

Evaluation of selected nutritional attributes among pigeon pea (*Cajanus cajan*) landraces

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Abstract

Pigeon pea (*Cajanus cajan*) is an important grain legume that provides highly nutritious food for human consumption and livestock feed and fixes considerable amounts of atmospheric nitrogen, improving soil fertility. It contains high amounts of protein, carbohydrates and fats as well as fair levels of both macro and micronutrients. The objective of the current study was to examine the genetic diversity in seed nutritional composition of twelve pigeon pea landraces (that were generated through successive selfing of single plant selections to uniformity) to select promising lines for cultivar development. There were very highly significant differences ($p \leq 0.001$) among the genotypes for most of the mineral elements, including calcium, copper, potassium, magnesium and manganese. Relatively higher amounts of calcium (2103.43 mg/kg) and magnesium (73.11 mg/kg) were observed in 'PTMN-3'. High amounts of potassium (15278.86 mg/kg), phosphorus (4945.12 mg/kg) and zinc (32.90 mg/kg) were present in genotypes 'PTMN-3', 'PTMN-4', and 'PTMN-14', respectively. Potassium showed a highly significant ($p \leq 0.01$) negative correlation with magnesium, manganese, phosphorus, and zinc. The principal component analysis showed that the first four principal components cumulatively explained 80.95% of the total variation among the pigeon pea genotypes. Cluster analysis allocated the tested genotypes into four main groups. Genotypes possessing high crude protein and high mineral concentrations in most nutritional traits ('PTMN-1', 'PTMN-3' and 'PTMN-10') could be used as potential parental sources for the genetic improvement of nutritional attributes in pigeon pea breeding programs.

1. Introduction

Pigeon pea (*Cajanus cajan*) is a drought-tolerant food legume grown widely in tropical and subtropical countries. In Southern Africa, it is grown in Mozambique, Malawi, Botswana, and Tanzania as well as in South Africa, where it is intercropped with cereals such as maize and sorghum (Gwata and Siambi, 2009). Furthermore, pigeon pea is relatively resistant to various abiotic and biotic stresses such as drought, weeds and insect pests, making it an ideal crop for production in resource-poor communities. This crop can play a vital role in food security and income generation, particularly in marginalized rural communities. In addition, pigeon pea enhances soil fertility through atmospheric nitrogen fixation. The crop is important in food and nutritional

security, particularly in rural communities in developing countries, as a major source of affordable protein (Sangle, 2015; Fiacre *et al.*, 2018). Fresh and succulent leaves and pods contain essential nutrients required for human growth and development.

The seed contains protein (20-26%), carbohydrates (65%), fats (1-2%), fibre (3%) and energy (326.8-345.23 kcal) (Ojwang *et al.*, 2021). Moreover, pigeon pea possesses both macro elements such as calcium (Ca) and phosphorus (P) and trace elements such as iron (Fe) and zinc (Zn) (Saxena, Kumar and Sultana, 2010). Medicinally, pigeon pea is used to treat various diseases such as measles, diabetes (Dinore and Farooqui, 2022), hepatitis and liver dysfunction (Oladunmoye and

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Kehinde, 2011). The grain of pigeon pea also contains both vitamin A and vitamin C (Saxena *et al.*, 2010). Moreover, it possesses various phytochemical properties such as antimicrobial, antioxidant, anticancer and anti-inflammatory properties.

Grain legumes such as pigeon pea have been identified as affordable sources of good quality protein, particularly in many parts of Africa where poor rural communities generally depend on starch-based diets leading to nutrient deficiencies such as anaemia, hypocalcemia and kwashiorkor (Dahiya *et al.*, 1977; Pele *et al.*, 2016). Nutrient deficiencies can be alleviated by biofortification and dietary diversification with nutrient-dense legumes such as pigeon peas. However, previous research efforts on pigeon pea focused largely on the agronomy of the crop with little emphasis on the nutrient profiles of the crop (Talari and Shakappa, 2018; Majili *et al.*, 2020). Likely, this is partly due to inadequate funding for research on orphan crops such as pigeon peas (Tadele and Bartels, 2019). These nutrients tend to vary depending on both the inherent genetic differences and environmental factors. Moreover, there is a dearth of effort aimed at developing new pigeon pea genotypes with superior nutritional attributes. Therefore, the objective of this study was to determine the nutritional composition of pigeon pea landraces grown in South Africa with a view to exploiting their potential in the human diet and selecting promising lines. The pigeon pea landraces were generated through successive selfing of single plant selections.

2. Materials and methods

2.1 Study location and genetic material

The study was conducted at Thohoyandou (22°56'59" S; 30°28'59" E; 724 m a.s.l.) in South Africa. The soils at the location are predominantly deep (> 1,500 mm), dystrophic, red, well-drained with apedal structure

and a high (60%) clay content (Mzezewa *et al.*, 2010). The study used pigeon pea genotypes that were raised without the application of chemical fertilizers to simulate typical agronomic practices that prevail in the smallholder production systems in the area. In general, the pigeon pea smallholder farmers in the area are resource-poor and cultivate the crop without chemical fertilizer inputs in poor soil conditions (Hartemink and van Keulen, 2005; Chianu *et al.*, 2012). The mean daily temperatures at Thohoyandou vary from about 25°C to 40°C in summer and between 18°C and 26°C in winter. Twelve genotypes of pigeon pea (that mature within 160 days from planting) were selected from a germplasm pool maintained at the University of Venda and utilised in this study (Table 1). The genotypes predominantly consisted of exotic and local landraces (Gwata and Silim, 2005). To address the heterogeneity associated with landraces, each one of them was previously selfed for several filial generations to attain uniformity (Kempf *et al.*, 2015).

2.2 Mineral and crude protein determination

A random sample of dry pigeon pea seeds (weighing 5.0 g each) of each genotype was ground to a fine powder using a mortar and pestle and sieved through a 1.0 mm stainless steel sieve to obtain a homogenised sample (Feleke and Tesfaye, 2021). For the determination of mineral elements, about 1.0 g of each sample was ashed at 450°C for 4 hrs after which a few drops of dH₂O followed by 2.0 mL of hydrochloric acid (HCl) were added. The samples were evaporated to dryness in a water bath prior to the addition of 2.5 mL of freshly prepared 1:9 HCl solution to each sample and then filtered using Whatman No. 1 filter paper discs thereafter. The filtered sample was diluted with de-ionized water at 5:20 and analyzed for mineral elements using the Varian 720 Inductively Coupled Plasma Emission Spectrometer (ICP-OES, Germany). The raw

Table 1. Information of pigeon pea genotypes that were used in the study.

Entry number	Genotype		Type
	Designation	Code	
1	PTMN-1	SST	Exotic landrace
2	PTMN-2	ENT-3	Exotic landrace
3	PTMN-3	MP-BLK	Local landrace
4	PTMN-4	HBR	Exotic landrace
5	PTMN-5	LW-AM	Local landrace
6	PTMN-6	MJ-ORIG	Exotic landrace
7	PTMN-7	T-POD	Exotic landrace
8	PTMN-8	MP-BRN-SPEC	Local landrace
9	PTMN-10	I-557	Improved genotype
10	PTMN-11	DC	Exotic landrace
11	PTMN-12	MJ-HBR	Exotic landrace
12	PTMN-14	EX-MLW-2	Exotic landrace

data from ICP-OES were taken for further calculations using the dry matter determined earlier and the weight of the weighed sample.

Total nitrogen was determined by Kjeldahl's method. About 1.0 g of each seed sample was mixed with 20.0 mL of concentrated sulphuric acid (H_2SO_4) in heating tubes. Two Kjeldahl selenium catalyst tablets were added to each tube, and the mixture was heated inside a fume cupboard. The mixture was boiled and subsequently distilled using a Buchi distillation unit K-350. The liberated NH_4-N was collected in a beaker containing 20.0 ml 4% boric acid (H_3BO_3), and three droplets of methyl red indicator were added prior to titration with 0.1 M HCl using Mettler Toledo DL15 auto titrator with pH electrode. The percentage of crude protein was calculated as total nitrogen \times 6.25. Replicate samples were analysed for each nutrient per genotype.

2.3 Statistical analysis

Data obtained was subjected to analysis of variance (ANOVA) using Minitab version 19.0, followed by mean separation at $P \leq 0.05$ using Tukey's test procedure. Pearson's correlation was used to test the strength of linear associations between the nutritional traits studied. The principal component analysis (PCA) was used to determine the significant variables that contributed to the variation observed among the pigeon pea genotypes. Cluster analysis was performed to generate a dendrogram showing the variations and similarities between genotypes.

3. Results

3.1 Analysis of variance of pigeon pea genotypes for selected nutritional elements

There were highly significant differences ($p \leq 0.001$) among the genotypes for most of the mineral elements including calcium (Ca), copper (Cu), potassium (K) and magnesium (Mg) (Table 2). The level of phosphorus (P) (4094.17 mg/kg) was more than double that of Ca (1280.70 mg/kg) and Mg (1407.36 mg/kg), respectively (Table 3). However, the Mg content ranged between 1231.20 - 1829.99 mg/kg. The local genotype 'PTMN-3' attained the highest (2103.43 mg/kg) Ca content, followed by 'PTMN-4' (1606.27 mg/kg) and 'PTMN-2' (1552.62 mg/kg) while 'PTMN-6' achieved the highest K content (15278.86 mg/kg) but similar to three ('PTMN-1', 'PTMN-8' and 'PTMN-10') other exotic genotypes (Table 3).

Among the micro-nutrients, the level of iron (Fe) ranged between 32.99 - 61.20 mg/kg, but the mean content was more than three-fold higher than the level of Cu. The genotype 'PTMN-3' attained a significantly

high manganese (Mn) content (73.11 mg/kg), which was >30.0% higher than that observed in the rest of the pigeon pea genotypes. The mean for zinc (Zn) content among the genotypes was 26.53 mg/kg. The highest Zn (32.90 mg/kg) was achieved by the exotic 'PTMN-14' followed by 'PTMN-5' (32.50 mg/kg), 'PTMN-7' (31.89 mg/kg) and 'PTMN-12' (30.76 mg/kg) (Table 3). The improved genotype 'PTMN-10' possessed >30.0% Mo than nine other genotypes.

The average crude protein was 21.41%, with a range between 18.25 - 23.50% observed among the genotypes. The high protein content observed in the improved cultivar 'PTMN-10' (23.50%) was comparable to that in the local landrace 'PTMN-8' (23.25%) and exotic 'PTMN-1' (23.36%), respectively.

3.2 Correlations among mineral elements

The nutrients in the pigeon pea genotypes exhibited various correlations. There was a highly significant ($p \leq 0.01$) positive correlation between Mg with Mn and P (Table 4). However, a highly significant ($p \leq 0.01$) negative correlation was observed between Ca and Cu (Table 4). K showed highly significant ($p \leq 0.01$) negative correlations with Mg, Mn, Mo and Zn. Mn showed a highly significant ($p \leq 0.01$) correlation with Zn but a negative correlation with Mo. Both the Fe and protein showed no significant correlation with any of the other mineral elements.

3.3 Principal component analysis and biplot

The principal component analysis revealed that the first four principal components accounted for 80.95% of the variation among the pigeon pea genotypes (Table 5). Furthermore, PCA identified three principal components with eigenvalues of more than one, which contributed 71.49% of the cumulative variance. Three variables, namely Mg, Mn and Zn were associated with PC1. In addition, Mn contributed the most variation to this component. The second principal component (PC2) accounted for 17.82% of the total variance, and it reflected positive loading of Fe and Zn, but P and protein showed negative correlations with this component.

The principal component biplot showed that the pigeon pea genotypes were scattered randomly across all the quadrants (Figure 1). Five genotypes, namely, 'PTMN-14', 'PTMN-1', 'PTMN-10', 'PTMN-4' and 'PTMN-3,' were on the extreme margins of the cartesian plane. There was a positive correlation for the variables in the first and second quadrants, namely Ca, P, Mg, Mn, Zn and Fe and these variables were associated with 'PTMN-5', 'PTMN-4', 'PTMN-3', 'PTMN-14' and 'PTMN-7' respectively (Figure 1). 'PTMN-2' showed

Table 2. Analysis of variance of pigeon pea genotypes for selected nutritional traits content.

Source	df	Mean Squares										
		Ca	Cu	Fe	K	Mg	Mn	Mo	P	Zn	Protein	
Replication	1	21059.41	0.10	138.50	350033.73	6734.03	3.24	0.00	7703.11	0.92	27.16	
Genotype	11	293931.41***	3.75***	194.20	9559302.21***	64739.81***	809.44***	14.90**	762608.50**	42.67**	3.11*	
Mean	-	1280.70	10.91	43.20	12599.35	1407.36	24.96	2.15	4094.17	26.53	21.41	
C.V. (%)	-	8.95	6.08	32.80	4.07	4.52	13.78	7.22	3.89	5.20	6.41	
R ² (%)	-	95.75	89.50	50.74	97.34	94.16	98.54	99.84	96.78	95.74	81.56	

***significant at 0.1% probability levels, **significant at 1.0% probability levels, *significant at 5.0% probability levels. Ca: calcium, Cu: copper, Fe: iron, K: potassium, Mg: magnesium, Mn: manganese, Mo: molybdenum, P: phosphorus, Zn: zinc.

Table 3. Mean values for nutritional traits content of twelve pigeon pea genotypes.

Genotype	Elements (mg/kg)											Protein (%)
	Ca	Cu	Fe	K	Mg	Mn	Mo	P	Zn			
PTMN-3	2103.43 ^a	8.74 ^g	41.77 ^a	12227.73 ^d	1620.56 ^b	73.11 ^a	0.17 ^f	4710.29 ^{ab}	28.42 ^{bc}	20.01 ^{cd}		
PTMN-4	1606.27 ^b	9.06 ^{fg}	36.50 ^a	8874.21 ^f	1829.99 ^a	32.25 ^{cd}	0.28 ^{ef}	4945.12 ^a	27.16 ^{cd}	21.94 ^{abc}		
PTMN-2	1552.62 ^{bc}	11.39 ^{bcd}	34.82 ^a	13988.90 ^{bc}	1231.20 ^f	15.80 ^e	0.81 ^d	2899.23 ^h	21.76 ^f	21.22 ^{abcd}		
PTMN-5	1432.60 ^{bcd}	9.99 ^{efg}	36.75 ^a	9975.85 ^{ef}	1563.27 ^b	34.12 ^c	0.47 ^{def}	4837.54 ^{ab}	32.50 ^a	23.06 ^{ab}		
PTMN-11	1410.56 ^{bcd}	10.01 ^{efg}	61.20 ^a	13376.11 ^c	1414.55 ^c	11.36 ^e	5.29 ^b	4043.87 ^{de}	22.57 ^{ef}	19.38 ^{cd}		
PTMN-12	1351.09 ^{cde}	11.71 ^{bcd}	55.25 ^a	13602.68 ^c	1315.95 ^{cdef}	14.91 ^e	0.57 ^{de}	3714.89 ^{efg}	30.76 ^{ab}	21.34 ^{abc}		
PTMN-6	1266.73 ^{de}	12.03 ^{abc}	32.99 ^a	15278.86 ^a	1290.49 ^{cdef}	12.43 ^e	0.23 ^f	4198.80 ^d	24.80 ^{de}	21.41 ^{abc}		
PTMN-1	1106.91 ^{ef}	13.45 ^a	42.38 ^a	14179.82 ^{abc}	1293.15 ^{cdef}	9.72 ^e	5.61 ^b	3839.85 ^{ef}	20.53 ^f	23.36 ^a		
PTMN-8	993.98 ^f	10.43 ^{def}	36.72 ^a	14283.12 ^{abc}	1271.89 ^{def}	9.50 ^e	4.15 ^c	3631.70 ^{fg}	22.71 ^{ef}	23.25 ^a		
PTMN-10	961.88 ^f	12.22 ^{ab}	35.26 ^a	14793.05 ^{ab}	1409.10 ^{cd}	9.04 ^e	7.69 ^a	4310.89 ^{cd}	22.48 ^{ef}	23.50 ^a		
PTMN-7	898.04 ^{fg}	11.36 ^{bcd}	46.76 ^a	9922.89 ^{ef}	1255.79 ^{ef}	24.98 ^d	0.27 ^{ef}	4550.84 ^{bc}	31.83 ^a	20.19 ^{bcd}		
PTMN-14	685.27 ^g	10.59 ^{cde}	57.94 ^a	10689.02 ^e	1392.35 ^{cde}	52.25 ^b	0.25 ^{ef}	3447.05 ^g	32.90 ^a	18.25 ^d		

Values with different superscripts in the same column are statistically significantly different ($P \leq 0.05$). Ca: calcium, Cu: copper, Fe: iron, K: potassium, Mg: magnesium, Mn: manganese, Mo: molybdenum, P: phosphorus, Zn: zinc.

Table 4. Pearson correlation coefficients (r) analysis showing association between the nutritional traits of pigeon pea landraces.

	Ca	Cu	Fe	K	Mg	Mn	Mo	P	Zn	Protein
Ca	1.0000									
Cu	-0.520**	1.0000								
Fe	-0.0480	-0.1190	1.0000							
K	-0.0610	0.547**	-0.1010	1.0000						
Mg	0.539**	-0.648**	-0.0070	-0.583**	1.0000					
Mn	0.408*	-0.637**	0.1040	-0.548**	0.532**	1.0000				
Mo	-0.3060	0.4020	-0.0010	0.537**	-0.2120	-0.556**	1.0000			
P	0.3120	-0.3810	-0.1610	-0.499*	0.667**	0.3370	-0.1260	1.0000		
Zn	-0.0500	-0.3120	0.2290	-0.672**	0.2810	0.591**	-0.682**	0.3490	1.0000	
Protein	-0.0050	0.2400	-0.2830	0.2340	0.0140	-0.3530	0.3460	0.1200	-0.2910	1.0000

**significant at 1% probability levels, *significant at 5.0% probability levels. Ca: calcium, Cu: copper, Fe: iron, K: potassium, Mg: magnesium, Mn: manganese, Mo: molybdenum, P: phosphorus, Zn: zinc.

Table 5. Principal component analysis showing the eigenvectors, eigen values, and cumulative percentages.

Parameter	PC1	PC2	PC3	PC4
Eigenvalue	4.21	1.78	1.16	0.95
Proportion	42.09	17.82	11.58	9.46
Cumulative	42.09	59.91	71.49	80.95
Eigenvectors				
Ca	0.237	-0.371	0.545	0.216
Cu	-0.384	0.121	-0.297	0.078
Fe	0.060	0.380	0.324	-0.725
K	-0.392	-0.099	0.346	0.147
Mg	0.367	-0.365	0.023	-0.252
Mn	0.405	0.080	0.137	0.120
Mo	-0.333	-0.267	0.039	-0.518
P	0.290	-0.376	-0.349	-0.219
Zn	0.344	0.342	-0.376	0.006
Protein	-0.162	-0.474	-0.326	-0.077

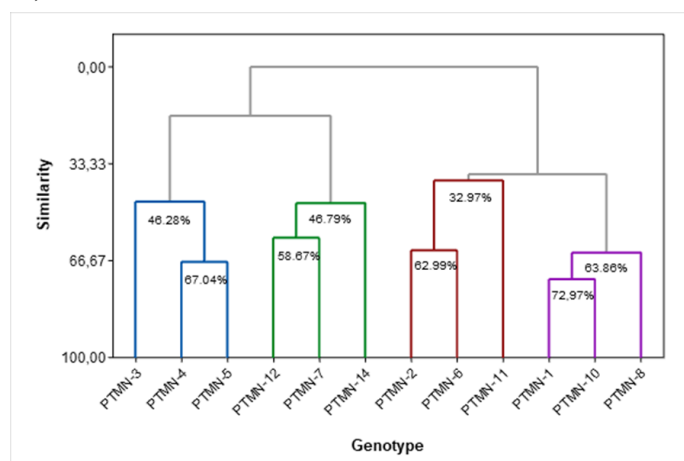


Figure 2. Dendrogram showing the similarities of pigeon pea genotypes based on 10 attributes for nutritional mineral content.

pigeon pea genotypes (Figure 2). Cluster I consisted of three pigeon pea landraces. The exotic genotype 'PTMN-4' was clustered together with 'PTMN-5', while the local landrace 'PTMN-3' was a singleton. Singletons are regarded as genotypes that are more diverse or superior to the rest in a cluster (Figure 2). The second cluster consisted of three exotic genotypes, 'PTMN-12' and 'PTMN-7' were clustered together, whereas 'PTMN-14' was a singleton. Similarly, in cluster III, 'PTMN-2' and 'PTMN-6' were clustered together with 'PTMN-11' as a singleton. Cluster IV also consisted of the local landrace 'PTMN-8' as the most diverse within the cluster, while the improved cultivar 'PTMN-10' was clustered with the exotic 'PTMN-1'.

4. Discussion

The study revealed wide variability in nutrients among the pigeon pea genotypes studied. The significant genotypic differences observed for mineral elements such as Ca, Cu, Fe, K, Mg, Mn, Mo, P and Zn as well as crude protein indicated genetic variability for nutrient compositions among pigeon pea germplasms. Pigeon pea is a rich source of crude protein, vitamins and essential

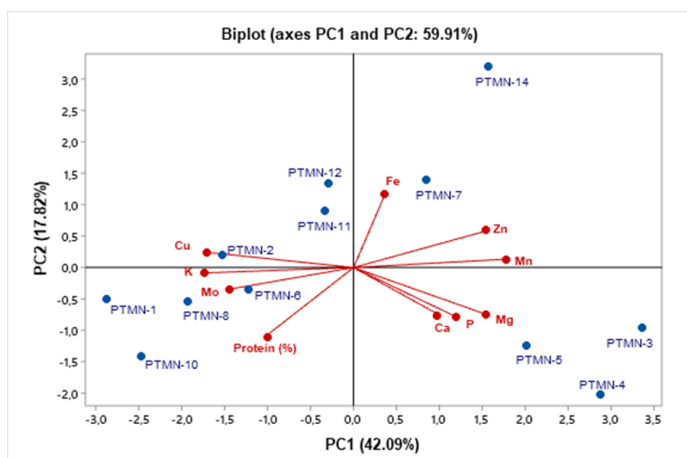


Figure 1. Principal component analysis of pigeon pea landraces with mineral content.

superior performance for Cu. Four genotypes ('PTMN-6', 'PTMN-8', 'PTMN-1' and 'PTMN-10') were associated with high K, Mo and protein (%), respectively.

3.4 Cluster analysis

The dendrogram produced four clusters out of twelve

minerals for human growth and development (Abebe, 2022). Crop improvement is hinged on the availability of genetic variation, and the significant differences in nutrient content exhibited by the evaluated genotypes indicate the potential use of the genotypes in pigeon pea improvement. Breeding efforts should be intensified to include pigeon pea in mainstream agricultural production for food and nutrition security, especially in developing countries where animal protein is expensive. Similar observations of genetic diversity in the nutritional attributes of pigeon pea were previously reported (Singh *et al.*, 2018; Anjulo *et al.*, 2021).

In the present study, calcium ranged between 685.27 mg/kg to 2103.43 mg/kg. Susmitha *et al.* (2022) reported a similar observation in Ca content (154.28 mg/100 g) and inferred that the Ca content in pigeon pea was higher than in many staple cereals such as rice, wheat and maize. Calcium is an important mineral element essential for maintaining strong bones and a normal heartbeat (Sekhon *et al.*, 2017; Ciosek *et al.*, 2021), which further asserts the importance of pigeon pea in alleviating calcium deficiency in cereal-based diets of sub-Saharan Africa. Furthermore, the high amount of K (15278.86 mg/kg) observed in 'PTMN-6' and Mg (1829.99 mg/kg) in 'PTMN-4' suggested that these genotypes could be significant in reducing the risk of cardiovascular diseases and diabetes when included in the diet (Stone *et al.*, 2016).

The Fe content observed with the genotype 'PTMN-11' was almost two-fold that observed in a study involving pigeon peas by Nwokolo (1987). This genotype could play a prominent role in fighting anaemia in women and children caused by Fe deficiency. Breeding for biofortification using this genotype as a donor parent for high Fe content is possible. Furthermore, 'PTMN-1' and 'PTMN-14' with significantly higher nutrient content for Cu and Zn could also be potential donor parents for mineral biofortification (Upadhyaya *et al.*, 2007; Hanumanthappa *et al.*, 2018). Zinc (Zn) is an important trace element essential for cell division and wound healing while Cu can act as an antioxidant, reducing free radicals that can damage cells and DNA in the human body. Molybdenum deficiency has previously been linked with the risk of developing esophageal cancer (Burrell *et al.*, 1966; Odularu *et al.*, 2019). Ray *et al.* (2012) reported that worldwide, one in 32 men has a lifetime risk of developing esophageal cancer, while in South Africa, the risk is twenty times more common. The results revealed that the investigated lines can effectively contribute towards meeting the daily recommended dietary intake.

Genotypes such as 'PTMN-10', 'PTMN-1' and 'PTMN-4' with high protein content could play a prominent role as supplements of cereal-based food in meeting the dietary and nutritional requirements in rural areas where diets are deficient in protein (Talari and Shakappa, 2018). Saxena and Sawargaonkar (2015) indicated that high crude protein and mineral genotypes could benefit end-users and be exploited as parental sources for the introgression of nutritional traits in the development of novel genotypes with superior nutritional attributes. Nonetheless, various reports suggested that the differences observed in some individual minerals were likely due to the substantial influence of the environment, climatic variations, agricultural practices, and inputs used for plant growth (Frossard *et al.*, 2000; Obala *et al.*, 2018; Murube *et al.*, 2021; Thovhogi *et al.*, 2021).

The positively correlated mineral elements could facilitate combined multi-nutrient biofortification. The Ca improvement in pigeon pea is favoured by the selection for Mg and Mn while the improvement for Mg would be favoured by the selection for Mn and P. Susmitha *et al.* (2022) indicated that the combined improvement of positively correlated minerals stays significant. The positive correlation of Ca and Mg in pigeon pea germplasm in this study is similar to that observed by Sharma *et al.* (2020). Furthermore, non-significant correlations observed among most minerals indicated that selection for a high concentration of these traits does not always lead to a greater concentration of the other trait and that selection for both should be performed simultaneously. A linkage drag could be experienced during the simultaneous selection of negatively correlated nutrients, which complicates breeding efforts. It would be prudent to investigate further the genetic basis of the expression of these nutrients to find ways to break unfavourable linkages for nutrients of interest.

The PCA is an important analytical tool for discriminating the importance of different traits and genotypes based on their contribution to the overall variation. The nutrients on the first PC are the most important in differentiating the genotypes. Because of their association with the first PC, Mg, Mn and Zn could be considered the most informative for assessing genetic variation for nutritional content among the pigeon pea genotypes. Subsequently, the genetic variation among the genotypes can be assessed by nutrients such as Fe, P and protein that were important on the second PC. High genetic gain in breeding is achieved when there is adequate genetic diversity, which is influenced by the ability to effectively assess the germplasm for variation. Thus, knowledge of which nutrients are important for

thorough evaluation and discrimination of genotypes is an important preliminary step in pre-breeding before the germplasm can be introduced into the breeding program. Alternatively, the discriminating nutrients will be important in germplasm maintenance and conservation.

On the other hand, the genotypes that were associated with certain nutrients could be useful as parents in breeding schemes. What would be prudent is to identify the genotypes that exhibited favourable phenotypic values for the trait of interest. Genotypes such as 'PTMN-5', 'PTMN-4', 'PTMN-3', 'PTMN-14' and 'PTMN-7' were positively associated with Ca, P, Mg, Mn, Zn and Fe, showing that they would be useful to introgress genes for improving these nutrients. Protein, K and Mo contents could be improved by using four genotypes, namely, 'PTMN-6', 'PTMN-8', 'PTMN-1' and 'PTMN-10'. Furthermore, it would be important to evaluate the relatedness of the genotypes before their use in breeding programs. Closely related genotypes may lead to inbreeding and genetic depression. Thus, cluster analysis was used in differentiating pigeon pea landraces into groups to get a better understanding of their similarities and differences.

The dendrogram partitioned genotypes into four main groups revealing the presence of high genetic diversity among the clusters. Similar studies in pigeon pea also revealed high genetic diversity based on cluster analysis (Kassa *et al.*, 2012; Kumara *et al.*, 2013; Upadhyaya *et al.*, 2013). The genetic diversity could assist in selecting the best parental genotypes based on the nutritional traits of interest. Genotypes such as 'PTMN-8', 'PTMN-1' and 'PTMN-10' that had high protein content may not be recommended for hybridization because they were clustered together showing that they could be related. However, there is a need to conduct molecular analysis of these genotypes to establish whether the observed phenotypic values in nutritional content are supported by a genetic basis. Phenotypic expression is influenced by the environment and provides a proxy indicator of genetic variation, but molecular markers are more reliable.

The significant genetic diversity in seed nutritional composition reported in this study indicated the potential for selecting and developing new and improved cultivars of pigeon peas. In addition, the identified genotypes possessing both high crude protein and high mineral concentrations can serve as source materials for researchers in many parts of the world who are interested in the improvement of food grain quality attributes in the crop for the benefit of consumers. The new information generated by the study is valuable for pigeon pea breeders since there is a dearth of information pertaining to pigeon pea landraces and their potential exploitation in

genetic enhancement of the nutritional attributes of this crop. The research has the potential impact to influence pigeon pea breeding programs as researchers acquire empirical evidence of the nutritional value of these landraces.

5. Conclusion

The study revealed variability in a wide range of mineral elements among pigeon pea genotypes. The genotypic variation observed indicated that there was genetic potential for the selection of parental genotypes for nutritional quality improvement in pigeon pea breeding programs. 'PTMN-1' and 'PTMN-10' were superior for Cu, K, Mo and crude protein, while 'PTMN-3' possessed significant levels of Ca, Mg, Mn and P. Genotypes possessing high crude protein and high mineral concentrations in most nutritional traits (i.e., 'PTMN-1', 'PTMN-3' and 'PTMN-10') could be used as potential breeding source materials for the genetic improvement of nutritional attributes in pigeon pea. Divergent genotypes were identified but further studies incorporating molecular markers to determine the genetic basis of the variation are recommended.

Conflict of interest

The authors declare no conflict of interest.

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