

Characterisation of agro-morphological traits of *corchorus* accessions

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Abstract

Purpose: The genus *Corchorus* includes nutrient rich indigenous leafy vegetables often grown or harvested in the wild in Africa. It has potential to contribute to food security, but there is need to improve it as a crop through plant breeding. However, not much is known about the genetic variability among *Corchorus* species. The aim of this study was thus to characterise the available germplasm of *Corchorus* accessions and investigate heritability of their agro-morphological traits.

Materials and methods: Eleven *Corchorus* accessions (4 South African and 7 from the World Vegetable Center) were evaluated in a field study at Roodeplaat, South Africa, for their morpho-agronomic traits using a randomised complete block design with three replications across two seasons (2015/2016 and 2016/2017). Data were subjected to ANOVA, principal component analysis and cluster analysis. Broad sense heritability, genetic advance, genetic parameters and correlations were determined among the accessions and traits.

Results and conclusions: The *Corchorus* accessions showed significant ($P < 0.05$) differences in all the quantitative traits evaluated. The data showed significant variability among the studied *Corchorus* accessions in their agro-morphological traits for exploitation in future breeding programs that in turn can contribute to the improvement of this crop.

Keywords: Genetic diversity, genetic parameters, indigenous leafy vegetable, principal component analysis, Wild jute

Introduction

Corchorus is a genus belonging to Malvaceae family and is commonly known as, wild jute or wild okra (Jansen van Rensburg et al. 2007). It is also widely known as jute mallow in other parts of Africa (Maina et al 2012; Ngomuo et al 2017; Nyadanu et al. 2017). Africa has been reported as the center of diversity and source of origin due to high species diversity of *Corchorus* on the continent and for the reason that both wild and cultivated types, including *Corchorus capsularis* and *Corchorus olitorius*, are distributed throughout Africa (Edmonds 1990). Adebo et al. (2015) estimate that the genus *Corchorus* contains about forty species. South Africa is endowed with wide biodiversity, having a large number of well adapted indigenous leafy vegetables (ILVs) (Dweba and Mearns 2011), with *Corchorus* being one of these. The ILVs have the potential to contribute to household food security, especially for underprivileged families (Bvenura and Afolayan 2015). However, researchers, policy makers, and farmers are neglecting the potential of ILVs in contributing to food security and are more focused on well-developed and domesticated vegetables (Mwai et al. 2007).

Corchorus species are among several other ILVs that grow in the wild as weeds in South Africa. It is not formally cultivated as a food crop but is semi-domesticated in some rural parts of South Africa (Jansen van Rensburg et al. 2007). Around the world, *Corchorus* species are cultivated for their fibre content, following after cotton (Ghosh et al. 2013), but in South Africa the leaves and tender shoots are harvested and consumed as a vegetable in a form of a relish (Mavengahama et al. 2013). Its leaves are also traditionally used to treat several illnesses around the world (Mensah et al. 2008). *Corchorus* species have been reported to be very rich in nutrients and minerals (Zeghichi et al. 2004; Ndlovu and Afolayan 2008; Choudhary et al. 2013; Islam 2013). *Corchorus* has been widely reported to be highly nutritious providing considerable quantities of beta-carotene, calcium, iron zinc, essential amino acids, protein and vitamins (Ndlovu and Afolayan 2008; Nwangburuka and Denton 2012; Maina et al 2012; Choudhary et al. 2013; Adebo et al. 2015; Helaly et al 2017; Ngomuo et al 2017; Nyadanu et al. 2017). *Corchorus olitorius* has been reported to be more nutritious when compared to the widely cultivated and commercialised leafy vegetable species such as cabbage (Ndlovu and Afolayan 2008; Njeme et al. 2014).

Little information is obtainable on the improvement of *Corchorus* foliage yield (Choudhary et al. 2013). Hence, this research gap needs to be addressed in future breeding programmes (Jansen van Rensburg et al. 2007; Choudhary et al. 2013) to secure *Corchorus's* place in the commercial vegetable production arena. Despite the benefits of molecular markers, knowing the morphological variability of a species is the first step before it can be genetically improved for the traits of interest in the breeding programme (Adebola and Morakinyo 2006; Osei et al. 2010). Any breeding programme depends on genetic variability for it to be successful. Das and Kumar (2012) also stated that the progress of plant breeding programmes depend on the nature and degree of variability present in the germplasm. Genetic variability enables the breeders to have a wide range

of traits that can be used to select parents. The study was aimed at investigating the variation in morphological characters of *Corchorus* accessions with the specific aim of quantifying the available genetic variability and identifying superior lines exhibiting desirable traits.

Materials and methods

Plant material

Four of the eleven *Corchorus* accessions used in this study were sourced from Agricultural Research Council (ARC) and seven from the World Vegetable Center (WVC) genebank. The four accessions from South Africa are SA001, SA002 and SA003 which were collected in KwaZulu-Natal (KZN) province and SA004 was collected in Limpopo province.

Study site

The study was carried out in the open field on the premises of the Agricultural Research Council, Vegetable and Ornamental Plants, Roodeplaat research farm, Pretoria. Roodeplaat is situated just outside Pretoria in the Gauteng Province of South Africa at an altitude of 1159 m above sea level and at 25°59' S and 28°35' E. The monthly rainfall and the mean monthly minimum and maximum temperatures for the two growing season are shown in Figures 1 and 2, respectively.

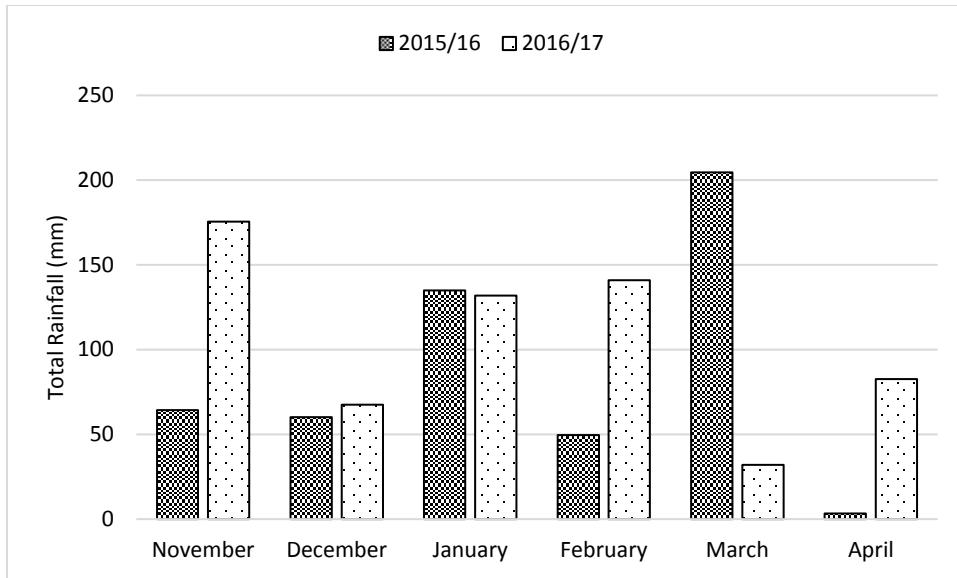


Figure 1. Total monthly rainfall received at Roodeplaat experimental farm during the duration of the experiment in 2015/16 and 2016/17 growing seasons.

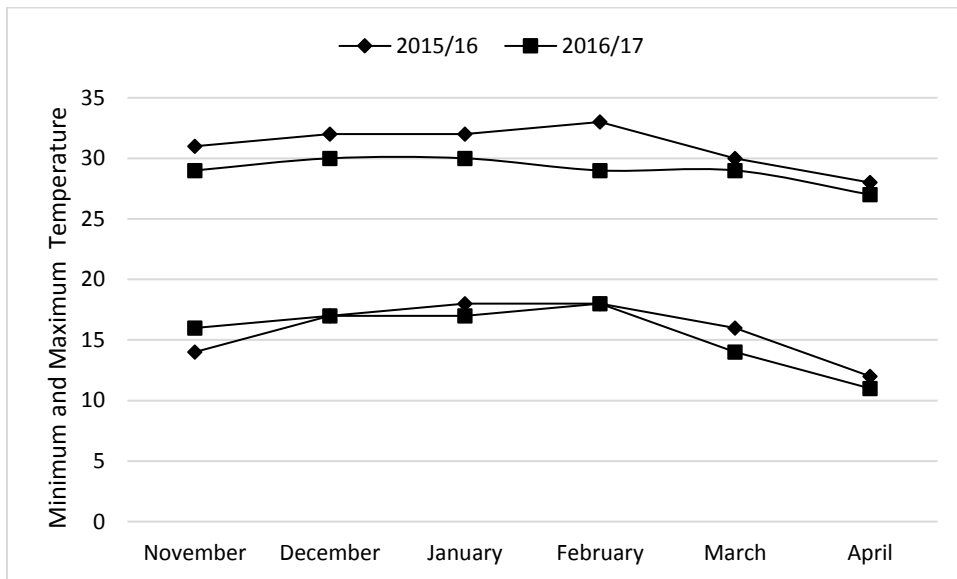


Figure 2: Mean maximum and minimum temperature (°C) at Roodeplaat experimental farm during the duration of the experiment in 2015/16 and 2016/17 growing seasons.

Experimental design and management

The agro-morphological evaluation was performed on 11 *Corchorus* accessions using a randomized complete block design with three replications. Each experimental plot had 4 rows, 3 m in length with an inter-row spacing of 50 cm and intra-row spacing of 30 cm. The experimental field was ploughed and harrowed with a tractor before the experiment started. Seedlings for each accession were germinated in trays in Hygromix® growth medium. Four weeks after emergence seedlings were transplanted to the field. The experiment was carried out over two seasons, November 2015 to April 2016 and November 2016 to April 2017. No fertilisers and chemicals (insecticides, fungicides etc.) were applied throughout the seasons since there are no registered fertilisers and chemicals for *Corchorus* in South Africa as well as to simulate the natural conditions under which it grows. Also, there were no diseases and pests noticed during the duration of the experiment in both growing seasons. Plants were kept weed free during the experiment by hand weeding. The experiment was conducted under rainfed conditions. However, supplemental overhead irrigation was applied when it was deemed necessary when plants started to show signs of wilting during some dry spells.

Data collection

Agro-morphological characterisation was conducted using a descriptor for *Corchorus* adapted from Ghosh et al. (2013). Ten plants from each accession were randomly selected from the two inner rows per plot and tagged for data collection. All traits apart from days to 50% flowering were taken at harvest maturity. Traits measured and counted are listed in Table 1.

Table 1. Quantitative trait descriptors used for characterisation of *Corchorus* accessions in the study

Traits	Code	Descriptors	How measurement was done
Days to 50% flowering	DF	Number of days from seed germination to 50% flowering	Measured as the number of number of days when half of the plants in plot had produced flowers
Plant height	PH	Plant height at maturity measured from the base of the plant to the tip of the main stem using a meter ruler (cm)	Measured from the soil surface to the tip of the highest leaf on a plant
Canopy width	CW	Canopy width at maturity measured at widest-point (cm)	Measured using a ruler at the widest point of the plant cacopy
Leaf length	LL	Length of a matured lamina from the proximal end of the mid-vein to the distal end, excluding the petiole (cm)	Measured using a ruler
Leaf width	LW	Length of matured leaf at widest-point (cm)	Using a ruler
Leaf length/leaf width ratio	LL/LW ratio	The ratio of the leaf blade length to the leaf width LL/LW	Measured as the ratio
Number of pods per plant	NPP	Total number of pods per plant	Counted as the number of matured pods with seeds inside
Pod length	PL	Pod length (cm)	Using a ruler
Pod diameter	PD	Diameter of the pod at the widest point (mm)	Measured using vernier caliper
Stem diameter	SD	Diameter of the plant base at soil level (mm)	Measured using Vernier caliper
Number of leaves	NL	Total number of leaves per plant	Counted as fully extended leaves attached to the plant
Number of branches	NB	Total number of primary branches	Counted as those branches originating on the stem only
Number of seeds	NS	Total number of seeds per pod	Pod was split and the total number of seeds inside counted
Fresh mass	FM	Total aboveground fresh mass per plant (g)	Weighed using a digital balance soon after harvesting. Included leaves branches and stems
Dry mass	DM	Total dry mass per plant (g)	Measured as the final mass obtained after drying in an oven at 60 °C until a constant mass was achieved

Source: (modified after Ghosh et al. 2013).

Data analysis

Data were subjected to ANOVA using the Genstat statistical software (12th edition, version 12.2; VNS International Ltd.2010). The least significant differences (LSD) test was applied for pair-wise comparisons of the means of traits. Differences were accepted as significant at $p < 0.05$. Multivariate analysis was performed to identify the most significant descriptors in capturing the morphological variation in the germplasm using XLSTAT statistical computer package (Version 2017.06.5). The principal component analysis (PCA) and cluster analysis (CA) were used to discriminate and group accessions, respectively. Pearson's correlation coefficients were used to decide on the relationship between selected traits.

Estimate of genetic parameters

An estimation of broad sense heritability was calculated as described by Allard (1960) in equation 1

$$H^2 = \frac{\delta^2_g}{\delta^2_p} \times 100 \dots\dots\dots (1)$$

Where H^2 represent broad-sense heritability, δ^2_g genotypic variance, δ^2_p phenotypic variance. Genotypic and phenotypic variances were obtained from the ANOVA table using equation (2) (Al-Tabbal and Al-Fraihat 2011):

$$\delta^2_g = \frac{Mg1 - Mg2}{rs}; \delta^2_p = \frac{Mg1}{rs} \dots\dots\dots (2)$$

Where r =replication, s = season, $Mg1$ = mean squares for genotype, $Mg2$ = mean square for accession by season interaction. Trait grand mean (\bar{x}) values were used for genetic parameter analysis to estimate the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) according to Singh and Chaudhary (1979) using Equations (3) and (4).

$$\text{GCV} = \frac{\sqrt{\delta^2_g}}{\bar{X}} \times 100 \dots\dots\dots (3)$$

$$\text{PCV} = \frac{\sqrt{\delta^2_p}}{\bar{X}} \times 100 \dots\dots\dots (4)$$

The genetic advance was estimated according to Farshadfar et al. (2013) as follows in Equation (5):

$$\text{GA} = \left(\frac{i \cdot \delta^2_g}{\sqrt{\delta^2_p}} \right) * 100 / \bar{X} \dots\dots\dots (5)$$

Where $i = 2.06$ is standard selection differential at 5% selection intensity.

Results

Genetic parameters

All the accessions evaluated in this study showed high variability with high significant differences in morphological traits. The phenotypic variance was higher than the genotypic variance in all traits (Table 3). High phenotypic and genotypic variance values were recorded for the number of pods per plant, number of seeds per pod, plant height, number of leaves per plant, and canopy width. Whereas low phenotypic and genetic variances values were recorded for leaf length, leaf width, the ratio of leaf length to leaf width as well as dry mass.

There were smaller differences between the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), but still the phenotypic values were a bit higher as compared to the genotypic values. The highest values were recorded for number of pods, pod diameter, leaf width and plant height. The lowest coefficient of variation values were recorded for days to 50% flowering and leaf length.

In this study, the broad-sense heritability for all the traits evaluated varied between 52% and 98%. Number of pods recorded the highest genetic advance (GA), followed by pod diameter, leaf width, plant height, and stem diameter. Leaf length recorded the lowest GA with fresh and dry mass unfortunately also on the low side (Table 3).

Correlation among traits

A strong positive correlation was observed between days to 50% flowering and the following traits: plant height, leaf width, stem diameter, pod diameter, fresh mass and dry mass (Table 5). Pod length was positively correlated with number of seeds per pod. The longer the pod the more were the number of seeds inside. Furthermore, number of branches was positively correlated with fresh mass and dry mass. Canopy width was positively correlated to number of pods per plant. Shorter accessions were spread having a larger canopy and produced more pods. A positive correlation was also observed between number of seeds per pod and pod diameter. Pods that were thick had more seeds inside whereas thin pods had few seeds inside.

A strong negative correlation was observed between days to 50% flowering and the following traits: leaf length-width ratio, canopy width, and number of pods per plant. It was observed that all accessions that flowered early produced more pods than those that flowered late. Another strong negative correlation was observed between plant height and canopy width, and also between plant height and number of pods per plant. Accessions that were taller had a narrow canopy and produced less pods whereas shorter accessions such as SA001 had a broad canopy and yielded more pods per plant. A moderate correlation was recorded between number of leaves and number of branches per plant.

Cluster analysis

A cluster analysis dendrogram clustered the 11 *Corchorus* accessions into two major clusters at 0.91 Euclidean distance based on the 15 phenotypic traits evaluated (Figure 4). The first main cluster (Cluster I) was subdivided into sub-cluster A which contained SA002 and SA004 accessions and a singleton SA001. The two accessions (SA002 and SA004) were more similar based on the highest number of pods per plant, shortest plant height with larger canopy, early flowering and low fresh and dry mass. The singleton, SA001 was more diverse than the other accessions but shares some similar characteristics with the accessions in the same cluster. SA001 flowered early, exhibited lowest number of seeds per pod, less number of branches per plant, and lowest fresh and dry mass. However, it recorded the highest number of leaves per plant, widest plant canopy width and highest number of pods per plant.

The second major (cluster II) was further subdivided into two main sub-clusters A and B. Sub-cluster A contained accessions SA003, AV003, AV005, AV001 and AV004 whereas sub-cluster B consisted of accessions AV007, AV002 and AV006. Cluster II was grouped together based on the tallest plants, larger stem diameter, lower number of pods and highest fresh and dry mass.

Principal component analysis (PCA)

The patterns of diversity were determined using multivariate analysis among accessions. Principal component analysis grouped 15 quantitative traits into 15 principal components, which accounted for the entire genetic variability among the 11 *Corchorus* accessions (Table 4). Traits that contributed the most to the variability among accessions both negative and positive loadings in the PC1 were days to 50% flowering, plant height, canopy width, pod diameter, stem diameter, dry

mass, fresh mass, number of seeds per pod, pod length, number of branches, leaf width, and number of pods per plant.

The second principal component (PC 2) had an eigenvalue of 2.59 and accounted for 17.29% of the genetic variability. In PC 2, the phenotypic attributes that mainly contributed to the variability among accessions were leaf width, pod length, leaf length, number of seeds per pod, and number of branches. The number of leaves per plant was the main contributing factor in the third principal component.

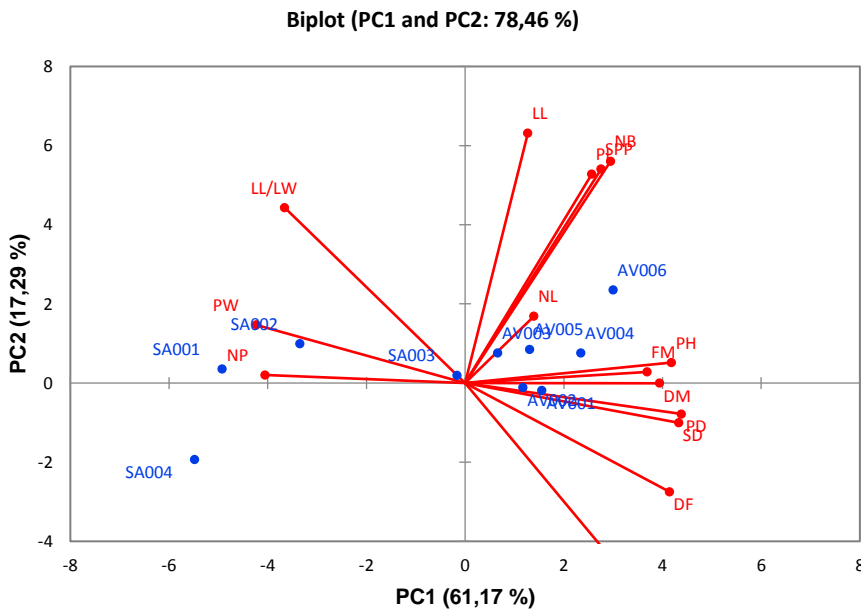


Figure 3: Principal component biplot showing variation of *Corchorus* accessions by phenotypic traits

The biplot clearly indicates the link between accessions (Figure 3). Accessions in the first and second quadrant, AV003, AV005, AV006, AV004, AV002, and AV001 are associated by plant height, high number of branches and pods per plant, wider stem and pod diameter, and high fresh and dry mass. Whereas, accessions in the opposite side, SA001, SA002, and SA004 are associated

by early flowering, widest plant canopy, high leaf length-leaf width ratio and number of pods per plant. Accession AV007 shared most characteristics with its fellow WVC accessions but slightly differed with regards to days to 50% flowering and leaf width.

Discussion

Morphological characterisation of plant species is an important step in crop improvement programmes as it permits breeders to identify and select superior lines for further crop advancement (Adebola and Morakinyo 2006; Das and Kumar 2012; Julia et al 2016; Peratoner et al 2016; Ngomuo et al. 2017). In this study, the *Corchorus* accessions were evaluated in the field for agro-morphological traits and revealed huge variability in days to 50 % flowering, plant height, canopy width, leaf length, leaf width, petiole length, stem and pod diameter, pod length, number of leaves, branches and pods per plant, number of seeds per pod, and fresh and dry mass as shown in Table 2. Similar findings to these presented were also reported by Benor et al. (2012) who described significant differences among accessions of *Corchorus olitorius* and Maina (2012, Nwangburuka and Denton (2012), Adebo (2015 and Ngomuo et al. (2017) who also observed variability in different *Corchorus* morphotypes for quantitative traits. Gichimu et al. (2009) also recorded significant variation among wild and cultivated species of watermelon. Oyekale et al. (2014) reported significant positive variation in 11 quantitative traits of *Corchorus olitorius* and Ahmed et al. (2016) reported significant variation in agro-morphological traits for 32 rice genotypes. The existence of significant genetic variability among the accessions indicate the potential for exploiting the evaluated germplasm for the improvement of the crop (Gerrano et al. 2014) in South Africa.

Table 2: Analysis of variance for 15 quantitative traits of 11 *Corchorus* accessions evaluated in the field for combined seasons

Traits	Year	Rep.	Accessions	S*S	Residual	CV%	GM
df	1	2	10	10	42		
DF	946.5*	15.6	117.3**	5.3 ^{ns}	12.4	6.5	53.8
PH	25750.5**	37.7	11494.5**	1246.5**	5.3	1.9	121.0
CW	626.8**	14.2	1004.4**	479.4**	5.5	4.8	48.5
LL	7.2**	1.1	3.7**	1.0**	0.2	4.9	8.0
LW	4.2**	0.2	7.1**	0.6**	0.1	10.8	2.9
LL/LW	2.8**	0.1	4.6**	1.0**	0.1	8.0	3.1
SD	141.4**	9.2	96.4**	15.4**	0.6	6.3	12.2
PL	3.3**	0.2	21.4**	0.6**	0.2	6.8	6.6
PD	6.6**	0.9	25.1**	0.5**	0.1	7.8	4.0
NL	26008.3**	293.1	10404.7**	2629.7**	36.9	3.9	157.3
NB	423.6**	10.1	154.9**	44.4**	1.0	5.9	16.6
NP	8033.4**	24.8	40357.3**	7348.5**	17.2	4.7	88.0
SPP	27585.0**	298.2	13917.8**	1616.5**	106.1	7.1	145.0
FM	1102.1**	1.9	148.6**	69.3**	0.8	5.9	15.5
DM	78.6**	1.2	6.7**	1.8**	0.2	11.5	4.3

*CV-coefficient of variation; GM-grand mean; S*S- season by species; *-significant; ** -highly significant; ns- not significant; DF- days to 50% flowering; PH-plant height; CW-canopy width; LL-leaf length; LW-leaf width; LL/LW ratio; SD-stem diameter; PL-pod length; PD-pod diameter; NL-number of leaves per plant; NB-number of branches per plant; NP-number of pods per plant; SPP-number of seeds per pod; FM-fresh mass; DM-dry mass.

The genetic parameters such as genetic variances and heritability are very important in selection for superior parental lines in breeding programmes (Alvi et al. 2003; Nwangburuka and Denton 2012). As displayed in Table 3, the *Corchorus* accessions evaluated in this study revealed relatively high genotypic and phenotypic variance values for plant height, canopy width, number of leaves, number of pods per plant, and number of seeds per pod. This is an indication that the genotype could be reflected by the phenotype and these traits could be selected and utilised in the breeding programme as also suggested other researchers (Nwangburuka and Denton 2012; Nyadanu and Dikera 2014). Furthermore, the high values of PCV and GCV obtained in the present study suggest that there is sufficient genetic variability among the accessions to facilitate

improvement through selection of the desirable traits as suggested by Shukla et al. (2006). There were very small differences between GCV and PCV, with PCV slightly higher than GCV in all traits. According to Alvi et al. (2003) the low differences in GCV and PCV indicates that there is a low environmental effect in the development of these traits. These results are in conformity with the findings by Shukla et al. (2006), Denton and Nwangburuka (2012) who reported small differences between GCV and PCV.

Table 3: Genetic parameters for quantitative traits in 11 *Corchorus* accessions

Variables	δ^2g	δ^2p	GCV	PCV	H ²	GA
DF	56.0	58.7	13.9	14.2	95.5	28.0
PH	5124.0	5747.2	59.2	62.7	89.2	115.1
CW	262.5	502.2	33.4	46.2	52.3	49.8
LL	1.3	1.8	14.4	16.9	72.9	25.3
LW	3.2	3.5	61.5	64.3	91.2	120.9
LL/LW	1.8	2.3	43.3	49.1	77.8	78.7
SD	40.5	48.2	52.2	57.0	84.1	98.6
PL	10.4	10.7	49.0	49.8	97.0	99.4
PD	12.3	12.5	88.7	89.6	98.0	180.9
NL	3887.5	5202.1	39.7	45.9	74.7	70.6
NB	55.3	77.5	44.8	52.1	71.4	78.0
NP	16161.9	20178.6	144.4	161.4	80.1	266.3
SPP	6150.7	6958.9	54.1	57.5	88.4	104.7
FM	39.6	74.3	40.8	55.8	53.3	34.2
DM	2.4	3.3	36.2	42.5	72.4	63.4

* δ^2g -genotypic variance; δ^2p -phenotypic variance; GCV-genotypic coefficient of variation; PCV-phenotypic coefficient of variation; H² –broad sense heritability; GA-genetic advance; DF- days to 50% flowering; PH-plant height; CW-canopy width; LL-leaf length; LW-leaf width; LL/LW ratio; SD-stem diameter; PL-pod length; PD-pod diameter; NL-number of leaves per plant; NB-number of branches per plant; NP-number of pods per plant; SPP-number of seeds per pod; FM-fresh mass; DM-dry mass.

The heritability estimates provide an indication of which trait could be transmitted from parent to an offspring (Usman et al. 2014; Khan et al. 2015). However, effectiveness of selection does not only depend on heritability but also on genetic advance. A combination of high GCV, high broad-

sense heritability (H^2), and genetic advance (GA) is the best for selection (Tefera et al. 2003; Nwangburuka and Denton 2012). When the GA and heritability are high for a certain trait it is mainly due to an additive gene effect (Shukla et al. 2006). In this study high GCV, H^2 , and GA were recorded for plant height, number of leaves per plant, pod length, number of pods per plant, and number of seeds per pod. These findings suggest the effect of additive genes in the inheritance of these traits. Similar results have also been reported by Immanuel et al. (2011) for grain yield and yield trait in 21 rice genotype and Denton and Nwangburuka (2012) for 6 yield and yield related traits in 15 *Corchorus* species.

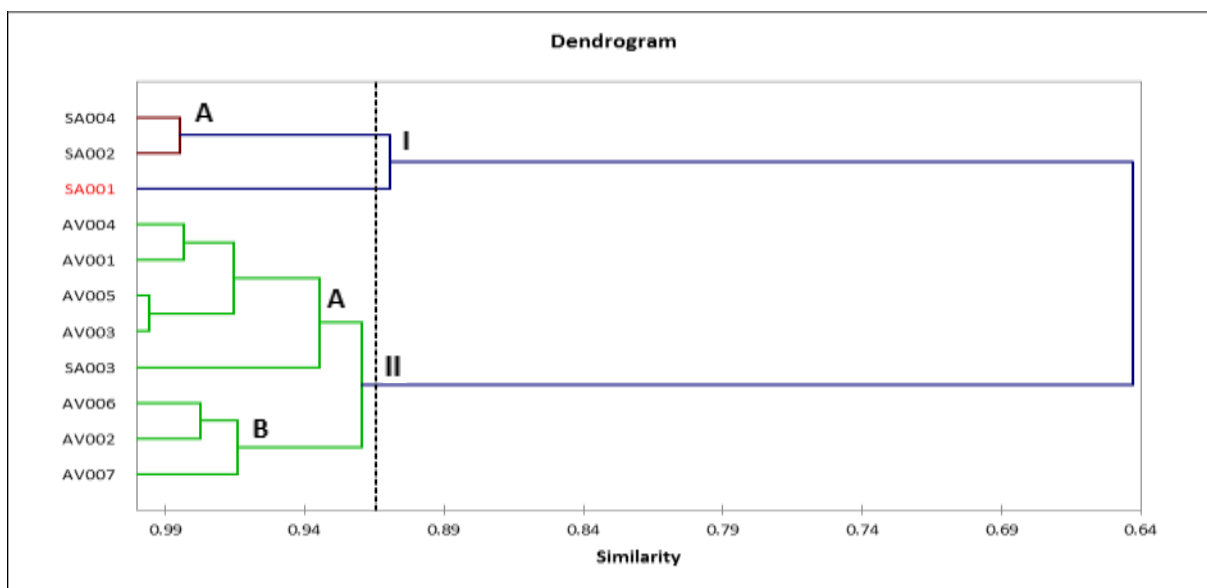


Figure 4: Hierarchical cluster analysis dendrogram displaying relationship among 11 *Corchorus* accessions using quantitative traits

The cluster analysis demonstrated the existence of variability among the 11 *Corchorus* accessions for the morphological traits studied (Figure 4). The clustering pattern shows that accessions from WVC were genetically distant from the ARC accessions and can be used to improve one another. Accessions from the same research centre were grouped together but there was also sub-clustering

of the major clusters, suggesting that was still variation within clusters. The clustering also revealed some singletons. Singletons are those accessions that are placed separately from the rest of the accessions in a cluster. They are more diverse and are to be given special attention during selection because of their superiority over other accessions as suggested by Choudhary et al. (2013).

Table 4: Principal component analysis (PCA) for quantitative traits of 11 *Corchorus* accessions

Traits	PC 1	PC 2	PC 3	PC 4	PC 5
Eigenvalue	9.18	2.59	1.19	0.72	0.65
Variability %	61.17	17.29	7.95	4.82	4.30
Cumulative %	61.17	78.46	86.41	91.23	95.54
Factor loading					
DF	0.92	-0.36	-0.02	-0.07	0.03
PH	0.93	0.06	0.00	0.27	0.18
CW	-0.94	0.17	-0.01	-0.12	0.13
LL	0.28	0.74	-0.03	0.42	0.40
LW	0.73	-0.58	0.06	0.15	0.07
LA	-0.81	0.52	0.09	0.00	0.18
SD	0.96	-0.12	0.09	0.19	-0.06
PL	0.57	0.62	-0.45	0.00	-0.20
PD	0.97	-0.09	-0.14	0.03	0.00
NL	0.31	0.20	0.87	0.18	-0.25
NB	0.65	0.66	0.22	-0.19	-0.01
NP	-0.90	0.02	0.29	-0.10	0.03
SPP	0.61	0.64	-0.08	-0.18	-0.35
FM	0.82	0.03	0.20	-0.36	0.36
DM	0.87	0.00	0.09	-0.37	0.20

*DF- days to 50% flowering; PH-plant height; CW-canopy width; LL/LW ratio; leaf length; LW-leaf width; LA-leaf length-leaf width ratio; SD-Stem diameter; PL-pod length; PD-pod diameter; NL-number of leaves per plant; NB-number of branches per plant; NP-number of pods per plant; SPP-number of seeds per pod; FM-fresh mass; DM-dry mass.

The principal component analysis explained the genetic diversity of the evaluated accessions.

Principal component analysis measures the contribution of each component to total variance, while

each factor loading specifies the amount of contribution of every trait with each principal component associated with that trait (Nachimuthu et al. 2014). Each trait was regarded as an important contributor to the variability in a component if its factor loading had total value ≥ 0.40 , irrespective of the plus or minus sign as also reported by other researchers (Nsabiyera et al. 2012; Nachimuthu et al. 2014). The first two components accounted for 78.46% of the total variance. The PC1 accounted for 61.17% and PC2 for 17.29% of variation (Table 4). These results are similar to the findings by Denton and Nwangburuka (2012) who reported the first two PCs in their study accounting for 80.45% variation with PC1 and PC2 accounted for 56.80% and 23.60%, respectively, among the 15 *Corchorus olitorius* genotypes.

Seven of the accessions were clustered together in relation to their traits in the first and second quadrants had a high level of similarity and are regarded as closely related. However, accessions SA001, SA002, SA003, and AV007 were isolated from the rest of the accessions and are considered to be more diverse and could be used for *Corchorus* improvement. Gerrano et al. (2015) reported similar findings among 32 amaranthus genotypes.

A strong positive correlation was observed between plant height and stem diameter, the taller the stem grew the thicker the stem (Table 5). Oboh (2007) also reported a positive correlation between plant height and stem diameter ($r^2=0.65$) in *Amaranthus hybridus* accessions. Such a relationship in which taller plants have thicker stems suggests the ability of the stem to provide stronger support to a bigger canopy. Adeyinka and Akintade (2015) also suggested that a strong positive correlation between plant height and thick stem is an indication of plant vigour. Another strong positive correlation was observed between days to 50% flowering and plant height, number of seeds per pod and pod diameter, number of branches and fresh and dry mass. Ghosh et al. (2013) and Nyadanu et al. (2017), similarly found a positive correlation between days to 50% flowering and

Table 5: Correlation table for 15 quantitative traits of *Corchorus* accessions evaluated in the field

TS	DF	PH	CW	LL	LW	LL/LW	SD	PD	PL	NL	NB	NP	SPP	FM	DM
DF	1														
PH	0.79	1													
CW	-0.90	-0.90	1												
LL	-0.01	0.46	-0.10	1											
LW	0.85	0.65	-0.72	-0.09	1										
LL/LW	-0.95	-0.66	0.86	0.21	-0.91	1									
SD	0.90	0.94	-0.95	0.22	0.79	-0.83	1								
PD	0.95	0.89	-0.92	0.23	0.76	-0.85	0.93	1							
PL	0.36	0.52	-0.42	0.56	0.04	-0.21	0.46	0.57	1						
NL	0.20	0.30	-0.31	0.19	0.18	-0.10	0.40	0.17	-0.04	1					
NB	0.38	0.60	-0.51	0.57	0.06	-0.18	0.54	0.53	0.68	0.48	1				
NP	-0.79	-0.88	0.90	-0.25	-0.60	0.75	-0.86	-0.89	-0.58	-0.05	-0.49	1			
SPP	0.38	0.47	-0.45	0.47	0.07	-0.25	0.47	0.53	0.84	0.31	0.81	-0.55	1		
FM	0.77	0.71	-0.67	0.23	0.56	-0.57	0.70	0.76	0.33	0.27	0.68	-0.60	0.45	1	
DM	0.79	0.76	-0.74	0.16	0.60	-0.64	0.77	0.81	0.40	0.25	0.62	-0.76	0.54	0.93	1

*TS-traits; DF- days to 50% flowering; PH-plant height; CW-canopy width; LL-leaf length; LW-leaf width; LL/LW ratio; SD-Stem diameter; PL-pod length; PD-pod diameter; NL-number of leaves per plant; NB-number of branches per plant; NP-number of pods per plant; SPP-number of seeds per pod; FM-fresh mass; DM-dry mass.

plant height, and stem diameter and plant height in *Corchorus* species. Plants that flower late have more time to grow taller and are able to grow more foliage, thus ensuring higher yield. Such plants are useful as parents for the development of cultivars with a prolonged growing and harvesting period, which trait is highly desirable in *Corchorus* and other leafy vegetables. The positive correlation between and among the traits is an indication that selecting and improving the primary desirable traits would have a positive effect on the secondary traits in the breeding programme (Gerrano et al. 2015).

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