REVIEW ARTICLE

Amino acids distribution in economical important plants: a review

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Abstract Amino acids (AAs) are abundantly found in the food plants and their individual concentration is of enormous importance in terms of nutrition. Therefore it is mandatory to explore the food plants for their nutritional importance. This review gives the overview of AA composition in different food plants. However, in most of the studies the complete AA concentration of food plants has not been reported. The data of 142 economical important plant species were collected from Google Scholar, Scopus and Google. Because the techniques applied by various authors, the units of content, and the conditions of analysis were different, in this review paper, for the purpose of statistical analysis the concentrations of AAs were changed into comparative units on Lys content basis, which is the utmost limiting, most variable species specific essential AAs in plants. The average concentration of relative AAs is: Leu > Asp > Glu > Ala > Glu > Arg > Gly > Ile > Ser > Pro > Lys > Thr > Val > His > Phe > Tyr > Cys > Met > Trp. The average relative content of non-essential AAs was recorded maximum, whereas relative content of aromatic AAs was low. The data was statistically analyzed by Pearson's correlation, cluster analysis (CA), heatmap analysis, principal component analysis (PCA) and non-metric multidimensional scaling (NMDS). Among the analyzed plant species, plants of Pentadipandraceae family recorded maximum total relative AAs content, while minimum total relative AAs content was found in Periplocaceae family.

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Introduction

AAs are the building blocks of proteins and are classified into essential and non-essential AAs based on their synthesis in the humans. The essential amino acids (EAAs) are synthesized only by plants, while non-essential AAs are synthesized by both plants and humans. The EAAs required to be taken from outside sources in animal or plant food forms. Animal food has high nutrition as compared to the plant food, but the environmental footprint of plant food manufacture is distant less in comparison with the production of animal food. Environmental foot printing ascertains the extent of resources on the earth that is needed for humans. The increasing growth in human population throughout the globe requires more food for better nutrition (Auestad & Fulgoni, 2015; Burch et al., 2007; Millward, Layman, Tomé, & Schaafsma, 2008; Tessari, Lante, & Mosca, 2016). According to Food and Agriculture Organization (FAO) approximately 15% population expecting scarcity of food, which inspired the food industry throughout the world to biofortification (Zhu et al., 2007; FAO, 2013).

Food plants such as Quinoa and Kaniwa are rich in proteins. The significance of proteins is established on their value with a balanced essential AAs concentration (Repo-Carrasco, Espinoza, & Jacobsen, 2003). Seeds of *Adenopus brevijorus* are rich sources of AAs and signify it's prospective for future food supplements and preparation of baby foods (Oshodi, 1996). *Cicer arietinum* is an essential crop throughout the world because of its nutritive value. The dietary fibre rich foods lower the glycemic index of diabetic peoples, help in prevention of cancer and cardiovascular diseases (de Almeida Costa, da Silva Queiroz-Monici, Reis, & de Oliveira, 2006; Hangen & Bennink, 2002; Lee et al., 2004; Viswanathan et al., 1989).

Pulses such as peas, lentils and beans have been used almost 10,000 years and are widely used as food throughout the world. These are rich sources of proteins and fibres, as well as of vitamins and minerals, i.e., Fe, Zn, Mg, etc. The pulses usage in the diet is a healthy approach to meet the dietary recommendations, and is linked with decreased risk of various chronic disorders (Mudryj, Yu, & Aukema, 2014). Legumes are the important staple foods and their seeds contain high content of carbohydrates, proteins and EAAs, whereas the sulphur containing AAs are the limiting ones. In countries where the consumption of legumes is more, the chances of colorectal cancer are lower (Sánchez-Chino, Jiménez-Martínez, Dávila-Ortiz, Álvarez-González, & Madrigal-Bujaidar, 2015). The quantity of legume seeds in the daily diet is reduced because of the use of meat and highly processed products. Their disproportion in the diet has a negative effect on the health of the humans. The year 2016 was considered as the International Year of Pulses (IYP) by the UNO to encourage the use of legumes in human nutrition. Leguminous plants contain numerous species, and their seeds vary in their chemical composition and nutritional values (Grela & Günter, 1995; United Nations, 2014). Seeds of legume plant are essential constituents of diet and these are used as health improving foodstuffs, especially for the control of obesity and management of diabetes (Grela et al., 2017). The commonly used legumes throughout the world are beans, chickpeas, lentil, peas, broad beans, soybeans,
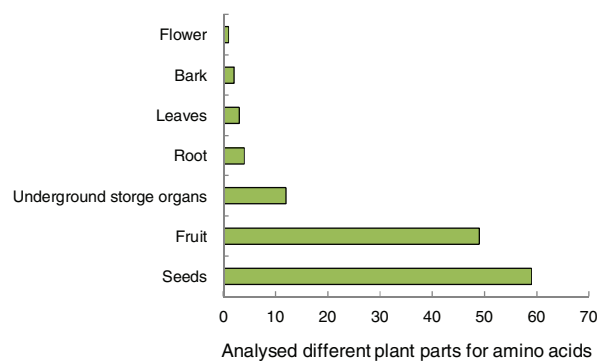
Figure 1 Different plant parts analyzed for amino acids content. The contents of amino acids were reported as mean values of AAs with respect to the lysine content.

peanuts, etc. (Guillon & Champ, 2002). Soybean is the important leguminous crops and its seed are the main source of food both for the humans and the livestock. The soya proteins are a rich source of AAs as these complement the nutritional value of that of the cereals. However, soybeans lack methionine although enough lysine is present to conquer the methionine deficiency (Lajolo & Genovese, 2002; Sharma, Kaur, Goyal, & Gill, 2014). Chickpea contains high protein and its addition to the foodstuffs will enhance the nutritive value that can decrease the acrylamide content. Acrylamide is an anti-nutritional substance existed in some junk foods, such as snacks, chips and bread etc. Chickpea flour and proteins are the alternatives to decrease the acrylamide contents in such type of products (Rachwa-Rosiak, Nebesny, & Budryn, 2015).

The review paper describes the AAs composition in the food plants, spices and pulses. The AA contents of food plants, spices and pulses are statistically analyzed by using various multivariate techniques, i.e., Pearson's correlation matrix, heatmap analysis, CA, PCA and NMDS. The overview of methods and techniques applied for AAs analysis was also presented in this paper.

Collection of data

In the present paper, data of food plants were collected and analyzed for various statistical analysis like Pearson's correlation analysis using PAST software v. 3.21, CA employing Minitab software v. 14, PCA using SPSS software v. 16, heatmap analysis using R-programming software v. 3.5.3 and NMDS scaling using PAST software v. 3.21. The data of 142 economical important plant species were collected from Google Scholar, Scopus and Google by searching the keyword ''amino acids in food plants'' and amino acids in economical plant species''. Because the techniques applied by various authors, the units of content, and the conditions of analysis were different, in the present review paper, for the purpose of statistical analysis the concentrations of amino acids were changed into relative units with respect to the contents of lysine which is the most limiting, most variable species specific essential amino acid in plants.

Fig. 1 showed the different parts of plant analyzed for AAs content. Among the reviewed literature for the present study, it was found that seed is the most analyzed part for
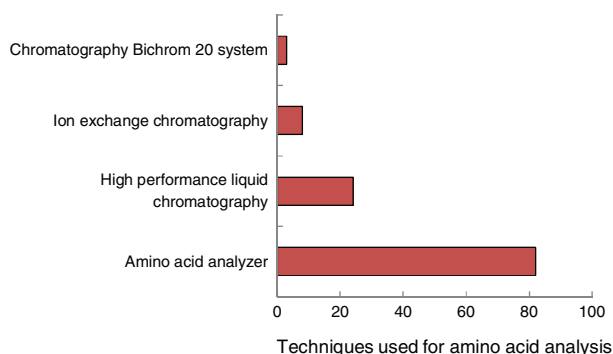
Figure 2 Techniques applied for amino acid analysis.
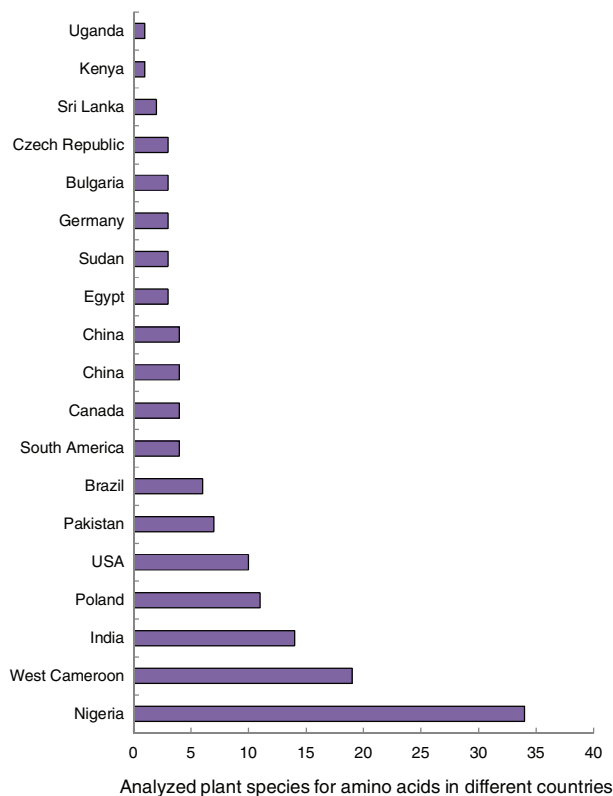
Figure 3 Analyzed plant species for amino acid in different countries.

AA composition (Abii & Amarachi, 2007; Bressani, Brenes, García, & Elías, 1987; Megias, Cortes-Giraldo, Giron-Calle, Vioque, & Alaiz, 2014; Oluwaniyi & Bazambo, 2016). Fruit is the second most abundant part analyzed for AA composition (Abdou Bouba et al., 2016; Ananthan, Subhash, & Longvah, 2016) followed by underground storage organs (Aremu, Nweze, & Alade, 2011; Ogbuewu et al., 2014; Oyarekua, 2009). Fig. 2 depicts the techniques used for the analysis of AAs. AA analyzer is the mostly used technique for the AA analysis (Ajayi, Akomolafe, & Akinyemi, 2013; Ananthan et al., 2016; Santos, Silveira, Martin-Didonet, & Brondani, 2013). The second most used technique for AA analysis is high performance liquid chromatography (Megias et al., 2014; Wright, Pike, Fairbanks, & Huber, 2002). Fig. 3 showed the analyzed plant parts in different countries for AA composition. Among the analyzed data for the current review, it was found that maximum plant species were analyzed for AAs in Nigeria followed by West Cameroon and India. Poland and USA are the fourth and fifth countries where maximum plants were analyzed for AA contents.

Results and discussion

Descriptive analysis of amino acids

The relative contents of different AAs analyzed by different researchers are presented in supplementary table (S1). Table 1 presents the structures, mean and S.E. of relative contents of AAs. The mean values of AAs with respect to the lysine content showed the trend, i.e., Leu > Asp > Glu > Ala > Glu > Arg > Gly > Ile > Ser > Pro > Lys > Thr > Val > His > Phe > Tyr > Cys > Met > Trp. The average leucine content was found to be maximum among all the analyzed AAs, whereas tryptophan content was found to be lowest with respect to the relative content of lysine. Since different authors used different techniques of analyses, and presented the data in different units, the AA contents were normalized with respect to lysine. Lysine is an essential AA and is the most limiting amino acid in Plants. The species from grass family generally contain very low amounts of lysine in legumes. It is also the most variable AA among the plants. For the purpose of data analysis, AA contents analyzed are presented as relative AA contents. Table 2 shows the average values of different categories of AA. The trend obtained is: non-essential AAs > EAAs > acidic AAs > basic AAs > aromatic AAs. The total relative AAs content was found maximum in Pentadipandraceae followed by Rutaceae, Asteraceae, Zingiberanceae and Cyperaceae families (Fig. 4).

Correlation analysis of amino acids

Pearson's correlation analysis showed associations among different AAs and is shown in the Fig. 5. The proline shows positive correlation with alanine, aspartic acid and glycine, and all these amino acids are non-polar. Positive correlations of arginine were found with glutamic acid, methionine, phenylalanine and valine. The aspartic acid showed correlation with glutamine, glycine, histidine, isoleucine, proline and serine. The correlation of aspartic acid and glutamine may be due to their acidic nature. The correlation of cysteine was found with methionine, phenylalanine, tyrosine and valine. Their correlation is attributed due to their non-polar nature. The correlation of cysteine and methionine may also be attributed because both are sulfur containing amino acids. Glutamine showed correlation with histidine, isoleucine and serine. The correlation of glutamine and serine attributed to their polar nature. Glycine, isoleucine and proline are non-polar in nature and are highly correlated with each other. The non-polar nature of methionine, phenylalanine and tyrosine may be associated with their high correlation. Both phenylalanine and tyrosine are aromatic and are highly correlated with each other.

Table 1   Mean, standard error and structures of different amino acids.
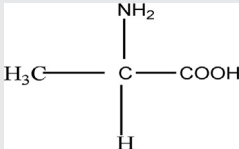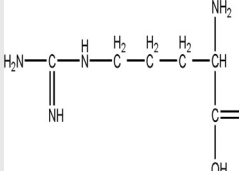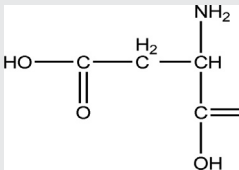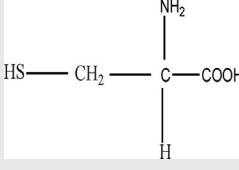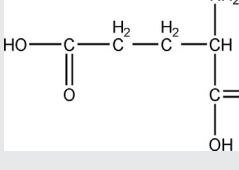
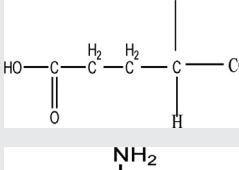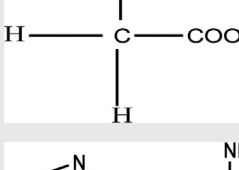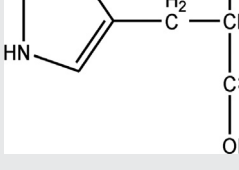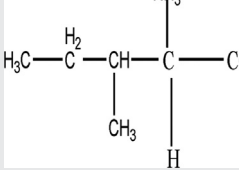| Name of amino acids	Abbreviation	Symbol	Structure	Mean of relative amino acid $\pm$ S.E
Alanine	Ala	A		2.09 $\pm$ 0.90
Arginine	Arg	R		1.66 $\pm$ 0.24
Aspartic acid	Asp	D		2.74 $\pm$ 0.45
Cysteine	Cys	C		0.41 $\pm$ 0.26
Glutamic acid	Glu	E		2.57 $\pm$ 0.62
Glutamine	Gln	Q		1.78 $\pm$ 0.70
Glycine	Gly	G		1.62 $\pm$ 0.33
Histidine	His	H		0.92 $\pm$ 0.32
Isoleucine	Ile	I		1.45 $\pm$ 0.44

Table 1 (*Continued*)
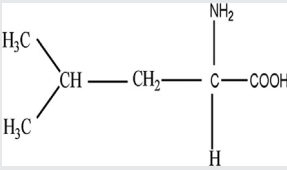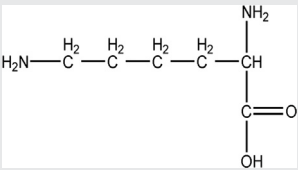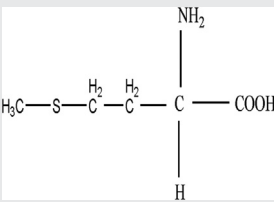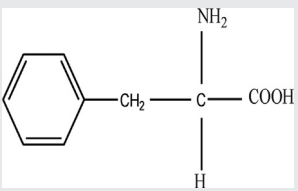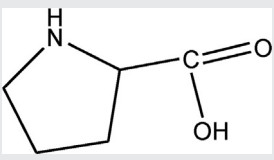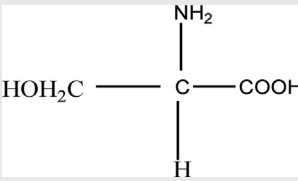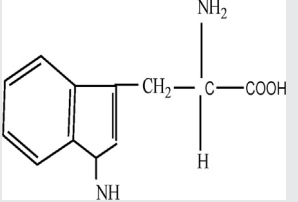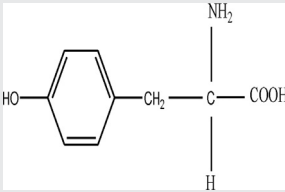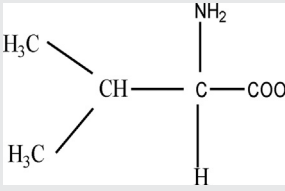
Name of amino acids	Abbreviation	Symbol	Structure	Mean of relative amino acid $\pm$ S.E
Leucine	Leu	L		3.33 $\pm$ 1.84
Lysine	Lys	K		1.00 $\pm$ 0.0
Methionine	Met	M		0.29 $\pm$ 0.05
Phenylalanine	Phe	F		0.65 $\pm$ 0.10
Proline	Pro	P		1.03 $\pm$ 0.13
Serine	Ser	S		1.42 $\pm$ 0.42
Threonine	Thr	T		0.95 $\pm$ 0.24
Tryptophan	Trp	W		0.17 $\pm$ 0.05

Table 1 (*Continued*)

Name of amino acids	Abbreviation	Symbol	Structure	Mean of relative amino acid $\pm$ S.E
Tyrosine	Tyr	Y		0.45 ± 0.09
Valine	Val	V		0.93 ± 0.11

Table 2 Mean of different categories of amino acids with respect to lysine content.

Types of amino acids	Mean of relative amino acid $\pm$ S.E
Essential amino acids	9.60 ± 0.33
Non-essential amino acids	14.12 ± 0.25
Acidic amino acids	6.74 ± 0.31
Basic amino acids	1.19 ± 0.18
Aromatic amino acids	1.02 ± 0.14

Multivariate statistical analysis of amino acids

CA was applied to different families on the basis of the relative contents of different AAs (Fig. 6) using Euclidean distance and Ward's method (Kumar et al., 2017; Kumar, Sharma, Bakshi, Bhardwaj, & Thukral, 2018). On the basis of the relati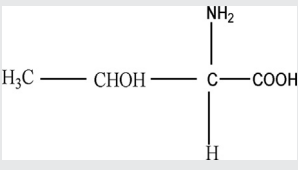ve contents of AAs, Asteraceae and Zingiberaceae families showed close proximities with each other. The Cyperaceae, Combretaceae and Moraceae families showed close association with each other on the basis of relative contents of AAs. The Fabaceae and Moringaceae, Apiaceae and Chenopodiaceae, Amaranthaceae and Annonaceae, Solanaceae and Piperaceae, Amaryllidaceae and Cucurbitaceae, and Fabaceae and Poaceae families showed close proximities with each other on the basis of relative content of AAs. Miyagi et al. (2010) while working on amino acids content in polygonaceous plants applied cluster analysis and heatmap analysis for the classification of amino acids. They concluded that grouping of amino acids are attributed to species differences. Heatmap analysis is the graphic representation of dataset found in 2-D matrix, representing each value as colour (Sun & Li, 2013). The similar colour of the amino acids or families represents same abundance or concentration of specific amino acid. Moreover, it presents grouping of all the studied amino acids by the use of cluster analysis and also presents impression of amino acids with greater concentration more directly (Tian, Gou, Niu, Sun, & Guo, 2018). Heatmap was also applied to the relative content of different AAs and
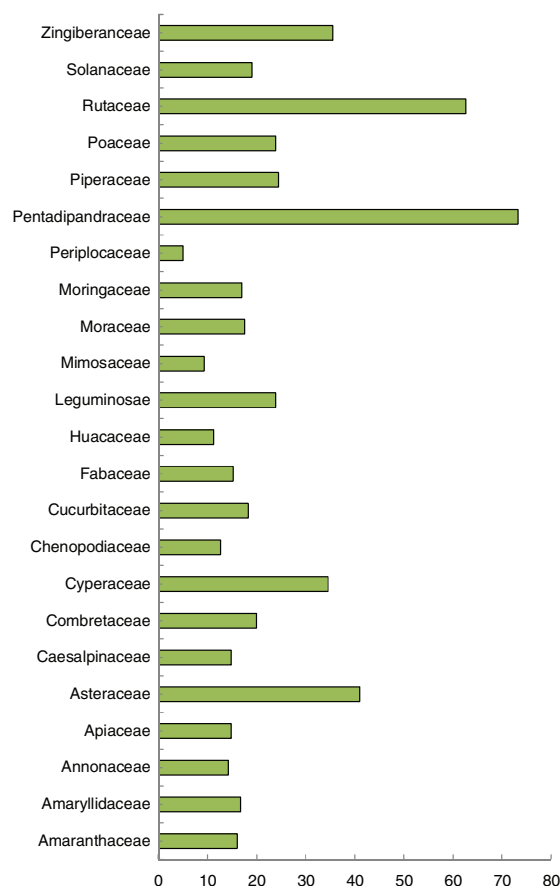
Figure 4 Total relative amino acids content in different families. The contents obtained in each family were reported as as mean values of AAs with respect to the lysine content.

families using R-programming software (Fig. 7). Glutamine and aspartic acid both are acidic amide and are included in the same group. Glycine, histidine, isoleucine and serine are included in the same group. Isoleucine and glycine both are non-polar AAs. Proline, alanine, valine and phenylalanine are non-polar AAs and are included in the same group.
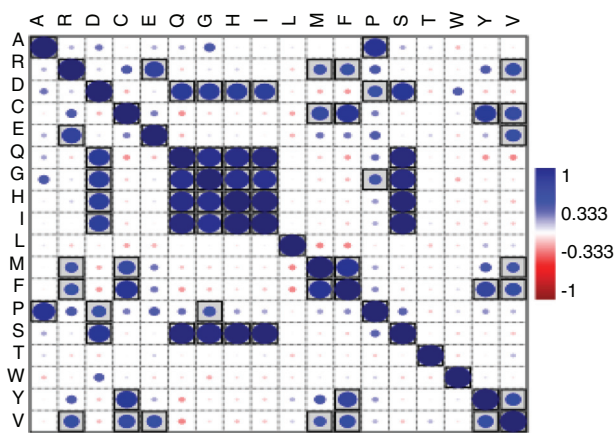
Figure 5 Pearson's correlation analysis of amino acids. The circles showed significant data at *p* < 0.05 (where A, alanine; R, arginine; D, aspartic acid; C, cysteine; E, glutamic acid; Q, glutamine; G, glycine; H, histidine; I, isoleucine; L, leucine; M, methionine; F, phenylalanine; P, proline; S, serine; T, threonine; W, tryptophan; Y, tyrosine; V, valine).

Tryptophan and tyrosine are aromatic AAs and included in the same group. Cysteine and methionine included in the same group and both are sulfur containing AAs. Fabaceae, Huacaceae, Leguminosae and Moraceae are included in the same group on the basis of relative content of AAs. Piperaceae, Solanaceae and Poaceae have similar proximities on the basis of relative AA contents. Cucurbitaceae, Chenopodiaceae, Combretaceae and Cyperaceae are also included in the same group.

PCA was conducted to determine the variations of amino acids in different plant species. It is an unsupervised method without previous knowledge of the dataset and reserved maximum variation of multidimensional dataset while decreasing its dimensionality into 2D or 3D (Gao et al., 2012; Worley, Halouska, & Powers, 2013). PCA results are given in Fig. 8 and Tables 3 and 4. The first four principal components explained 73.16% of the total variance. PC1 displayed 29.99% of the variance and included aspartic acid, glutamine, glycine, histidine, isoleucine and serine. Both aspartic acid and glutamine are acidic in nature. The sulfur containing AAs (cysteine and methionine) and aromatic AAs (phenylalanine and tyrosine) contributes to PC2 and accounted for 19.49% of the variance. PC3 displayed 11.46% of the variance and included arginine, glutamic acid and valine. The non-polar AAs (alanine and proline) have maximum loadings on PC4 and explained for 10.82% of the total variance. Zhu et al. (2017) while working on the amino acids content in *Angelica sinensis* applied PCA to find the source of variations among the amino acids. Pierce, Hope, Hoggard, and Synovec (2006) applied PCA to compare the amino acids content in *Ocimum basilicum*, *Mentha piperita*, and *Stevia rebaudiana* and also showed the alterations among different amino acids.

NMDS is an indirect gradient assessment techniques which generates an ordination based on a distance or dissimilarity
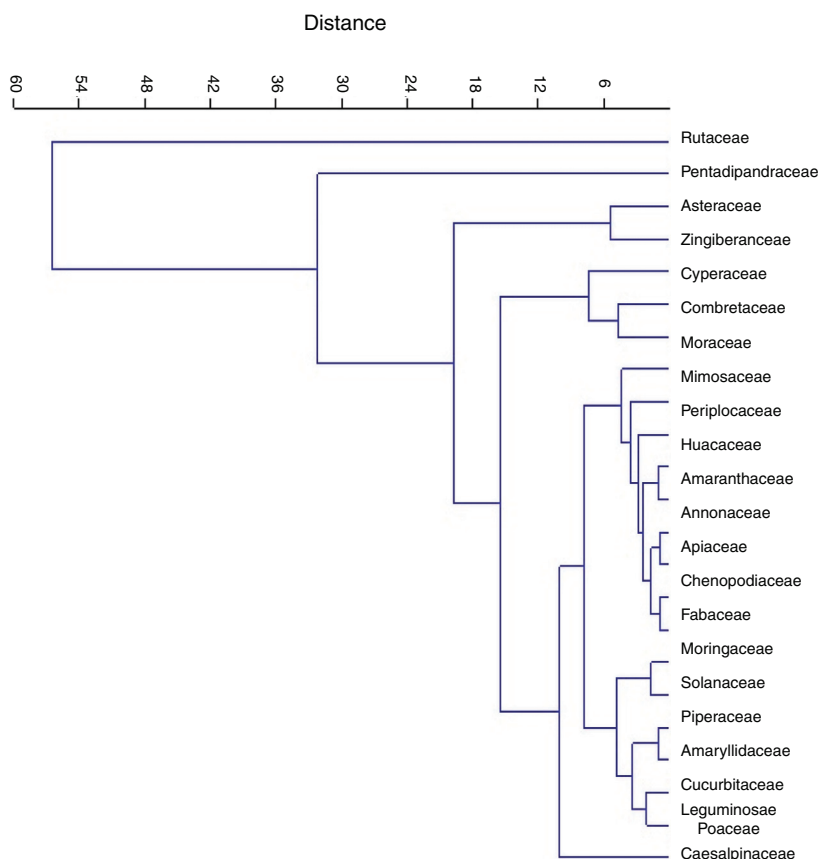
Figure 6 Cluster analysis of different families on the basis of contents of amino acids with respect to lysine.
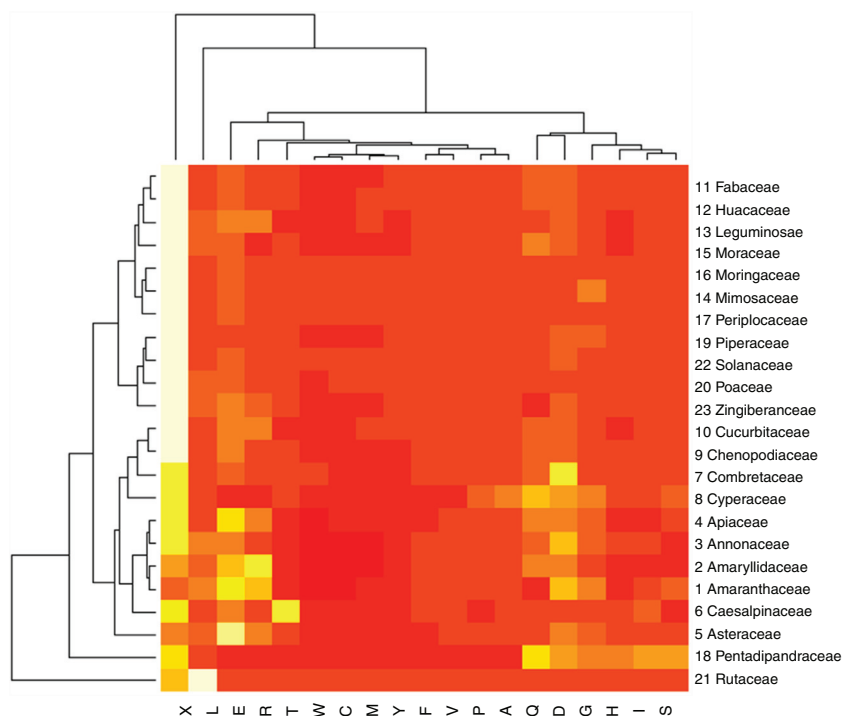
Figure 7 Heatmap analysis of different amino acids and families. The same colour in the row and column representing little variations in the content of amino acids in particular families (where A, alanine; R, arginine; D, aspartic acid; C, cysteine; E, gl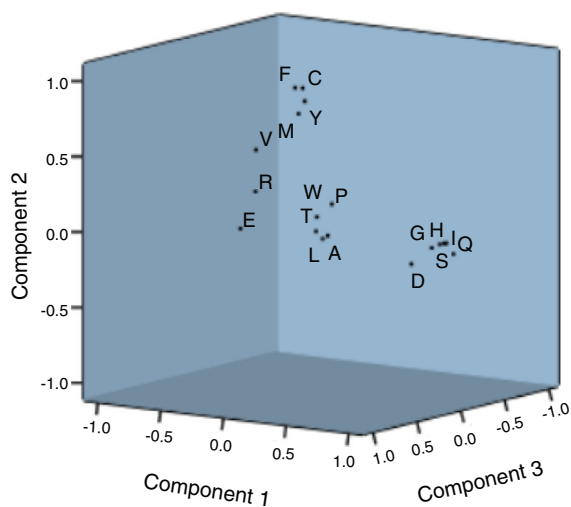utamic acid; Q, glutamine; G, glycine; H, histidine; I, isoleucine; L, leucine; M, methionine; F, phenylalanine; P, proline; S, serine; T, threonine; W, tryptophan; Y, tyrosine; V, valine).

Figure 8 PCA plot for different amino acids.

matrix. The ranks were compressed into three dimensions. NMDS scatter plot revelaed that Pentadipandraceae and Rutaceae are separated from other families on the basis of relative AA contents (Fig. 9a). Shepard plot (Fig. 9b) indicated a stress level of 0.06065. The coefficient of determination (R^2) was 0.9338 and 0.6114 respectively. Stress values equal to or less than 0.1 regarded as fair, whereas values similar or less than 0.05 represent good fit of the data (Kaur et al., 2018). Allocating the algorithm to ordinate in further dimensions can decrease the stress; while allocating higher than 3 dimensions fastly makes explanation more challenging (Kumar et al., 2019).

Future prospects

In present scenario vegetal sources contribute 57% of the protein supply globally (FAO, 2010). The plant derived proteins is of enormous significance and attention has been paid to meet the protein increasing requirements of people from

Table 3 Percent variance explained by PCA for different amino acids.

Component	Initial Eigen values			Extraction sums of squared loadings			Rotation sums of squared loadings		
	Total	% Of variance	Cumulative %	Total	% Of variance	Cumulative %	Total	% Of variance	Cumulative %
1	5.73	31.85	31.85	5.73	31.85	31.85	5.39	29.99	29.99
2	4.24	23.57	55.42	4.24	23.57	55.42	3.50	19.49	49.48
3	1.77	9.88	65.31	1.77	9.88	65.31	2.06	11.46	60.95
4	1.41	7.84	73.16	1.41	7.84	73.16	1.94	10.82	71.77
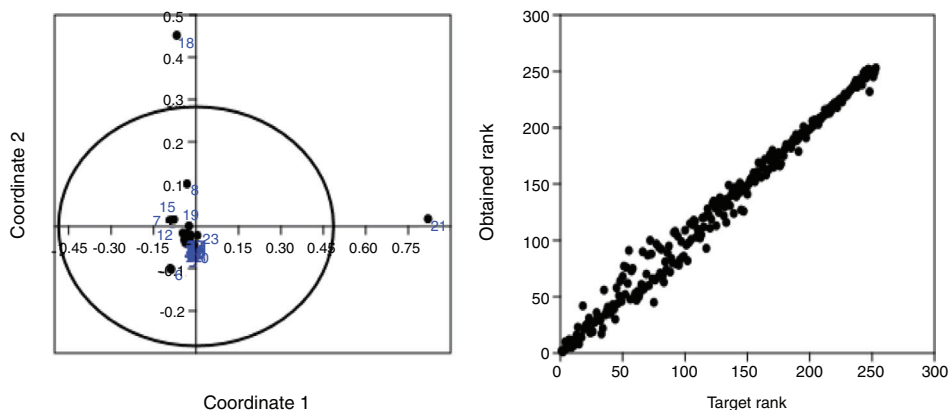
Figure 9 (a) NMDS scatter plot (95% ecclipse) of different families on the basis of amino acids relative content using Elucidean as a similarity measure. (b) NMDS Shepard 2-D plot of different families on the basis of amino acids relative content (Stress = 0.06065, R^2 for Axis 1 = 0.9338, Axis 2 = 0.6114) (where Amaranthaceae = 1; Amaryllidaceae = 2; Annonaceae = 3; Apiaceae = 4; Asteraceae = 5; Caesalpinaceae = 6; Combretaceae = 7; Cyperaceae = 8; Chenopodiaceae = 9; Cucurbitaceae = 10; Fabaceae = 11; Huacaceae = 12; Leguminosae = 13; Mimosaceae = 14; Moraceae = 15; Moringaceae = 16; Periplocaceae = 17; Pentadipandraceae = 18; Piperaceae = 19; Poaceae = 20; Rutaceae = 21; Solanaceae = 22 and Zingiberanceae = 23).

Table 4 Loadings of PCA for different amino acids.

	Component			
	1	2	3	4
A	.084	−.058	.043	.972
R	.051	.344	.820	.135
D	.798	−.164	.111	.261
C	−.063	.916	.119	.036
E	−4.486E−5	.107	.919	.139
Q	.953	−.119	−.146	.106
G	.909	−.056	.037	.25
H	.983	−.023	.053	−.057
I	.986	−.026	−.020	−.069
L	−.018	−.102	−.045	.008
M	−.054	.757	.180	.019
F	−.084	.924	.174	.022
P	.250	.196	.234	.884
S	.993	−.021	.016	.089
T	−.016	−.040	.034	.000
W	−.065	.038	−.045	−.025
Y	−.062	.826	.096	.049
V	−.099	.573	.601	−.065

plant derived products (Henchion, Hayes, Mullen, Fenelon, & Tiwari, 2017). The increased demand for plant proteins as compared to animal based proteins is due to the reason that these are coupled with less land utilization need, and usually established that plant derived food form less greenhouse gases, which are linked with climate change (Tilman & Clark, 2014). Several plants present distinctive benefits like pulses, being legumes have capability to fix nitrogen. Moreover, because of its high cost and reduced accessibility of animal proteins in many countries and customer worries above health advantage of animal derived proteins, consideration should paid on more use of plant derived proteins, as probable resources of less price dietary proteins for food utilization (Wang, Li, Wu, & Lan, 2008). Among the plant

derived proteins, pulses are regarded as essential resources of dietary protein, and are included as main sources of proteins in the diet (Henchion et al., 2017). The diet that contains plant derived proteins as main proteins are nutrient poor owing to inappropriate protein sources (Elorinne et al., 2016). As compared to animal proteins, plant proteins do not contain all vital AAs in appropriate amount. Among the nine essential AAs needs for human beings, pulses lack methionine. Diverse anti-nutritional components like hydrolase inhibitors and lectins also found in the pulses which comprises a portion of defensive mechanism of the seed, which further hinders many biological roles (Campos-Vega, Loarca-Piña, & Oomah, 2010; Thompson, 1993). Products formed by mingle of cereal and pulses balances the AAs and enhances the nutritive significance. In general likely in the future, advancement in the technology will carry out to position plant derived proteins as advisable opportunity from a sustainability perception. The current review gives the status about AAs rich plants and families which requires more attention for the scientists to explore such plants for plant derived proteins to meet the demands of increasing population.

Conclusions

An increasing worldwide population, coupled with factors like altering socio-demographics, put enhanced pressure on the resources to give diverse food types. Enhanced demand for animal derived proteins is likely to have bad environmental influence, producing greenhouse gas discharge, needs more water and land. Alternative protein rich sources are plants, and current review presents the AAs composition in plants. The food plants are rich sources of AAs and are important for nutrition point of view. From the results of AAs, it has been concluded that in food plants leucine is the most abundantly found AA, whereas tryphtophan is the least found AA in the food plants. Out of the studied families maximum total relative AAs content was found in Pentadipandraceae and lowest total relative AAs content

was recorded from Periplocaceae. CA showed that Asteraceae and Zingiberaceae families are closely related with each other.

Conflicts of interest

The authors declare no conflicts of interest.

Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at doi:10.1016/j.biori.2019.06.004.

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