for both essential and non-essential amino acids. Column under Factor B means showed values at a close range of 35.1 to 39.2g/100gcp. On the whole, the mean of Factor A means and Factor B means gave a value of 37.2g/100gcp.

3.2.8. Amino acid functions

Various amino acids have different types of functions in the human body. Phe is a precursor of neurotransmitters which help in the production of other amino acids and their functioning. Val assists in muscle stimulation to grow, regeneration and it produces energy. Thr is a principal component of some structural proteins such as collagen and elastin which are present in skin and connective tissues, helps in fat metabolism and immune function. Trp is a precursor to serotonin, a neurotransmitter that helps in appetite, sleep and mood regulation. Met plays an important role in metabolism, detoxification, helps in tissue growth and in the absorption of minerals such as Zn and Se needed by the body. Leu helps in regulating blood sugar levels, enhances wound healing and stimulates growth hormones. Ile helps in muscle metabolism, immune function, haemoglobin production and energy regulation. Branched-chain amino acids are Val, Leu and Ile. Lysine is involved in protein synthesis, calcium absorption, immune function, energy production, hormone production and in collagen production. His, a neurotransmitter helps in maintaining the protective barrier called myelin sheath that surrounds the nerve cells, helps in digestion, immune response, sleep-wake cycles and sexual functions (Walther et al., 2008).

4.Conclusions

This work had reported the amino acid composition of three forms of two common Nigerian vegetables; they were *Celosia argentea* and *Amaranthus hybridus* on dry weight basis. The experimental sample forms were: *Celosia argentea*: raw, leaf protein concentrate (LPC) and 'waste' denoted as CR, CC and CW respectively. In *Aramanthus hybridus*, we have: raw, leaf protein concentrates and 'waste' denoted as AR, AC and AW respectively. For most concentrated amino acids (AAs), observations were: Glu, *A. hybridus* > *C. argentea;* Asp, *C. argentea* > *A. hybridus* (similar to Leu and Lys). Least concentrated AA was Met in *C. argentea* but it was Cys in *A.hybridus.* Most varied AA was Cys whereas Thr was the least varied. Trend in concentration was: CC (except Cys) > CR (except Ile) > CW although CR > CC in Pro; and A C (except Glu) > AR > AW showing in both samples that LPC was highest in all the samples, that is, CC > CR > CW; AC > AR > AW as seen in both TAAs and protein content. There was a reverse trend in digestibility: CR>CC>CW; AR>AC>AW. Individual AA percent variation were Met to Glu (*C. argentea)* and in *A. hybridus,* Cys to Glu. Leu range in sample was 5.24 to 6.69 < 11g/100g cp, it made the samples safe and beneficially exploitable to prevent pellagra in endemic areas. TArAA was 10.8 to 13.4g/100g cp > 68 to 118mg/g cp qualifying the samples as supplements to foods of lower ArAA with best concentration from CC = 12.5g/100gcp and AC = 13.4g/100g cp. In %Cys/TSAA, values of 50.4 to 59.4 in *C. argentea* followed trends in plant AAs; this ratio may make it in Cys functionality than *A. hybridus* where %Cys/TSAA range was 31.3 to 35.1 which followed literature values in animal proteins. P-PER 1,2,3, in all *C. argentea* was consistently higher than *A. hybridus.* P-PER 1 and 2 were in super class in *C. argentea* but in moderate class in *A. hybridus* whereas P-PER 3 was in poor class in both samples. *C. argentea* might likely be more physiologically utilized as protein source. Phe/Tyr of 1.10 to 1.39 had highly comparable percentage ratio of 52.3: 47.7 to 58.1: 41.9, optimal proportion being 60:40. EAAI (egg standard): 93.0 to 93.5 (CR to CW), 96.1 to 97.2 (AR-AW) and corresponding BV values being 89.6 to 90.2 (CR-CW), 93.0 to 94.2 (AR to AW) all values being better than vegetables and also in many animal proteins. In AA scores, Tables 10 + 11: egg/PDCAAS were observed as follows CR (Ala), CC (Met), CW (Ala), AR = AC= AW= Cys. In Tables 12 + 13, (provisional EAA/PDCAAS) we observed: CR (Thr), CC = CW = AR= AC=AW= Met + Cys. In Tables 14 + 15, (pre-school EAA requirement/PDCAAS) we observed: CR=CC=Thr,CW=AR=AC=AW= Met + Cys. TEAA requirements for 10 + 12y at 30kg school boys is 7830mg/kg/day; present results within this standard were (mg/kg/day): CC (10158), AC (8216), CR (7906). Therefore, total comparisons would go thus: CC > AC > CR> AR>CW=AW showing quality concentration gradient of the samples. 'Waste' in these samples was the fibrous residue. From this work the fibrous residue had good levels of quality AAs, hence instead of its being thrown away as 'waste' or used as animal feed, it could be made into powder and be sprinkled into cooked rice, beans or soup for human consumption. Leaf protein concentrate took a pride of place in many parameters considered and constantly competed with the raw samples AAs. In the samples, % TEAA of 11 to 39 (for all ages) would be satisfied by all the samples. The two null hypotheses were rejected. The statistical analysis showed that significant differences

existed between: (i) The intra-sample amino acids as CR/CC, CC/CW, CR/CW and AR/AC, AC/AW, AR/AW; (ii) significant differences also existed in the inter-sample AAs as CR/AR,CC/AC, CW/AW at $r_{xy=0.01}$ and n-2 (df). All C_A << IFE in all sample pairs and since this is the case, it meant that any member of a pair could be used to predict the relationship in the functionality of its pair and vice versa at very low error of prediction. Since this is a cross sectional report, it has contributed to information in the Food Composition Table on vegetables on raw, LPC and fibrous residue. For comparisons, Table 18 contained the LPC of CC, AC and the LPC of *Solanum aethiopicum* and *Solanum macrocarpon* (Taylor, 1983).

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Conflict of interest

The authors declare no conflict of interest.