

# Genotypic diversity and trait profiles of some *Amaranthus* accessions

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*Key words:* *Amaranthus*, biplot, improvement, trait profile, variability.



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All relevant data are within the paper and its Supporting Information files.

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The authors declare no competing interests.

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**Abstract:** Knowledge of the pattern of trait variation among accessions, and the trait profiles of the accessions is crucial for improvement of a crop. Twenty-one *Amaranthus* accessions were evaluated in 2018 and 2019 to investigate the extent of genotypic diversity among the amaranth accessions and their trait profiles. Data were subjected to analysis of variance, and correlation and principal component analyses. Taking stem weight (SWT) as the yield, the accession × yield-trait combination (GYT) biplot was employed to investigate the trait profiles of the accessions. Accession, year, and accession × year mean squares were significant ( $P \leq 0.05/0.01$ ) for most of the measured traits. The first three principal components explained 88.18% of observable variation among the accessions and identified plant height (PHT), number of leaves per plant (NOL), and root weight (RWT) as the major contributors. Significant ( $P \leq 0.01$ ) correlation was observed in the association of SWT with NOL, TBM, and RWT. Accessions NGB00019 and NGB00061 were associated with the sector containing all the YT combinations considered. However, NGB00019 was identified as the best combiner of yield with other traits. Further studies involving more traits should determine the trait profiles of the remaining accessions.

## 1. Introduction

*Amaranthus* is a member of the Amaranthaceae family and is believed to have originated from South America (Janovská *et al.*, 2012). Despite the level of under-development, the genus is one of the most diverse among cultivated crops, with about 70 species (Ebert *et al.*, 2011). Amaranths are classified based on the part of the plant for which they are grown. The leaf types including *A. hybridus* and *A. tricolor* are grown for their leaves consumed as vegetables while the grain amaranths such as *A. caudatus*, *A. cruentus*, and *A. hypochondriacus* are popular for the grains. In addition, some amaranth like *A. tricolor* are valued as ornamental, while some (e.g. *A. palmeri* S. Wats., *A. powellii* S. Watt., *A. retroflexus* L., and *A.*

*spinosa* L.) are considered as weeds. In general, cultivated amaranths are of nutritional importance because they produce edible leaves, stems, and grains (e.g., *A. hybridus* and *A. tricolor*) (Akin-Idowu *et al.*, 2016; Neelesh and Pratibha, 2018). The leaves and stem are rich natural stores of vitamins (A, B, and C), and dietary minerals including calcium and iron (Stallknecht and Schulz-Schaeffer, 1993). *Amaranthus* has also been found to be a source of lysine, an essential amino acid that is lacking in diets based on cereals and tubers (Schippers, 2000). The vegetable is reported to be adapted to a wide range of agro-ecology habitat (Katiyar *et al.*, 2000) and can tolerate biotic (i.e. diseases and pests) and abiotic (i.e. heat and drought) stresses (Shukla *et al.*, 2010). As is with many other under-utilized leaf vegetables, the genetic and economic potentials of *Amaranthus* have not been fully harnessed.

Although the amaranth is essentially self-pollinating, there is significant level of natural outcrossing and inter-specific and inter-varietal hybridization, leading to the occurrence of wide differences among accessions (Akin-Idowu, 2016). There is a growing interest in research on amaranth because of the high genetic diversity and phenotypic variability of the crop which are of immense use in designing strategies for improvement of the crop. Plant breeders have found differences in plant observations among genetic materials as effective means to deduce estimates of genetic diversity (Akin-Idowu, 2016) and to determine genotypic superiority. However, identification of genetic superiority is hindered by unfavourable associations among a set of target traits since the decision is often based on multiple traits (Yan and Fregeau-Reid, 2018). This implies that a successful cultivar must attain desirable levels for several key traits. Thus, knowledge of the pattern of trait variation among accessions and the trait profile (strength and weakness) of available Amaranth accessions will aid the exploitation of existing genotypic diversity for improvement of the crop for desired traits. Recently, the accession x yield-trait (GYT) biplot approach was proposed by Yan and Fregeau-Reid (2018) to combat the challenge posed by evaluation of accessions based on multiple traits. In this approach, the worth of an accession is determined by its value for yield in combination with other traits (Y-T) rather than its levels for an individual trait. Therefore, this study investigated the extent of genotypic diversity among amaranth accessions, as well as the trait profiles of the accessions with a view to pro-

viding information to aid effective future improvement strategies.

## 2. Materials and Methods

### Genetic materials

Twenty-one (21) amaranthus accessions (NGB00001, NGB00005, NGB00019, NGB00022, NGB00025, NGB00027, NGB00028, NGB00029, NGB00031, NGB00024, NGB00058, NGB00059, NGB00060, NGB00061, NGB00070, NGB00078, NGB00082, NGB00108, NGB00111, NGB00112, and a local check named LASPO-COL-001). All the accessions, except the local check, were obtained from the National Agency for Crop Genetic Resources and Biotechnology (NACGRAB), Ibadan, Nigeria. Seeds of the local check were collected from a reputable farmer in Ikorodu. All the accessions belong to the species *A. hybridus*, and are of Nigerian origin (Table 1).

### Field evaluation and phenotyping

The 21 amaranthus accessions were evaluated on the field during the main seasons of 2018 and 2019.

Table 1 - Origin of the 21 *Amaranthus hybridus* accessions used in the study

Serial number	Accession name	Origin
1	NGB00001	Katsina State, Nigeria
2	NGB00005	Kebbi State, Nigeria
3	NGB00019	Lagis State, Nigeria
4	NGB00022	Zamfara State, Nigeria
5	NGB00025	Niger State Nigeria
6	NGB00027	Osun State, Nigeria
7	NGB00028	Osun State, Nigeria
8	NGB00029	Ondo State, Nigeria
9	NGB00031	Oyo State, Niigeria
10	NGB00034	Oyo State, Niigeria
11	NGB00058	Ogun State, Nigeria
12	NGB00059	Ondo State, Nigeria
13	NGB00060	Oyo State, Niigeria
14	NGB00061	Osun State, Nigeria
15	NGB00070	Ogun State, Nigeria
16	NGB00078	Oyo State, Niigeria
17	NGB00082	Oyo State, Niigeria
18	NGB00108	Oyo State, Niigeria
19	NGB00111	Oyo State, Niigeria
20	NGB00112	Oyo State, Niigeria
21	LASPO-COL-001	Lagis State, Nigeria

The land was initially tilled mechanically by ploughing twice and then harrowing. Subsequently, raised beds; 2x1 m in diameter, were made manually. Cured poultry manure was applied on the bed at a rate of 10 tons/ha. The trial was laid out in randomized Complete Block Design with two replications. Each accession was grown in a 2-row plot fitted into a bed in each replicate. A seed rate of 1.5 kg/ha was used, and planted by drilling. Seeds were mixed with dry fine sand to enhance even distribution within the drills. The experiment was exclusively rain-fed. Weeds were controlled manually by rogueing, subject to field inspection, and chemical insecticides were not used throughout the experiment.

At maturity, a random sample of five plants per row; making 10 plants per replicate per accession, were observed for plant height (PHT) (cm), number of leaves per plant (NOL), and stem girth (STG) (mm). All the plants in each plot were uprooted, and the roots washed carefully, to record data on total biomass (TBM) (g), root weight (RWT) (g), stem weight (SWT), and harvest index (%). Observations were recorded according to the *Amaranthus* descriptors of IPGRI (1999). Data on TBM, RWT, and SWT were converted to kg/ha. Harvest index was computed as the percent of the total biomass that is made up by the stem weight.

#### Data analyses

Test for homogeneity of variance was not significant and thus analysis of variance (ANOVA) was performed on combined data from the two-year evaluation using 'proc glm' in SAS (SAS, 2011). Means of data collected for each accession were subjected to correlation (Pearson coefficients) analysis among all pair-wise combinations of measured traits while the standardized mean values were subjected to principal component analysis. To reveal the level of pheno-

typic divergence among pairs of accessions, estimates of genetic distance (Euclidean) among all possible pairs of accessions were obtained using 'proc distance' while the accessions were distributed into clusters from dendrogram obtained using 'proc tree' (SAS, 2011). To investigate the trait profiles of the accessions, a accession × yield-trait combination (GYT) (Yan and Fregeau-Reid, 2018) biplot approach was employed where stem weight was taken as the yield. The GYT biplots were obtained using the GGEBiplotGUI package in R. To select accessions for the GYT biplots, a superiority index (SI) was computed for the accessions, based on standardized GYT estimates. The SI value of a accession was computed as the arithmetic mean of its standardized estimates. Ten accessions comprising seven and three accessions with the highest and lowest SI values respectively were selected for the GYT biplot.

### 3. Results

Results of analysis of variance of amaranth accessions are summarized in Table 2. Mean squares of accession were significant ( $P \leq 0.05/0.01$ ) for all the measured traits except stem girth, while mean squares of year were significant ( $P \leq 0.05/0.01$ ) for number of leaves per plant, root biomass, and harvest index. Accession × year mean squares were also found to be significant ( $P \leq 0.05/0.01$ ) for plant height, number of leaves per plant, and harvest index.

The first three principal components (PCs) jointly accounted for 88.18% of the total variation among accessions, with PCs 1, 2, and 3 having Eigen values of 2.64, 1.39, and 1.25, respectively, and explaining 44.06, 23.21, and 20.91% of the total variation in that order (Table 3). Plant height, root weight, and number of leaves per plant had high loadings ( $\geq 0.30$ ) of

Table 2 - Mean squares of measured traits of *Amaranthus* evaluated in 2018 and 2019

Source of variation	DF	PHT	NOL	STG	TBM	RWT	SWT	HI
Rep (Year)	2	4.160	7.043**	0.010	0.039	0.005	0.023	0.002
Year	1	0.481	7.346*	0.004	0.007	0.036**	0.061	0.264**
Accession	20	10.989**	9.745**	0.014	0.057**	0.007**	0.031*	0.015**
Accession × Year	20	5.800**	6.517**	0.011	0.019	0.004	0.011	0.022**
Error	40	2.110	0.332	0.008	0.023	0.049	0.015	0.005

Rep = Replicate; DF = degrees of freedom; PHT = Plant height; NOL = Number of leaves per plant; STG = Stem girth; TBM = Total biomass; RWT = Root weight; SWT = Stem weight; HI = Harvest index.

\* and \*\* significant at 5 and 1% probabilities respectively.

Table 3 - Loadings from principal component axes of the compost used in this study

Trait	Principal component axis 1	Principal component axis 2	Principal component axis 3
Plant height	0.55	-0.14	0.09
Number of leaves per plant	0.44	0.21	0.40
Stem girth	0.25	-0.14	0.57
Root weight	0.50	0.02	-0.49
Stem weight	0.27	0.66	-0.35
Harvest index	-0.23	0.69	0.37
Eigen value	2.64	1.39	1.25
Proportion (%) of variation	44.06	23.21	20.91
Cumulative (%) variation	44.06	67.27	88.18

0.55, 0.50, and 0.44 respectively in PC 1. High loadings in PC 2 were 0.69 and -0.66 observed for harvest index and stem weight respectively while PC 3 was characterized by stem girth, root weight, number of leaves per plant, harvest index, and stem weight with loadings of 0.57, -0.49, 0.40, 0.37, and -0.35, respectively. The PCA biplot grouped the amaranthus accessions into clusters over the four quadrants based on the contributions of the measured traits as explained by the PCs (Figs. 1 and 2). The accessions were scattered on the score biplot with the local check distinctly placed. Accessions NGB00022, NGB00031, NGB00060, and NGB00070 in the top left quadrant were associated with harvest index. The top right quadrant, associated with number of leaves per plant and stem and root weights, had NGB00005, NGB00019, NGB00025, NGB00058, NGB00061, and

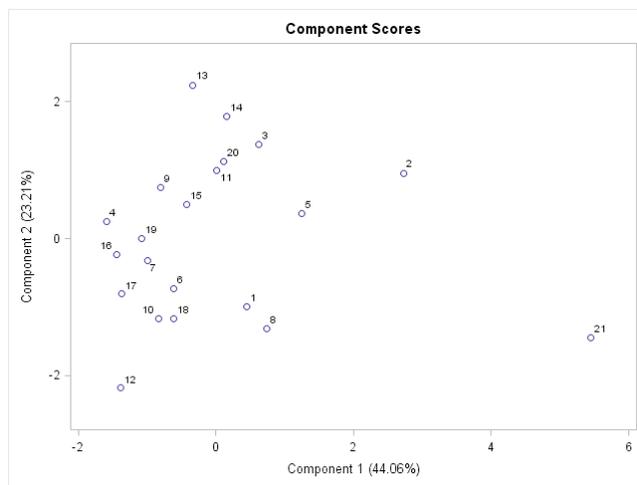


Fig. 2 - Principal components score plot for 21 Amaranthus accessions.

NGB00112 as the corresponding accessions. The bottom right quadrant, characterized by plant height and stem girth, was composed by NGB00001, NGB00029, and the Local check. Other accessions, clustered in the bottom left quadrant, were not associated with any of the traits measured in this study.

Estimates of correlation coefficient revealed significant ( $P \leq 0.05/0.01$ ) associations among pairs of measured traits (Table 4). Positive and significant ( $P \leq 0.05/0.01$ ) correlation was observed in the association of plant height with number of leaves per plant ( $r = 0.52$ ), stem girth ( $r = 0.27$ ), total biomass ( $r = 0.29$ ), and root weight ( $r = 0.47$ ). Number of leaves per plant showed positive and significant ( $P \leq 0.05$ ) correlation with stem girth, total biomass, root weight and stem weight with a correlation coefficient of 0.27, 0.24, 0.22 and 0.22, respectively. Furthermore, total biomass and root weight had a significant positive correlation ( $r = 0.70$ ;  $P \leq 0.01$ ) while there was positive and significant correlation in the association of stem weight with total biomass, root weight and harvest index ( $r = 0.93, 0.43$ , and  $0.27$ , respectively). Finally, harvest index had negative and significant correla-

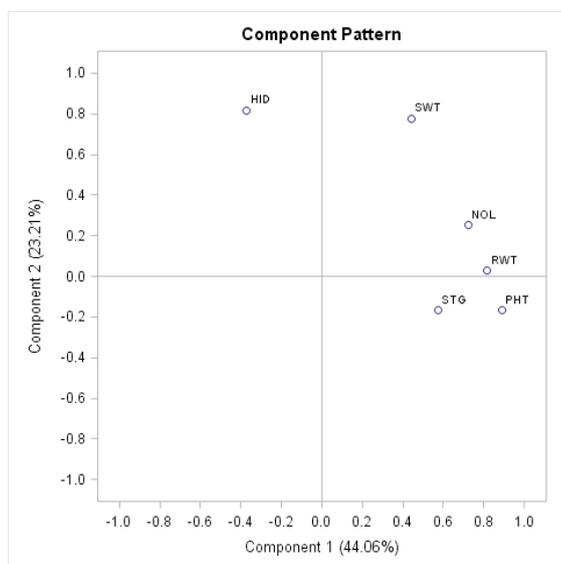


Fig. 1 - Principal component loading pattern of six traits of Amaranthus accessions.

Table 4 - Pearson correlation coefficients among measured traits of 21 Amaranthus accessions evaluated in 2018 and 2019

	NOL	STG	TBM	RWT	SWT	HI
PHT	0.52**	0.27*	0.29**	0.47**	0.14	-0.27*
NOL		0.27*	0.24*	0.22*	0.22*	0.10
STG			0.16	0.14	0.15	-0.02
TBM				0.70**	0.93**	-0.04
RWT					0.43**	-0.68**
SWT						0.27*

Re\* and \*\* significant at 5 and 1% probabilities respectively.

tions ( $P \leq 0.05/0.01$ ) with plant height ( $r = -0.27$ ) and root weight ( $r = -0.68$ ).

The estimates of genetic distance among pairwise combination of accessions based on composited traits (Table 5) ranged from 0.99 between NGB00028 and NGB00111 to 7.90 between NGB00078 and the local check. In particular, high genetic distance estimates were obtained between the local check and NGB00022 (7.45), NGB00059 (7.72), NGB00060 (7.02), and NGB00082 (7.21).

At a genetic dissimilarity of 0.50, the grouping of the accessions by the dendrogram (Fig. 3) fairly compares with the groupings on the PC scores biplot. For instance, cluster 1 was composed of eight accessions, six of which were NGB00060, NGB00058, NGB00112, NGB00025, NGB00061, and NGB00019 which were grouped together, and associated with total biomass and stem and root weights on the PC scores biplot. The other two accessions in cluster 1, NGB00031 and NGB00070, were also grouped together on the PC score plot, and were associated with harvest index. Cluster 2 contained NGB00005 and the local check. The two accessions were also grouped together by the PC score biplot, and associated with plant height, number of leaves per plant, and stem girth. Similarly, all the accessions in cluster 3; NGB00001, NGB00029,

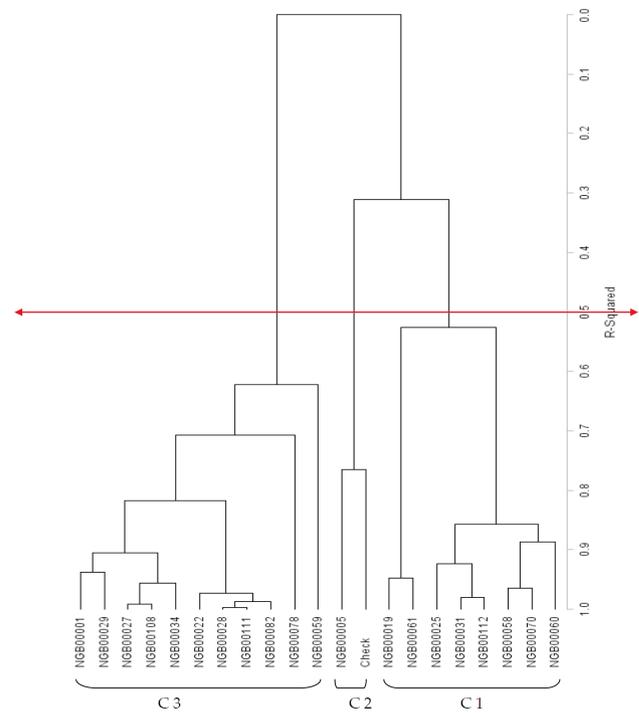


Fig. 3 - Dendrogram of relatedness among *Amaranthus* accessions, (X-axis) based on genetic dissimilarity (Y-axis) from Single-Linkage Cluster analysis. The red double-headed line delineates the accessions into clusters at approximately 0.50 level of dissimilarity; C1, C2, C3 are clusters 1, 2, and 3, respectively.

Table 5 - Pair-wise genetic distance estimates based on observed phenotypes of 21 *Amaranthus* accessions

ID	ACCESSION	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
1	NGB00001	0.00	3.62	3.86	2.52	1.82	1.37	2.13	1.65	2.34	1.62	2.73	3.81	3.91	4.02	2.27	4.23	2.58	1.84	2.47	2.44	5.33
2	NGB00005		0.00	3.68	4.89	2.26	4.36	4.50	3.88	3.80	4.80	3.39	6.27	3.94	3.50	3.50	5.66	5.32	4.77	4.73	3.11	3.81
3	NGB00019			0.00	4.14	2.97	4.24	4.54	4.93	2.82	4.71	4.00	5.09	4.45	1.54	3.70	6.57	5.08	5.21	4.83	2.61	6.33
4	NGB00022				0.00	3.19	1.42	1.19	2.97	1.69	2.14	2.23	3.79	3.01	3.88	1.68	3.28	1.54	2.06	1.26	2.26	7.45
5	NGB00025					0.00	2.67	3.07	2.70	2.15	3.06	2.35	5.10	3.10	3.20	2.45	4.98	3.75	3.19	3.17	1.63	4.79
6	NGB00027						0.00	1.00	1.80	2.12	1.35	2.37	3.38	3.58	4.14	1.70	3.26	1.41	1.15	1.45	2.46	6.39
7	NGB00028							0.00	2.10	2.21	1.85	2.01	3.55	3.17	4.17	1.31	2.47	1.12	1.25	0.99	2.52	6.80
8	NGB00029								0.00	3.34	2.52	2.55	4.16	3.96	4.94	2.52	3.54	2.28	1.56	2.27	3.06	5.07
9	NGB00031									0.00	2.53	2.18	4.31	2.69	2.57	1.63	4.26	2.93	2.94	2.41	1.33	6.76
10	NGB00034										0.00	3.32	3.54	4.27	4.56	2.46	3.67	2.31	1.52	2.35	3.25	6.79
11	NGB00058											0.00	5.06	1.54	3.69	1.51	3.41	2.62	2.65	1.75	1.48	6.10
12	NGB00059												0.00	6.32	4.96	4.01	4.94	3.43	3.87	4.34	4.80	7.72
13	NGB00060													0.00	4.03	2.58	4.15	3.78	3.81	2.72	2.15	7.02
14	NGB00061														0.00	3.10	5.78	4.93	5.05	4.60	2.61	6.74
15	NGB00070															0.00	2.90	2.32	2.29	1.81	1.78	6.36
16	NGB00078																0.00	2.88	2.87	2.73	4.50	7.90
17	NGB00082																	0.00	1.40	1.18	3.12	7.21
18	NGB00108																		0.00	1.44	3.18	6.50
19	NGB00111																			0.00	2.48	6.99
20	NGB00112																				0.00	6.00
21	Local check																					0.00

NGB00027, NGB00108, NGB00034, NGB00022, NGB00028, NGB00111, NGB00082, NGB00078, and NGB00059, except NGB00022 and NGB00001 were also grouped together on the PC scores biplot, and were not associated with any of the traits measured in this study.

The trait profiles of the *Amaranthus* accessions are displayed on the polygon view of the GYT biplot (Fig. 4). The polygon view revealed four sectors with the NGB00019, local check, NGB00060, and NGB00078 as the vertex accessions in their respective sectors. Accessions NGB00019 and NGB00061 belonged to sector 1 which was characterized by all the measured yield-trait (Y-T) combinations. This sector contained the highest ranked accessions. Sector 2 with the local check as vertex accession, also contained NGB00005 and NGB00025, thus comprising accessions that were next in rank to the accessions in sector 1. Similarly, the accessions in sector 3; NGB00060 and NGB00112, ranked next to those in sector 2 while the-poorest ranked accessions; NGB00082, NGB00059, and NGB00078, constituted sector 4. Sectors 2, 3, and 4 were not associated with

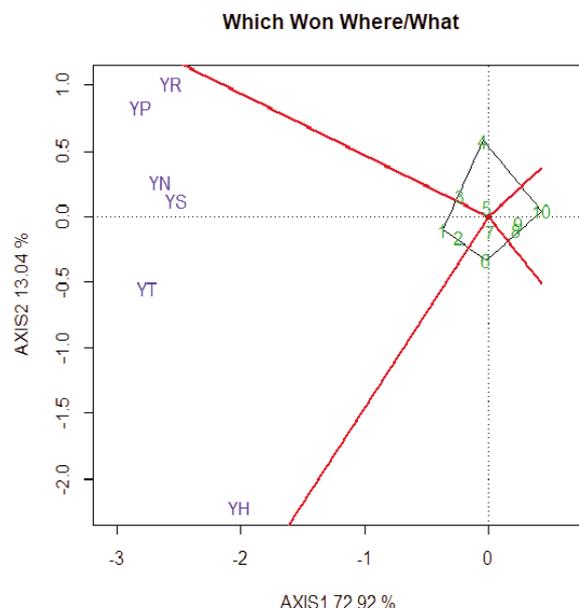


Fig. 4 - The accession x yield-trait biplot of ‘which won where’ of selected seven best and 3 worst *Amaranthus* accessions.

any of the Y-T combinations considered in this study.

The names of the accessions 1 to 10 are available in Table 6.

Table 6 - Genotype x yield-trait combination data matrix for 21 *Amaranthus* accessions evaluated in 2018 and 2019

ID on GYT biplot	Accession	YxPHT	YxNOL	YxSTG	YxTBM	YxRWT	YxHI	Superiority index
1	NGB00019	1.779	1.183	1.386	2.337	2.299	1.774	1.793
2	NGB00061	1.291	1.564	0.793	1.903	1.701	1.655	1.485
3	NGB00005	1.426	1.923	1.337	1.200	1.470	0.943	1.383
4	Local check	1.564	1.081	1.098	0.553	1.476	-0.230	0.924
5	NGB00025	0.791	0.833	1.272	0.783	0.856	0.683	0.870
6	NGB00060	0.831	1.186	1.313	0.595	-0.367	1.576	0.856
7	NGB00112	0.886	0.676	1.005	0.766	0.462	1.087	0.814
Not selected	NGB00031	0.070	0.244	0.441	0.561	0.156	0.576	0.341
Not selected	NGB00058	0.427	0.394	0.423	0.005	-0.326	0.560	0.247
Not selected	NGB00070	-0.188	0.060	-0.251	-0.244	-0.245	0.017	-0.142
Not selected	NGB00001	-0.294	-0.365	-0.041	-0.295	0.003	-0.453	-0.241
Not selected	NGB00022	-0.499	-0.537	-0.340	-0.438	-0.531	-0.101	-0.408
Not selected	NGB00111	-0.584	-0.635	-0.466	-0.710	-0.826	-0.388	-0.602
Not selected	NGB00028	-0.685	-0.633	-0.707	-0.726	-0.740	-0.576	-0.678
Not selected	NGB00027	-0.758	-0.802	-0.692	-0.694	-0.490	-0.707	-0.690
Not selected	NGB00034	-0.978	-0.748	-0.593	-0.682	-0.499	-0.822	-0.720
Not selected	NGB00029	-0.638	-0.784	-0.737	-0.825	-0.614	-0.950	-0.758
Not selected	NGB00108	-0.990	-0.959	-0.879	-0.946	-0.881	-1.005	-0.943
8	NGB00082	-0.883	-1.093	-1.010	-0.955	-0.972	-0.879	-0.965
9	NGB00059	-0.952	-1.269	-1.518	-0.874	-0.612	-1.251	-1.079
10	NGB00078	-1.617	-1.321	-1.833	-1.317	-1.318	-1.509	-1.486
Mean		0	0	0	0	0	0	
Standard deviation		1	1	1	1	1	1	

YxPHT, YxNOL, YxSTG, YxTBM, YxRWT, YxHI = Yield combination with plant height, number of leaves per plant, stem girth, root weight, and harvest index respectively.

#### 4. Discussion and Conclusions

The significant difference observed among the accessions indicated the existence of variation with respect to the measured traits except for stem girth, and underscored the possibility of selection for improvement. Idehen *et al.* (2018) reported same result for stem girth among 10 accessions of *Amaranthus* spp. On the contrary, Mandal and Dhangra (2012) studied 17 *Amaranthus* accessions and observed significant differences among the accessions for all the characters considered including stem girth. Plant height, number of leaves per plant, root biomass and harvest index can be relied upon as important tools in long term selection gain. Gerrano *et al.* (2015) found high phenotypic variability among 32 *Amaranthus* accessions using plant height, leaf length, leaf width, leaf area, leaf area index, number of leaves, stalk diameter, panicle or inflorescence length, number of primary branches, fresh biomass, dry biomass, harvest index, thousand seed weight and grain yield per plant.

The loadings of plant height, number of leaves per plant, and root weight indicated that these characters chiefly accounted for most of the variation observed among the accessions. This suggests that these traits are crucial in maintaining variability within the breeding population and they should be considered for selection in *Amaranthus* improvement programme. Gerrano *et al.* (2015) reported comparable results on 32 *Amaranthus* species of South African origin.

The positive significant correlation observed between plant height and number of leaves per plant, stem girth, total biomass, root weight and harvest index implied that direct selection for any of the trait could lead to improvement in the other. Gerrano *et al.* (2015) reported that plant height correlated positively with fresh biomass and dry biomass when evaluating the genetic diversity of *Amaranthus* species in South Africa. Thanapornpoonpong *et al.* (2007) also reported a significant and positive relationship between plant height and fresh biomass. Strong positive correlation of stem girth, total and root biomass and stem weight with number of leaves per plant, total biomass and root biomass, stem weight with total biomass, root biomass and harvest index indicated that the use of any of the characters can help to improve selection process in breeding programs. The significant negative correlation of harvest index with plant height and root

weight suggested that an attempt to breed for high harvest index will lead to short plant height and less root weight in *Amaranthus*.

The clustering pattern of accessions into groups showed the phenotypic diversity among the accessions for the different characters studied. Genetic diversity, evidenced by phenotypic variability, is essential in the initiation of a breeding program because when absent, there cannot be meaningful selection and genetic advancement becomes impossible (Govindaraj *et al.*, 2014). The accessions within a cluster are closely associated and this suggests that the variability within group could be useful in the selection process for improvement of associated desired traits. Variability between groups could be explored in heterotic breeding where members of a cluster could serve as parents in crosses involving members from distinct clusters. For instance, accessions in Cluster 1 were mostly associated with harvest index, number of leaves per plant, and stem and root weights suggesting the presence of favourable alleles for yield-related traits within the group and a potential to improve these traits via selection. Whereas, individuals in Cluster 2 were generally associated with plant height and stem girth. A cross between members of the two groups could give higher yielding progenies with good standability which would be invaluable to the vegetable industry.

The GYT biplot is useful for multiple-trait-based evaluation of accessions, permitting a graphical ranking of entries based on their levels in combining yield with related traits. Like in the GGE biplot, the GYT polygon is delineated into sectors, with their associated closely-related Y-T combinations, a vertex and other associated accessions (Yan and Frégeau-Reid, 2018). Thus, NGB00019 and NGB00061 were associated with all the Y-T combinations considered in this study which is an indication of superior trait profile. However, NGB00019 was the vertex accession and was thus identified as the best combiner of yield with other traits.

There was sufficient genetic variability among the *amaranthus* accessions, to permit improvement through selection, with greater chances of success with plant height, number of leaves per plant, and root weight. Harvest index; which is the edible portion of the plant, can be simultaneously improved with plant height, and stem and root weights. Information from principal component analysis, genetic distance estimates, and cluster analysis can

be utilized for parental selection in breeding programmes. Accessions NGB00019, NGB00025, NGB00058, NGB00060, NGB00061, and NGB00112 would be good genetic materials for total biomass, and root and stem weights while NGB00031 and NGB00070 have potentials to improve harvest index, and NGB00005 and the local check would be useful for plant height, number of leaves per plant, and stem girth. NGB00019 followed by NGB00061 had the most diverse trait profile among the evaluated accessions. Further studies involving more traits are required to determine the trait profiles of the remaining accessions used in the study.

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