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EVALUATION OF GENETIC DIVERSITY IN AGRONOMIC TRAITS AMONG DUAL-PURPOSE COWPEA GENOTYPES IN KENYA

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ABSTRACT

Availability of diverse genetic materials is central in any plant breeding programme. Genetic diversity is important in ensuring survival of a species; and buffering of crops from climate change effects through crop improvement programmes. The objective of this study was to determine the genetic diversity among a panel of dual purpose cowpea (*Vigna unguiculata* L.) genotypes to inform crop breeding programmes in Kenya. The study was conducted at the Jomo Kenyata University of Agriculture and Technology (JKUAT) Demonstration Farm in Kenya; during four cropping seasons (2021-2022). A total of 224 dual-purpose cowpea (*Vigna unguiculata* L.) genotypes were evaluated using an alpha lattice design with two replications. Data were recorded on agronomic traits, and were subsequently subjected to correlation and principal component analysis (PCA), biplot and hierarchical cluster analyses. Total grain yields positively correlated ($P<0.05$) with grain yield per row and pods plant^{-1}. Principal component analysis dissected total variation into three components, namely PC1, PC2 and PC3. The first three PCs (with eigenvalues >1), accounted for 71.6% of the total variability among the accessions. PCA and Bi-plots showed that pods plant^{-1}, grain yield plant^{-1} and per row were the best (farthest from the origin indicating largest divulgence) agronomic traits for selection towards improvement of Kenyan dual- purpose cowpea genotypes. The dendrogram also grouped the genotypes into three clusters, namely I (101), II (53) and III (70). There was congruence between the PC and hierarchical cluster in grouping the accessions, based on the Euclidean distance; with the highest values to be used for genetic improvement. The genotypic and phenotypic differences among the accessions could be leveraged as a basis for genetic improvement, through selection and crossing of parents with desired phenotypic traits in future breeding programmes.

Key Words: Bi-plots, hierarchical cluster, *Vigna unguiculata*

RÉSUMÉ

La disponibilité de matériel génétique diversifié est essentielle à tout programme de sélection végétale. La diversité génétique est importante pour assurer la survie d’une espèce et pour protéger les cultures des effets du changement climatique grâce à des programmes d’amélioration des cultures. L’objectif de cette étude était de déterminer la diversité génétique d'un panel de génotypes de niébé à double usage (*Vigna unguiculata* L.) afin d'éclairer les programmes de sélection végétale au Kenya. L'étude a été menée à la ferme de démonstration de Jomo Kenyata University of Agriculture and Technology (JKUAT) au Kenya, pendant quatre saisons de culture (2021-2022). Au total, 224 génotypes de niébé (*Vigna unguiculata* L.) à double usage ont été évalués à l'aide d'une conception de réseau alpha avec deux réplications. Les données ont été enregistrées sur les caractères agronomiques, puis soumises à une analyse de corrélation et de composantes principales (PCA), à des analyses de biplot et de cluster hiérarchique. Les rendements totaux en grains étaient positivement corrélés ($P<0{,}05$) avec le rendement en grains par rang et par gousses par plante^{-1}. L'analyse des composantes principales a disséqué la variation totale en trois composantes, à savoir PC1, PC2 et PC3. Les trois premières composantes principales (avec des valeurs propres > 1) représentaient 71,6 % de la variabilité totale entre les accessions. PCA et les bi-plots ont montré que les gousses plante^{-1}, le rendement en grains plante^{-1} et par rangée étaient les meilleurs caractères agronomiques (les plus éloignés de l'origine indiquant la plus grande divulgation) pour la sélection en vue de l'amélioration des génotypes de niébé à double usage du Kenya. Le dendrogramme a également regroupé les génotypes en trois groupes, à savoir I (101), II (53) et III (70). Il y avait une congruence entre le PC et le groupe hiérarchique dans le regroupement des accessions, sur la base de la distance euclidienne; les valeurs les plus élevées étant utilisées pour l'amélioration génétique. Les différences génotypiques et phénotypiques entre les accessions pourraient être exploitées comme base pour l'amélioration génétique, par la sélection et le croisement de parents présentant les traits phénotypiques souhaités dans les futurs programmes de sélection.

Mots Clés: Bi-parcelles, cluster hiérarchique, *Vigna unguiculata*

INTRODUCTION

Cowpea (*Vigna unguiculata* (L.) Walp) is by far the most important indigenous pulse crop in sub-Saharan Africa (SSA), playing key roles in the livelihoods of communities. Its seeds and leaves provide proteins, vitamins and minerals; while its haulms are used as a nutritious animal feed or silage (Araméndiz-Tatis *et al.*, 2018). Besides, cowpea greatly enhances soil fertility through symbiotic biological nitrogen fixation (Edematie *et al.*, 2021) .

Genetic diversity in crops like cowpea, is important as it ensures a means of survival for plant species. It buffers crops from climate change and can be conserved through germplasm collection, conservation and utilisation within crop improvement programmes (Mukhopadhyay and Bhattacharjee, 2016). Genetic diversity can be assessed using variation in morphological traits, isozymes, DNA markers and seed protein (Salgotra and Chauhan, 2023).

Preference of cowpea varieties among farmers and consumers varies in terms of grain yield, drought tolerance, time to physiological maturity, pest resistance, capacity to improve soil fertility, cooking time, storage quality, palatability and rate of growth attributes (Karikari *et al.*, 2023). Patil *et al.* (2022) revealed positive correlations between grain yield with days to 50% flowering, number of seeds pod^{-1} and pod length. Nkoana *et al.* (2019) also reported that grain yield ha^{-1} correlated positively with number of pods plant^{-1} and grain yield plant^{-1}; thus indicating that the traits were important in cowpea yield improvement through direct selection. Owusu *et al.* (2021) and Kindie *et al.* (2022) conducted PCA and Cluster Analysis that are essential for grouping the genotypes, to provide the breeder with an opportunity to select appropriate parents for crossing.

However, cowpea as a minor crop with diverse uses, its evaluation for genetic variability has been limited (Chen *et al.*, 2017), due to scanty attention, thus rendering it an "orphan crop".

In order to permit efficient genetic improvement, a basis for crossing parents with improved agronomic superiority is necessary, and that calls for assessment of genetic diversity and identification of parental lines for crossing and hybridisation (Salgotra and Chauhan, 2023; Begna and Teressa, 2024).

The objective of this study was to determine genetic diversity among a panel of dual-purpose cowpea (*Vigna unguiculata* (L.) Walp) genotypes to inform crop breeding programmes in Kenya.

MATERIALS AND METHODS

Experimental site. The experiment was conducted over four cropping seasons, in the experimental field of Jomo Kenyatta University of Agriculture and Technology (JKUAT), Juja in central Kenya. The site is located at latitude 3° 35"S and longitude of 36º 35"E. The site experiences semi-arid continental monsoon climate type, with a mean annual temperature of 19.8 °C, and annual precipitation of 675.8 mm (Jaetzold *et al.*, 2007).

The area has three soil types, which are shallow clay soils over trachytic tuff, very shallow sandy clay soils over murram; and deep clay (Vertisols) soils (Soil Survey Staff, 2010). The pH ranged from 5.2 to 5.8 in the top soil and from 4.8 to 7.0 in the sub-soil (Bankole *et al.*, 2016).

Experimental materials. The experiment was conducted using 224 genotypes, obtained from the Legumes Breeding Project of JKUAT. The genotypes comprised of the following as illustrated in Table 1.

Treatments and design. Treatments included 224 cowpea genotypes, laid out in an alpha lattice design, with incomplete blocks design and with two replications. Plant spacing was 50 cm between and 30 cm within rows; while plot size was 5 m by 1 m. The study was repeated four times during 2021 and 2022, long and short rain seasons.

Routine field maintenance. Fertiliser application 60 kg ha^{-1} P_2O_5 as single super phosphate (SSP); 60 kg ha^{-1} N in the form of urea; and 50 kg ha^{-1} K as muriate of potash. SSP was applied all at planting; while the latter

TABLE 1. Characteristics of the cowpea genotypes used in the study

Genetic materials	Locality	Specific locality	Number of accessions
National Gene Bank of Kenya	Lower Eastern Kenya	Machakos	74
		Makueni	3
		Kitui	5
Landraces	Lower Eastern Kenya	Machakos	14
	Rift-valley	Baringo	9
Single plant selections			113
Commercial varieties	Registered seed companies		6
Total			224

two were applied in two splits, half at planting and the rest at 20% flowering.

Supplementary irrigation was done at the rate of 20 mm per week, during dry spell, usually in the months of June-September 2021 and June-December, 2022. Insecticides were sprayed once at vegetative growth, flowering and pod maturing stages; using Dimethoate 50% to control aphids at the rate of 1 litre ha^{-1}. Hand weeding was done thrice, at three weeks after planting (two to three leaves stage), at two months after planting, and at 75 days after planting, to ensure weed-free plots.

Data collection. Data were collected on eight agronomic traits (days to 50% flowering and 75% physiological maturity, pod length, seed pod^{-1}, pods plant^{-1}, grain yield plant^{-1} and row^{-1}; and seed yield ha^{-1}) (Table 2), based on the International Board for Plant Genetic Resources descriptors for cowpea (IBPGR, 1983). To avoid border effects, a composite sample of three randomly selected plants, were taken from each plot in the centre row.

Statistical analysis. The data collected were subjected to analysis of variance (ANOVA), using the *Agricolae* package in RStudio Version 4.2.2 software (R Core Team, 2022). Mean separation was done using Least Significant Differences (LSD) at 5% level of significance. The genotypic mean values were standardised to a mean zero and a variance of unity, using R Studio Version 4.3.1 software; before analysis, to remove biases due to differences in the scale of measurements.

The means were then used to calculate phenotypic correlation, using *Corrplot* package at $P < 0.05$. Principal components, Eigen values and scores were computed using correlation matrix in *ggbiplot* package; and hierarchical cluster analyses were performed using Ward's Method. A dendrogram was constructed using *Hclust* package in R (R Core Team, 2022).

RESULTS AND DISCUSSION

Days to 50% flowering and to 75% maturity. Days to 50% flowering was not significant among the tested cowpea genotypes ($P>0.05$); however, days to physiological maturity was highly significant ($P <0.001$) for the test genotypes evaluated (Table 4).

The days to 75% maturity was significantly shorter for genotypes 52 (GBK 003682), 177 (selection from within variety), 137 (GBK 022545) and 128 (GBK 022473). The high variation among cowpea genotypes underscores the significance of genetic variation as an input in the Kenyan cowpea breeding programmes (Dorvlo *et al*., 2022). This provides the requisite genetic information for the selection of useful parents for application in a cowpea improvement programme that would contribute substantially to food security in sub-Saharan Africa.

Similar findings were reported by Gerrano *et al*. (2015) and Mofokeng *et al*. (2020), that early flowering might be attributed to inherent genetic variation in cowpea, as well as prevailing environmental factors, such as altitude, temperature and soil conditions. Furthermore, flowering time varies significantly among cowpea genotypes and is influenced by environmental factors prevalent during growth and development. Kinfe and Tsehaye (2015) also opined that genotypes should be first screened for genetic diversity, to ensure success in developing new high yielding cultivars; by relying on the availability of genetically diverse germplasm (Buckler *et al.,* 2009). The higher the genetic diversity possessed, the greater the prospects for improvement of traits of interest; as well as increasing chances for developing new superior high yielding cultivars, with consistent performance.

The significant seasonal differences between the long and short rains arise from environmental differences, particularly as a result of rainfall and temperatures. The short

TABLE 2. List of quantitative traits recorded in field trials for morpho-agronomic variability

Trait	Denotation	Unit	Description
Phenological traits			
Flowering days	DTF	Days	Number of days from date of seedling emergence to when 50% of plants have at least one open flowers
Maturity days	DTM	Days	Number of days from date of seedling emergence to date when 90% of plants have reached physiological maturity
Yield and yield components			
Pods plant^{-1}	NPP	no	Average total number of pods from five randomly tagged plants per plot at maturity
Pod length	PL	no	Average length of five randomly tagged plants pods from each plot using a ruler
Seeds pod^{-1}	SPP	no	Average number of seeds from five randomly selected pods from each plot
Grain yield plant^{-1}	GYP	g	Average yield plant^{-1}
Grain yield row^{-1}	GYR	g	Average yield row^{-1}
Grain yield ha^{-1}	TW	Kg ha	Total seed yield per plot extrapolated to yield ha^{-1}

Source: Author’s work

TABLE 3. Four seasons analysis of variance for yield and yield-related traits among 224 dual-purpose genotypes evaluated in JKUAT in 2021 and 2022

SV	Df	BLUPs-DTF	BLUPs-DTM	BLUPs-PL	BLUPs-NPP	BLUPs-NSP	BLUPs-GYP	BLUPs-GYR	BLUPs-TW
Genotype Unadj.	223	<2.2e-15***	<2.2e-17***	<2.22e-16***	<2.22e-16***	1.744e-4***	<2.22e-16***	<2.22e-15***	<2.22e-15***
Geno.Seas	224	1.14e-11***	1.937e-11***	1.38e-4***	7.63e-4***	1.61e-2*	8.706e-4***	0.663ns	0.735ns
Seas.Rep	1	4.54e-2*	0.789ns	0.346ns	0.0722ns	0.4853ns	0.870ns	0.215ns	0.380ns
MS. Residual	446	8.424	14.389	0.384	40.135	3.6955	84.93	2369	2568
CV%		8.15	4.57	6	27.82	14	27.4	11.41	10.89

TABLE 4. Combined seasons analysis of variance for yield and yield-related traits among 224 dual-purpose genotypes evaluated in JKUAT in 2021 and 2022

SV	Df	BLUPs-DTF	BLUPs-DTM	BLUPs-PL	BLUPs-NSP	BLUPs-NPP	BLUPs-GYP	BLUPs-GYR	BLUPs-TW
Rep	1	0.509^{ns}	0.0065**	0.299^{ns}	0.455^{ns}	0.587^{ns}	0.603^{ns}	1.14e-10***	0.880^{ns}
Genotype Unadj	223	0.969^{ns}	0.021*	<2e-16 ***	0.012 *	<2e-16 ***	<2e-16 ***	2.09e-295***	<2e-16 ***
Block/Rep	12	0.883^{ns}	0.330^{ns}	0.373^{ns}	0.445^{ns}	0.383^{ns}	0.109^{ns}	0.437^{ns}	0.119^{ns}
MS Residual	211	8.59	27.13	2.714	2.915	38.72	60.14	1106	3502
CV (%)		6.54	5.55	10.33	12.43	23.73	22.1	7.2	12.67

Note: SV = Source of variation, df = Degree of freedom, DTF = Days to flowering (days), DTM = Days to maturity (days), PL = Pod Length (cm), NSP = Number of seeds per pod, NPP = Number of pods per plant; GYP = Grain yield per plant; TW = Grain yield per plot; CV = Coefficient of Variation, ns: not significant, *, **, *** = significant (at 0.05, 0.01, 0.001 level, respectively)

TABLE 5. Descriptive statistics for days to flowering, days to maturity and yield- related traits for 224 dual-purpose cowpea accessions grown at Juja in 2021 and 2022

Traits	Seas.	Mean	Range		MSE	SE	MSS	CV%	P.value
			Max	Min					
DTF	SR	41	55	25	2.416	3.416	43.36	8.3	<0.001
	LR	40.94	56	27	3.796	2.684	38.55	9.27	<0.001
	CSR	40.91	52	28.5	1.354	1.915	37.274	4.7	<0.001
DTM	SR	94.14	118	78	3.207	4.536	89.45	4.78	<0.001
	LR	94.18	116	78	3.181	4.499	90.81	4.8	<0.001
	CSR	94.16	115.5	79.5	2.718	1.926	82.713	2.9	<0.001
PL	SR	16.44	23.73	10.5	0.6617	0.9358	7.008	5.7	<0.001
	LR	16.52	23.6	11.03	0.7119	1.0067	6.357	6.1	<0.001
	CSR	16.48	24.07	11.65	0.508	0.719	6.167	9.5	<0.001
NPP	SR	25.04	57	7	5.342	7.554	115.403	31.6	<0.001
	LR	25.04	66	5.67	4.672	6.608	4.209	26.4	0.106
	CSR	24.48	61	7.94	3.103	4.389	109.37	17.9	<0.001
NSP	SR	14.24	28.67	8.67	1.547	2.188	5.049	15.4	0.344
	LR	14.45	20.67	9.67	1.3344	1.88871	4.209	15.4	<0.001
	CSR	14.34	22	9.84	0.968	1.37	2.766	9.5	0.002
GYP	SR	35.99	114.7	11	8.588	12.145	288.5	33.7	<0.001
	LR	35.86	88.5	7.33	6.2	8.768	241.5	24.5	<0.001
	CSR	35.92	89.83	10.1	4.066	5.75	231.7	16	<0.001
GYR	SR	420.6	913.7	81	35.71	50.5	46721	12	<0.001
	LR	425.8	1070	96.67	32.91	46.55	50464	10.9	<0.001
	CSR	423.2	1036	100.5	23.89	33.79	47460	8	<0.001
TW	SR	457.4	943	100	36.93	52.23	46804	11.44	<0.001
	LR	461.6	1101	118	33.94	48	52400	10.4	<0.001
	CSR	459.5	1070	119.5	35.31	24.94	48980	7.7	<0.001

season is characterised by higher temperatures, triggering early termination of the flowering phase and initiation of the reproductive phase. Genotypes that flower early and mature early, tend to be more adapted to warm- or tropical season food legumes than their late maturing counterparts (Sita *et al.*, 2017).

In the present study, 10 genotypes were found to mature earlier than the second most physiologically maturing commercial variety, C2 (M66); and eight reasonably higher yielding variety than the second commercial variety, (C3 (KAT-KUNDE) (Table 6). These cowpea genotypes are more suitable for the warm tropical and sub-tropical regions of Kenya. K80 was the earliest to flower among the commercial varieties, with the highest seed yielding potential; attributed to prolonged pod filling period.

The genotypes that flowered and matured earliest tended to be more adapted to the growing conditions, than the late maturing genotypes; thus were able to escape the drought conditions. This provided an advanced drought adapted production strategy in cowpea under conditions of eminent terminal drought.

These genotypes could be used in future plant breeding programmes, through recurrent

TABLE 6. Mean values of agronomic traits for top 10, bottom 5 and checks of Kenyan dual-purpose cowpea genotypes grown in Juja in 2021 and 2022 ranked based on days to maturity

Field ID and Genotype	DTF	DTM	PL	NSP	NPP	GYP	GYR	TW
Early maturing								
52 -GBK 003682	48.75	81	14.69	12.42	29.75	36.84	204.92	239.25
177-Selection from within variety	33.5	81.25	14.1	15.54	29.17	33.71	205.54	239
137-GBK022548	34.5	81.5	15.2	13.67	18.5	21.17	143.83	165
128-GBK 022473	41	82.75	14.23	14.75	22.59	31.58	133.42	165
99-GBK 003705-1	41.75	83	14.6	15.98	18.56	35.42	118.83	154.25
199-Selection from within variety	42	83	11.74	16.43	19.77	33.2	200.06	241.75
146-GBK 022518	36	83.75	13.88	14.42	20.95	24.42	220.25	244.75
184-Selection from within variety	42.75	83.75	15.76	14.92	23.83	31.08	302.17	332.5
159-GBK 022486	42.25	84.25	14.38	14.58	19.13	49.84	152.67	200.25
86-MAR.5	35.25	84.5	15.44	14.34	43.83	57.42	212.33	269.75
Late maturing								
53- GBK 003720-1	45	113	15.96	14.71	23.67	35.5	794.75	830.25
161-GBK022548	42.5	112.75	19.57	17.25	28.08	50.75	595	646.25
100- GBK 034722-2	49.25	111.25	18	14.58	27.92	37.165	476.84	514
176- GBK 026931	45.25	109.75	17.83	15.92	34.78	51	476	527
162- GBK 022477	44.75	108.25	18.33	13.92	20.46	36.42	483.33	519.75
Commercial varieties (Controls)								
C1- K80	34.75	80.25	17.58	14.34	32.33	42.58	621.92	664.5
C2-M66	32.25	85.25	19.67	15.34	19.83	64.99	817.92	883
C4- KUNDE SOKO	36.25	85.25	17.56	15.42	23.58	42	609.75	651.75

TABLE 6. Contd.

Field ID and Genotype	DTF	DTM	PL	NSP	NPP	GYP	GYR	TW
C5- KUNDE-FAULU	41.75	86	15.77	13.69	20.39	35.33	453.42	488.75
C3- KAT-KUNDE	36.25	86.75	17.27	14.84	13.41	31.67	708.34	739.75
C6- KUNDE-TAMU	33.75	88.5	15.7	15.63	18.64	35.42	374.33	409.75
Mean	40.97	94.16	16.48	14.34	24.48	35..92	423.21	459.52
LSD genotypes	6.1^{ns}	7.9*	1.8***	3.7*	12.4***	18.0***	88.2***	91.5***
LSD seasons	8.9*	7.5**	3.3**	4.7*	7.1***	13.6**	31.5***	69.3***
CV (%)	8.15	4.57	5.99	14	27.83	27.39	11.41	10.9

Note: DTF = Days to Flowering (days), DTM = Days to maturity (days), PL = Pod Length (cm), NSP = Number of seeds pod^{1-}, NPP = Number of pods plant^{1}; GYP = Grain yield plant1-; TW = Grain yield per plot, CV = Coefficient of Variation, LSD = Least significance difference, ns = not significant, *, **, *** = significant (at 0.05, 0.01, 0.001 level respectively)

selection, as earliness is a crucial adaptation in agro-ecological zones with short growing seasons especially in sub-Saharan Africa. This could allow cowpea escape from biotic and abiotic stresses (Owusu *et al.*, 2018) and hinders early floral development, leading to sterility (Kazan and Lyons, 2016; Abdou, 2021), that would counteract adverse effects of water stress typical in Kenya.

Furthermore, evaluation of early maturing cowpea genotypes, in diverse environments, is crucial to identify lines with wide adaptations and stability in yield performance. This would answer to the needs of the farmers in arid and semi-arid regions of Kenya who tend to prefer early maturing and high yielding cowpea varieties that are tolerant to diseases (Kuruma *et al.*, 2019).

Breeding efforts should, therefore, focus on developing genotypes that combine early maturity with desirable agronomic traits, such as pod length and yield components that meet farmer preferences. In addition, effective dissemination of early maturing cowpea varieties, along with training about improved production practices, could accelerate adoption by smallholder farmers in semi-arid areas. By leveraging the development and adoption of early maturing and high yielding cowpea genotypes, Kenya could achieve higher cowpea productivity, improve food security, and increase incomes of smallholder farmers in drought-prone regions.

Pod characteristics and grain yield

Pods per plant. A significantly small number of pods plant^{-1} was recorded for 201(SFV) (8.01) and 85 (GBK 003770-1), with the highest recorded in 136B (SFV) (51.67), 147 (GBK022484); followed by 113 (GBK 005173-2) (Table 5). Pods plant^{-1} recorded an overall mean of 14.33 pods plant^{-1}, ranging from 8.01-51.67, compared to the best performing commercial variety, K80 which yields barely 32.33 pods plant^{-1}. The wide range of pods per plant suggests presence of genotypes with superior genetic traits that can be selected for breeding programmes that can significantly enhance productivity and sustainability. The genotype with the highest pod count, 136B, could be particularly valuable for developing new varieties aimed at maximising yield. Furthermore, the best-performing commercial variety, K80, yields only 32.33 pods per plant, indicating that the identified genotypes have the potential to significantly outperform established varieties.

The significant difference between the highest-yielding genotype and the commercial standard (K80) underscores the potential for breeding programmes to improve pod production. Incorporating high-yielding traits from genotypes like 136B into existing varieties could lead to substantial increases in overall yield.

Further research could focus on understanding the environmental and agronomic factors that contribute to the high pod counts in genotypes like 136B; and exploring their adaptability across different growing conditions. Additionally, studies on disease resistance and stress tolerance would provide a more comprehensive view of their potential applications in diverse agricultural settings.

These findings presents significant opportunities for enhancing pod yield through selective breeding and improved agricultural practices, ultimately contributing to greater food security and sustainability in agriculture. This diversity is essential for breeding programmes focused on developing varieties that can withstand environmental stresses such as drought, pests, and diseases. Utilising diverse genetic backgrounds can enhance resilience and adaptability in changing climatic conditions, against a backdrop of climatic stress that limits yields, owing to shifts in pests and pathogens, precipitation, heat-waves and other weather extremes (Bailey-Serres *et al.*, 2019).

Seeds per pod. The highest mean for the trait was recorded in genotypes 175 (GBK 005163), 33(GBK-003668 D) and 46 (KOL 3), with 19.00, 18.36 and 17.96 seeds per pod, respectively (Table 6). The lowest value was recorded in 157 (GBK 022559) and 179 (GBK 017474), with 10.00 and 11.75 seeds plant^{-1}, respectively; compared to the best performing check variety, Kunde-Tamu (15.63). The high-yielding genotypes identified, such as GBK 005163, GBK-003668 D, and KOL 3, have several potential applications in agriculture that can significantly enhance productivity and sustainability.

These high-yielding genotypes can contribute to greater food production, addressing food security challenges, especially in regions facing population growth and climate change impacts (Bailey-Serres *et al.*, 2019). The high-yielding genotypes may possess traits that enhance resilience to environmental stresses, making them suitable for cultivation in changing climatic conditions (Zhang *et al.*, 2018; Bailey-Serres *et al.*, 2019). This is crucial for maintaining yields in the face of unpredictable weather patterns.

In addition, these genotypes can serve as valuable genetic resources in cowpea breeding programmes aimed at developing new varieties with enhanced traits such as disease resistance, drought tolerance, and enhanced nutritional quality by application of modern breeding strategies such as CRISPR/Cas9 for accelerated crop improvement leveraging on these naturally evolved traits (Richards, 2000).

Pod length. Mean pod length was significant among genotypes, with the trait mean at 16.47 cm and ranging from 11.74 to 23.06 cm (Table 6). The longest mean values were recorded in 126 (GBK 003676-2), 133 (GBK 003723) and 131 (GBK 003671-1); which recorded 23.06, 21.90 and 20.87, respectively. The shortest recorded pod length was in 199 (SFV); followed by 84B (MAR.6-1), which recorded 11.74 and 12.57 cm, compared to the best check variety; (C2) M66, which recorded 19.67 cm (Table 5). The significant differences in pod length among genotypes indicate a rich genetic diversity that can be exploited in breeding programmes. Genotypes with longer pods, such as GBK 003676-2, could be prioritised for breeding to enhance this desirable trait in new varieties. Pod length is often correlated with other yield components, such as pod weight and seed number per pod. Selection for longer pods could indirectly improve overall yield through these associated traits, making it a strategic focus in breeding programmes (Edematie *et al*., 2021).

Grain yield. Grain yield is dependent on the three factors; the longer the pods, the greater the seeds space; the higher the number of pods the more the seeds and the higher the number of seeds pod^{-1}; the higher the seed yield ha^{-1}. However, this may pose a grain quality problem as over proliferation of seeds per pod may lead to production of small and incompletely developed seeds per pod; hence low grain yield per ha. Sometimes, fewer but larger seeds per pod and per unit area may be desirable for hybridisation of the best parents selection for high yielding varieties in future. Hence, an optimum yield that combines high seed quality and quantity may be the most desirable (Ezin *et al*., 2023).

The three factors can be considered in cowpea breeding by selection of genotypes with desirable traits in breeding strategy and hybridisation for grain yield (Owusu *et al*., 2021; Gerrano *et al*., 2022).

Days to flowering and physiological maturity. Days to flowering was not significant (P>0.05) among the 224 genotypes used in the present study. However, days to 75% physiological maturity, were significantly different (P<0.05) and ranged from 80.25-113.00 days; with a mean of 94.13 days (Table 6). Genotypes 53 (GBK 003720-1), 161 (GBK022548) and 100 (GBK 00366-1) recorded the longest days to physiological maturity, with 113.00, 112.75 and 111.25 days; and shortest maturity periods recorded in genotypes 52 (GBK 003657-2) and 177 (GBK 022519, recording 81.00 and 81.25 days, compared to the check variety C1 (K80) taking 80.25 days to mature.

Of necessity, farmers tend to prefer short term maturing cowpea genotypes that are capable of escaping terminal drought, and insect pests and diseases, prevalent at the end of cropping season in the dry SSA, which is characterised by short and erratic rainfall (Owusu *et al*., 2018).

The late maturing genotypes were high yielding (Table 6), as long grain filling period and pod development resulted in more grains per pod. Additionally, the longer pods had heavier grains due to the maximum period taken for plant growth and development; hence superior dry matter accumulation. Breeding cowpea for early maturation and high yielding cowpea genotypes is a challenge as earliness embodies decline in yield potential due to short growth cycle and sub-optimal foliage development owing to the short cropping season (Mduruma *et al*., 1998).

Grain yield. Results in Table 7 revealed that mean grain yield varied significantly among the genotypes, with the highest yields ranging from 734 to 908 kg ha^{-1}, with accession 222 yielding the highest (908 kg ha^{-1}) and accession 85 (GBK 003770-1) producing the lowest (122 kg ha^{-1}), compared with the commercial varieties in which C1 (K80) with mean yield of 664.5 kg ha^{-1} (Table 7). On the other hand, commercial varieties C2 (M66) yielded more (883 kg ha^{-1}), but less than the highest yielding genotype. The significant variation in grain yield among the genotypes indicates a rich genetic potential that can be harnessed in breeding programmes. Accession 222, with the highest yield, serves as a valuable genetic resource for developing new high-yielding varieties. This can lead to improved productivity in agricultural systems.

The performance of commercial varieties, C1 (K80) and C2 (M66), demonstrates that while they provide reliable yields, there is still room for improvement. The fact that accession 222 outperforms these varieties by substantial

TABLE 7. Mean values of agronomic traits for top 10, bottom 5 and checks of Kenyan dual-purpose cowpea genotypes grown in Juja in 2021 and 2022 ranked based on grain yield ha^{-1}

Field ID and Genotype	DTF	DTM	PL	NSP	NPP	GYP	GYR	TW
High yielding								
222- SV	42.00	102.00	19.93	16.03	24.57	29.39	878.62	908.00
AA4- SV	44.00	106.80	18.84	15.42	20.60	27.93	812.47	840.40
233- SV	29.50	90.50	19.12	14.51	25.29	35.05	796.45	831.5
53-GBK 003720-1	45.00	113.00	15.96	14.71	23.67	35.50	794.75	830.25
79-GBK 003820-4	36.75	91.50	18.39	14.17	27.5	36.58	770.17	806.75
153-GBK 022471	43.25	106.00	20.75	15.17	23.42	31.33	772.67	804.50
133-GBK 003651	37.75	89.50	21.90	15.25	23.34	43.42	732.09	775.50
163-GBK 022520	40.25	105.50	18.48	14.42	31.42	40.25	705.75	746.00
124-GBK 003706-3	40.00	96.75	19.89	13.83	15.17	28.34	711.67	740.00
126-GBK 003676-2	34.25	94.00	23.06	16.43	27.83	41.92	692.84	734.75
Low yielding								
85-GBK 003770-1	36.75	86.75	13.95	12.42	10.25	17.33	105.17	122.00
99-GBK 037732-1	41.75	83.00	14.60	15.98	18.56	35.42	118.83	154.25
128-GBK 003687-1	41.00	82.75	14.23	14.75	22.59	31.58	133.42	165.00
137-SV	34.50	81.50	15.20	13.67	18.50	21.17	143.83	165.00
26-GBK 003697	42.25	86.75	15.94	13.08	17.83	35.42	141.08	176.50
Commercial varieties (Controls)								
C2-M66	32.25	85.25	19.67	15.34	19.83	64.99	817.92	883.00
C3-KAT-KUNDE	36.25	86.75	17.27	14.84	13.41	31.67	708.34	739.75
C1-K80	34.75	80.25	17.58	14.34	32.33	42.58	621.92	664.50

TABLE 7. Contd.

Field ID and Genotype	DTF	DTM	PL	NSP	NPP	GYP	GYR	TW
C4-KUNDE SOKO	36.25	85.25	17.56	15.42	23.58	42.00	609.75	651.75
C5-KUNDE-FAULU	41.75	86.00	15.77	13.69	20.39	35.33	453.42	488.75
C6-KUNDE-TAMU	33.75	88.50	15.7	15.63	18.64	35.42	374.33	409.75
Mean	40.97	94.16	16.48	14.34	24.48	35..92	423.21	459.52
LSD (G)	6.1^{ns}	7.9*	1.8***	3.7*	12.4***	18.0***	88.2***	91.5***
LSD (S)	8.9*	7.5**	3.3**	4.7*	7.1***	13.6**	31.5***	69.3***
LSD (GxS)	7.1**	8.9*	1.9**	4.1**	14.0***	20.8*	95.4***	98.6***
CV (%)	8.15	4.57	5.99	14.00	27.83	27.39	11.41	10.90

Note: LSD = Least significance difference, CV = Coefficient of variation, DF = Days to flowering, DM = Days to maturity, SV = Selection from a variety, G = Genotype, S = Season

margins suggests that breeders can achieve better results by incorporating traits from high-yielding genotypes into commercial lines. By focusing on genotypes like accession 222, breeders can contribute to increased food production, which is essential for sustaining growing population in the country.

Breeding programmes can employ targeted strategies such as marker-assisted selection to incorporate desirable traits from high-yielding accessions into existing commercial varieties. This approach could accelerate the development of new cultivars that combine high yield with other beneficial traits, such as disease resistance or drought tolerance. The significant differences in grain yield among genotypes underscore the importance of continued research and breeding efforts aimed at enhancing crop productivity. By focusing on high-yielding accessions like accession 222, breeders could develop improved varieties that meet both market demands and food security needs.

Cowpea grain yield ha^{-1} is the most important trait to farmers and the ultimate goal of the present study. Crossing the identified high yielding with early maturing cowpea genotypes would avert hunger and food insecurity to approximately 400 million of the population living in rural areas as smallholder farmers in sub-Saharan Africa (Porciello *et al.*, 2020), with future food demand projected to worsen with the emergence of urbanisation, land degradation and climate change exerting food supply pressure on already worst condition to the future projected 9 billion in the world by 2050 (Lenaerts *et al.*, 2019)

Descriptive statistics. Results revealed that the coefficient of variation ranged from 5.7% (days to maturity) to 33.7% (grain yield plant^{-1}) during long rain seasons and 4.80 % (days to maturity) to 26.4% (pods plant^{-1}) during short rain seasons (Tables 3 and 4). These results provide valuable insights into the variability of different agricultural traits across genotypes. The low CV (5.7% in long rain seasons and 4.80% in short rain seasons) for days to maturity, suggests that this trait is relatively stable across different genotypes despite environmental variations. This stability may be advantageous for breeding programmes aiming for consistent maturity times.

The highest coefficient of variation was recorded in grain yield plant^{-1} at 33.86% and number of pods plant^{-1} at 31.83%, respectively. This showed a significant environmental impact among the genotypes assessed for these traits. The highest CV recorded at 33.7% during long rain seasons, indicates substantial variability in grain yield among the genotypes. This suggests that environmental conditions, such as rainfall patterns, soil fertility and pest pressures, significantly impacted yield outcomes. Breeders may focus on identifying genotypes with higher resilience to these environmental stresses

Similarly, the high CV of 31.83% for pods plant^{-1} reflects considerable variability in this trait as well, emphasizing its sensitivity to environmental factors. A high CV (>30%) indicates substantial differences among individual plants regarding their yield and pod production capabilities, suggesting that these traits are influenced by both genetic and environmental factors. The high CV for grain yield per plant suggests that there is considerable potential for improvement through selective breeding. This suggests considerable potential for improvement through selective breeding. Breeders could target genotypes that consistently produce higher yields, thereby enhancing overall crop productivity.

Similarly, the significant variability in the number of pods per plant indicates that selecting for this trait could also lead to increased grain yield, as pod number is often positively correlated with yield. This variability could inform selection strategies, where genotypes that consistently produce more pods under varying conditions could be prioritised.

The significant environmental impact observed on grain yield and pod production highlights the need for targeted breeding strategies that consider both genetic potential and environmental adaptability. Breeders should prioritise genotypes that demonstrate consistent performance across varying environmental conditions, particularly those with high yields and pod counts despite fluctuations in weather. Farmers can benefit from understanding which cowpea genotypes are likely to perform better under specific seasonal conditions, allowing for more informed decisions regarding crop selection and management practices. These findings underscores the importance of environmental influences for assessing genetic variation in agronomic traits in cowpea. By focusing on traits with high CVs, such as grain yield and pods plant^{-1}, breeders and farmers can enhance crop productivity and resilience in changing climates.

These results are in close conformity with the findings of Wahome *et al.* (2023) with 257 common bean genotypes with grain yield (32.3%) and number of pods plant^{-1} (36.1%). This depicts a strong environmental influence among the cowpea genotypes traits evaluated.

The low coefficient of variation for days to maturity (5.55%), and days to flowering (6.54%); suggest that these traits are stable across different environments or genotypes, which is advantageous for breeding programmes aimed at consistent quantitative and qualitative yield attributes. This stability can help farmers to predict performance and make informed decisions about which varieties to fit to which environments.

Conversely, a high CV indicates greater variability in a trait, which can reflect genetic diversity among cowpea accessions as observed in number of pods plant^{-1} (23.73%), and grain yield plant^{-1} (22.10%) . This diversity can be leveraged to select for desirable traits that may perform well under varying environmental conditions, enhancing adaptability and resilience in production systems. The observation of both stable and diverse traits will be important in arid and semi-arid cowpea breeding programmes in Kenya. For instance, Mofokeng *et al.* (2020) and Horn and Shimelis (2020) showed that high genetic variability in cowpea traits allowed for better selection of high yielding and early maturing varieties, which are crucial for improving cowpea production in Kenya. Therefore, understanding the coefficients of variation among traits can guide breeding strategies to enhance cowpea production, ensuring both consistency and adaptability response to environmental challenges.

Mean seed yield was surprisingly greater in short rainy season than in its long rain counterpart in 2021 and 2022 (Table 4). This could have been occasioned by warmer temperatures and longer day lengths experienced in SSA, marking early flower initiation and short grain filling period allowing the early flowering and maturing escape of terminal drought, heavy incidences of pests and diseases; and unfavourable temperatures during flowering and pod formation (Haisirikul *et al*., 2020).

In addition, the low yields during the wet long rainy seasons could have been attributed to luxuriant vegetative growth, at the expense of grain formation, causing a yield penalty as most photosynthates are translocated to foliage (Atakora *et al*., 2023).

Heavy rainfall in poorly drained soils and high temperatures in the study area (Table 10), could have led to excessive soil water, causing poor root nodulation and decreased yields (Iizumi *et al*., 2024). This could have resulted from supersaturation of water in soil micro- and macropores, leading to impaired soil aeration, otherwise necessary for root growth and Biological N-fixation.

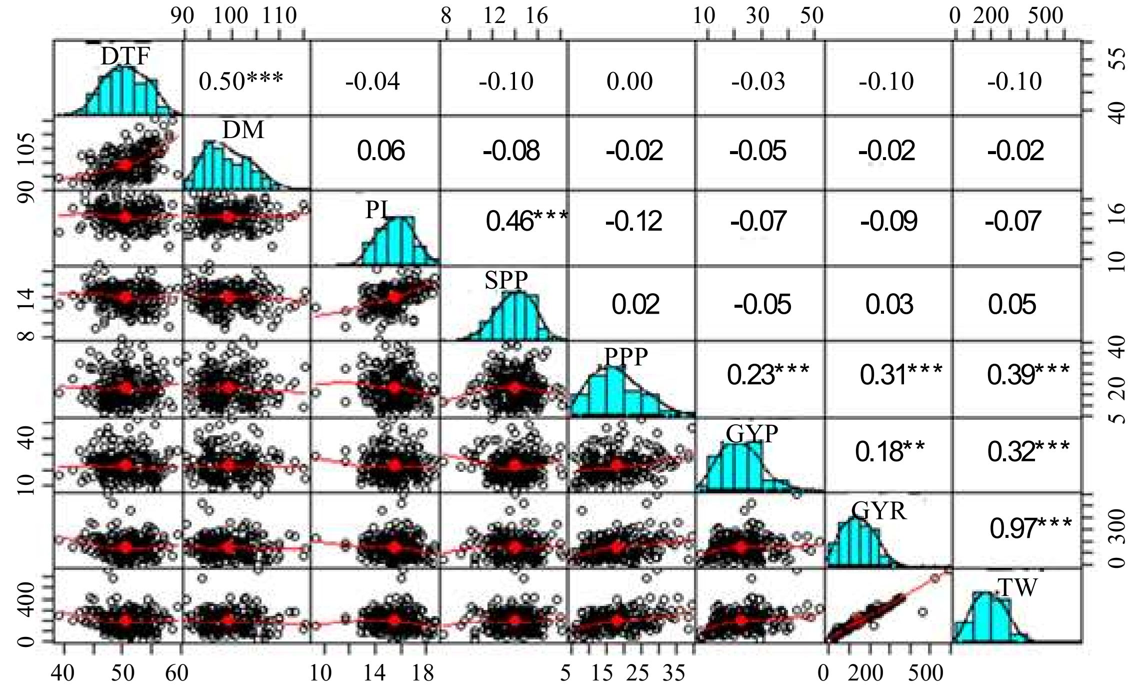
Iseki *et al*. (2021) and Iizumi *et al*. (2024) reported that cowpea grown under excessive soil water in the Sudan Savannah, showed reduced yields due to suppression of biological nitrogen fixation in roots; thereby limiting plant growth and yield. Our findings conformed to those of Atakora *et al.* (2023), that heavy rainfall normally reduces temperatures causing poor flower and pod development with interactions of seasons x genotype influencing most traits evaluated limiting achievement of maximum yield in cowpea.

Character associations. The correlation among traits of tested genotypes is presented in Table 8. Days to flowering was highly ($P<0.01$) and positively correlated with days to physiological maturity ($r = 0.50^{***}$) indicating a moderate to strong positive relationship for the traits. This relationship can guide breeders in selecting for early-flowering varieties that may also reach maturity sooner, potentially allowing for earlier harvests and better adaptation to varying climatic conditions. This is useful to farmers in managing planting schedules more effectively, ensuring that flowering and maturity align with optimal growing conditions.

Grain yield plant^{-1} was also highly significant ($P<0.01$) and positively correlated with grain yield row^{-1} ($r= 0.18^{***}$). The weak correlation implies that improvements in grain yield plant^{-1} do not necessarily translate into proportional increases in yield per row. This highlights the importance of considering multiple factors affecting yield, such as plant density, competition for resources, and environmental conditions while grain yield row^{-1} was highly significant ($P<0.01$) and positively correlated with pods plant^{-1} ($r= 0.31^{***}$). This moderate positive relationship suggests that an increase in the number of pods per plant is associated with an increase in grain yield per row emphasizing the importance of selecting genotypes that produce a higher number of pods, as this trait appears to be a significant contributor to overall yield potential. By leveraging this information, breeders can make informed decisions when selecting for desirable traits, while farmers can adopt management practices that optimise yield outcomes.

Understanding these relationships is crucial for enhancing agricultural productivity and sustainability. These results provides better choice of Kenyan dual-purpose cowpea genotypes adaptable to unfavorable sub-Saharan environmental conditions influencing overall yield by careful selection and breeding. Apart from the seed yield, early maturing cowpea ranks second in importance in

TABLE 8. Pearson's correlation values among the studied traits in dual purpose cowpea genotypes evaluated in JKUAT



marginal sub-Saharan Africa regions characterised with unpredictable onset and termination of rainfall (Martey *et al*., 2022). Late maturing crop succumbs to a yield penalty, although not always, as reported by Owusu *et al*. (2018); with terminal drought which occurs mostly at flowering and pod filling stage of the crop, causing as high as 80% yield loss (Agbicodo *et al*., 2009).

This informs breeders in selection and development of new varieties of cowpea in breeding programme with novel genes allowing farmers with an opportunity to shift to extra-early maturing varieties (those maturing in less than 60 days after planting), enhancing drought tolerance for cost effective and sustainable crop yield in the ever changing harsh and dry sub-Saharan climatic conditions posing food and income threat to resource poor smallholder farmers. Owusu *et al*. (2021) and Yaw *et al*. (2022) inferred that early maturing varieties do not always translate to small seeds, hence low yield plant^{-1}. Aliyu *et al*. (2022) suggested that the strong correlation between flowering days and maturity days indicates that flowering days is a reliable indicator for selection of maturity period enhancing cowpea seed yield in marginal short wet season in sub-Saharan Africa.

Kenyan breeders may infer that other traits such as pod development or environmental factors may play significant roles in determining yield, explore presence of genetic diversity within early maturing varieties that affects seed size and yield to identify lines that combine early maturity with desirable yield traits, focus on selection of multiple traits rather than single traits to achieve optimal yield outcomes and conduct additional studies to understand relationship between maturity, seed size, and yield guiding future cowpea breeding programmes more effectively in Kenya.

Pod length was highly significant ($P<0.01$) and positively correlated with number of seeds pod^{-1} ($r= 0.46$***). This implies that pod length forms a fundamental selection index for number of pods per plant in the cowpea breeding programmes. These results are in consonance with the findings of Chay and Thurling (2009), who suggested that long pods produced greater number of seed than short pods. However, the short pods produces more seeds per unit length of pod due to less efficient distribution of assimilates required to support growth of pod walls within the longer pods in cowpea (Canci and Toker, 2014), in mung bean (Thorat and Gadewar, 2013; Snehal *et al.* 2021) in cowpea. This indicates that selection of genotypes with longer pods creating more seeds space could provide baseline for greater acceptability by cowpea farmers alleviating food insecurity and provision of adequate genetic materials for breeding. Longer pods selection could be an effective strategy for improving the number of seeds per pod. Breeders might prioritise these traits in their selection processes to enhance yield potential ultimately contributing to improved agricultural outcomes.

Seed yield was highly significant ($P<0.01$) and positively correlated with grain yield row^{-1} ($r = 0.97$***), grain yield plant^{-1} ($r= 0.32$***) and number of pods plant^{-1}($r=0.39$***). As yield is a complex trait influenced by polygenes, genetic heterogeneity and environment variety of factors (Usman *et al.*, 2017), correlation among yield and related agronomic component traits assessment is necessary to identify traits with significant effect on cowpea yield and elimination of those with undesirable correlative changes. Seed yield is influenced by agronomic, genetic and environmental factors hence the need of cowpea breeders to identify their interactions to ascertain the most appropriate for seed production to feed the ever increasing population in sub-Saharan Africa.

Principal component analysis. The presence of agronomic traits variances among the genotypes was further validated by principal component analysis, which indicated that the overall diversity observed could be elucidated by a few eigenvectors (Fig. 2). The cumulative contribution was split into eight PCs equal to the variables in the study based on Kaiser-Guttmann rule (Guttman, 1954). The resulting three PCs with eigenvalues >1 provided a potential criteria in the selection of the critical principal components contributing to the total

TABLE 9. Contribution of 8 yield and yield-related traits to the variation among 224 cowpeas genotypes showing eigenvectors, eigenvalues, variance percent and cumulative variation

Traits	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Days to flowering	-0.094	**-0.3295**	**0.7167**	-0.118	**-0.5108**	**0.244**	-0.186
Days to pod maturity	**0.274**	**-0.4341**	**0.4489**	0.0403	**0.6018**	**-0.3205**	**0.2617**
Pod length	**0.4561**	-0.1507	-0.1577	-0.0774	-0.0361	**0.7007**	**0.4962**
Seeds pod^{-1}	0.1575	-0.0361	-0.1097	**-0.9463**	0.104	-0.0761	-0.2232
Pods plant^{-1}	**0.2456**	**0.5513**	**0.351**	0.0969	**0.4098**	**0.3793**	**-0.4374**
Grain yield plant^{-1}	0.2221	**0.5955**	**0.3136**	-0.1491	**-0.3014**	**-0.3422**	**0.5144**
Grain yield row^{-1}	**0.5317**	-0.1213	-0.1268	0.1672	-0.2203	-0.1871	**-0.2911**
Seed yield ha^{-1}	**0.5394**	-0.0755	-0.1018	0.1531	-0.2398	-0.2123	**-0.2454**
Eigenvalues	3.0446	1.447	1.237	0.984	0.496	0.415	0.377
% variance	38.1	18.1	15.5	12.3	6.2	5.2	4.7
Cum. variance %	38.06	56.14	71.6	83.9	90.1	95.29	99.996

Bold figures represent vector loadings >0.24 for a trait contribution for a given principal component towards cumulative variation

TABLE 10. Mean monthly rainfall and temperature for the year 2021 and 2022

Month	2021 Rainfall (mm) (°C)	2022 Rainfall (mm) (°C)	2021 Mean monthly temperature	2022 Mean monthly temperature
January	33.1	2.3	18.6936	19.0936
February	94	64	18.8286	19.7929
March	52.2	39.1	19.2345	19.5
April	254.2	224.6	19.2862	19.6867
May	134.3	37.8	18.5129	19.5419
June	0	1.5	16.7767	17.6367
July	6.5	11.8	15.8032	16.3742
August	8.9	28	16.7	16.53
September	1.2	0	17.2333	17.4933
October	66.6	0	19.8032	19.7533
November	161.9	0	20.32	19.3621
December	205.4	0	19.1839	19.2194

variation as suggested by Gerrano *et al.* (2019).

The present study has revealed three important PCs (PC1, PC2 and PC3) among the evaluated agronomic traits, contributing 36.1, 19.3 and 16.1%, respectively; totaling to 71.6% of cumulative variation (Table 8). This forms the basis for characterisation and classification of genotypes for improvement programmes and submission to gene bank for long-term storage; although Gixhari *et al.* (2014) suggested that pulse crops genetic characterisation, acceptable total variation should be greater than 75%.

Principal Component 1 accounted for 36.1% of the total variation; mainly influenced and impacted by variation due to days to flowering, pod length, pods plant^{-1}, grain yield row^{-1}, and seed weight ha^{-1} among Kenyan dual-purpose cowpea genotypes, as the main positive contributors with eigenvalue of 3.0446 accounting for the greatest amount of variance of the original data. The identified traits highlight their collective impact on the overall performance and adaptability of cowpea genotypes. Days to flowering is a critical trait determining the growth cycle and can influence overall yield potential. Early flowering may allow for better adaptation to varying climatic conditions, especially in regions with unpredictable rainfall patterns. Longer pods may indicate better seed development and higher yield potential. This trait is essential for assessing the crop quality and quantity of produce. A higher number of pods plant^{-1} is directly associated with increased yield. This trait reflects the plant's reproductive success and its ability to maximise output under optimal conditions.

Grain yield row^{-1} measure provides insight into how effectively a genotype can convert its growth resources into harvestable grain, making it a critical factor for farmers focused on maximising productivity. The overall seed weight indicates seed quality and vigor. Heavier seeds often correlate with better germination rates and stronger seedlings, contributing to overall crop success. Breeders can focus on enhancing these specific traits to improve overall cowpea performance. By selecting genotypes that exhibit desirable characteristics in these areas, they can develop varieties that are more productive and resilient. A better understanding of these traits contributing most to variation allows for more efficient evaluation and selection processes in breeding

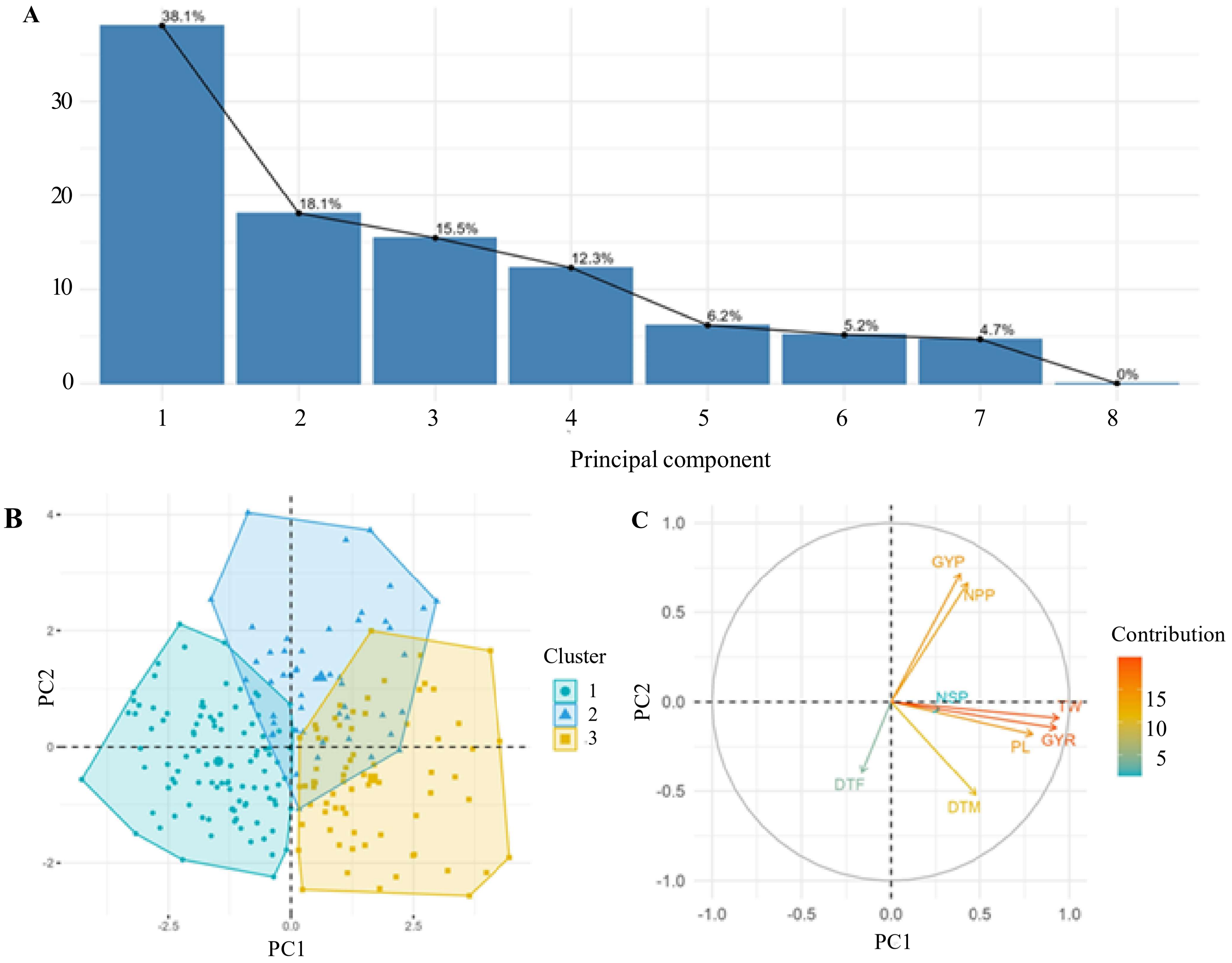


Figure 1. Loading plot showing the contribution of the 8 quantitative characters to the variation observed in PC1 and 2.

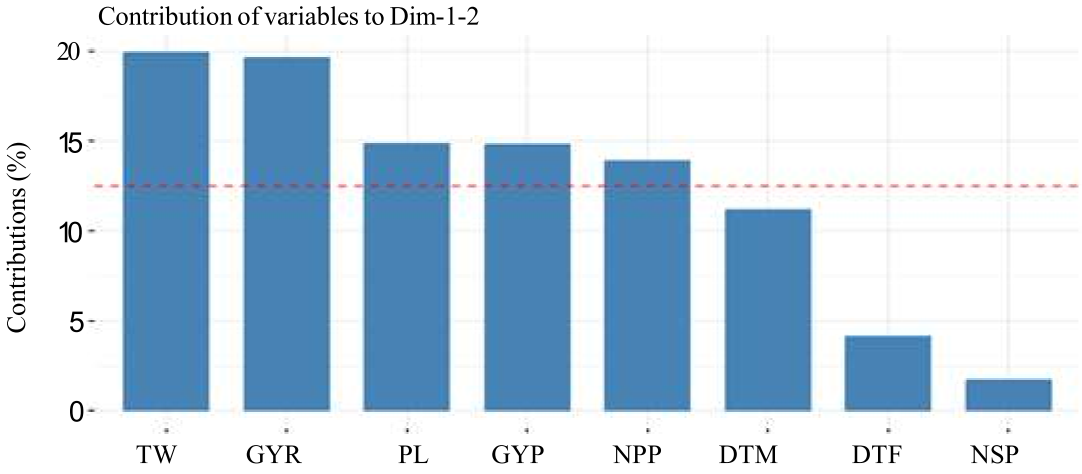


Figure 2. Contributions of the various traits to dimension 1 and 2.

programmes. This can lead to faster development cycles for new cultivars. By leveraging these insights, stakeholders can enhance both breeding efforts and agricultural practices for optimal outcomes.

Genotypes with high PC1 scores could provide good genitors for diversity could be used as a selection criteria to improve seed yield of Kenyan dual-purpose cowpea. The rich diversity endowed within the genotypes, provides greater chance of selection in cowpea breeding programmes in Kenya. The results of our findings were close to those obtained by Vijayakumar *et al.* (2020), who observed that grain yield plant^{-1}, pods plant^{-1}, seeds pod^{-1}, pod length, except days to maturity that contributes maximum towards divergence in the PC1. Similarly, Mwangi *et al.* (2021) used PCA to identify major traits for detecting phenotypic diversity Kenyan mung bean (*Vigna radiata* L. Wilckzek) genotypes, and observed that pod length, seeds pod^{-1}, grain yield plant^{-1} and pods plant^{-1} contributed significantly to PC I and II. Therefore, seeds pod^{-1}, seeds plant^{-1}, and pod length are mainly the yield contributing traits mostly preferred by cowpea farmers among the studied traits and traits utilised as morphological quantitative marker traits for characterisation and classification of cowpea germplasm (Gixhari *et al.*, 2014).

Principal Component 2 contributed 18.1% of the total variation; which accounted for the greatest variance in the residual variation, which was not accounted in the first principal component (Table 8). The variance explained by PC2 may be indicative of other important traits or interactions among traits that influence cowpea performance. Understanding these relationships can provide deeper insights into how different traits contribute to overall plant health and yield. By considering both PC1 and PC2, breeders can develop more comprehensive strategies that take into account a wider variety of traits. This holistic approach can enhance selection processes and lead to the development of more resilient and productive cowpea varieties ultimately leading to improved breeding strategies and better crop performance.

PC2 was negatively dominated by days to flowering and maturity; but positively associated with the pod length and grain yield plant^{-1}. The negative dominance of days to flowering and maturity in PC2 suggests that genotypes exhibiting shorter durations for these traits are likely to score higher on this principal component. This could indicate a selection pressure towards early flowering and maturity, which is advantageous in environments with variable climatic conditions. This helps plants escape adverse conditions, such as drought or extreme temperatures, thus enhancing survival and productivity. Breeding efforts that focus on increasing pod length may align well with the goals of improving yield, particularly in genotypes that also exhibit early flowering. This dual focus can enhance adaptability while maximising yield potential.

PC3 explained 15.5% of the variation and mainly contributed positively to days to flowering and maturity, grain yield plant^{-1} and to pods plant^{-1}. This component provides valuable insights into the relationships among these traits in cowpea genotypes. This could indicate that longer flowering and maturity times are linked with better overall plant performance, possibly due to extended growth periods allowing for greater resource accumulation to produce more grain, aligning with agricultural practices that favor extended growth cycles in favorable environments. selecting for genotypes that exhibit favorable flowering and maturity characteristics alongside high yield and pod production.

This dual focus can lead to the development of varieties that perform well under diverse environmental conditions. By leveraging these insights, breeders and farmers can enhance selection processes aimed at improving both adaptability and productivity, ultimately contributing to more resilient agricultural systems. The positive significant contribution of phenological and yield and yield-related traits could allow genotypes stability and escape from the impact of the unfavorable soil and erratic rainfall conditions in sub-Saharan Africa.

Vijayakumar *et al.* (2020) reported similar findings for pods plant^{-1} and grain yield plant^{-1} in PC2 and days to flowering and maturity in PC3, respectively. In PC, days to flowering had the greatest residual variation unaccounted for by PC2 with vector loading of 0.717. These selection based on these traits could effectively allow improvement in cowpea yield improvement programme.

Variables with vector loadings of ± 0.4 and above, had the greatest contribution to total variation (Fig. 2). These characters were grain yield row^{-1}, total seed weight, days to flowering and maturity, pod length, grain yield plant^{-1} and pods plant^{-1} being the significant contributors towards the divergence. These results to certain extent are in accordance with the findings of Hutchinson *et al.* (2017) and Nkhoma *et al.* (2020).

PCA biplots are very effective in identification of the existence of wider phenotypic variability by providing the contrast among variables and interrelationships among genotypes possessing multiple traits facilitating designation of a suitable breeding strategy (Owusu *et al.*, 2021). The biplot grouped the genotypes with characteristics explained by the first two dimensions (PC1 *vs*. PC2), based on combined data across seasons showing groupings of cowpea genotypes and agronomic traits were scattered into the four quadrants depicting wide genetic variability of characters studied (Fig. 1). All the genetically dissimilar cowpea genotypes are viable genotypes that can broaden the genetic base of the cowpea materials for population bulking and utilisation in breeding programme that would contribute to food security and nutrition.

In the present study, the eight characters are placed in all the four quadrants with pod length having negative association with pods plant^{-1} (Fig. 1) in the opposite quadrant indicating that genotypes are genetically distinct. The extent of variation among the quantitative variables depicted that characters such as pod length, grain yield plant^{-1} and pods plant^{-1} are closer to the origin, thus are considered to have lower loadings, with least contributions towards the divergence. Variables placed further away from the origin (x, y) such as total weight and grain yield row^{-1} were considered to have the highest loadings score; having maximum contribution towards the divergence. In order to enhance the productivity of dual-purpose cowpea in Kenya, leveraging the insights from variables such as total weight and grain yield is essential. These variables indicate the potential for improved agricultural practices and resource management.

Mwadzingeni *et al.* (2016) also reported occurrence of a great phenotypic trait association in discriminating evaluated genotypes with narrow angles between the dimensions vectors in the same direction. On the contrary, parameters such as days to flowering and seeds pod^{-1} were placed closer to the origin and were considered to have the least loading scores having minimal contribution towards the divergence (Figs. 1 and 2). These results are in conformity with previous studies by Gerrano *et al.* (2015) and Walle *et al.* (2019) in cowpea who reported similar observations regarding the limited impact of these traits on overall variation among genotypes. There studies emphasize that these traits with lower loading values are less significant in distinguishing between different genotypes, supporting the findings of Mwangi *et al.* (2021) regarding yield-contributing traits.

In light of these observations, it can be inferred that traits prioritisation such as pod length, pods plant^{-1}, and seed yield plant^{-1} are more critical for improving cowpea yields, as they exhibit greater variation and loading scores in PCA analysis. This suggests that breeding programmes should prioritise these traits to enhance overall productivity. There is also minimal impact of flowering as minimal loading scores for days to 50% flowering indicate that this trait may not influence the phenotypic diversity among Kenyan dual-purpose cowpea genotypes.

The consistency of these previous studies by Gerrano *et al*., 2015; Walle *et al*., 2019) reinforces the reliability of PCA in understanding trait contributions to phenotypic diversity and highlights the importance of focusing on traits that have been validated by multiple studies. The results suggest the need for further research to explore the genetic basis and their interactions that could lead to more effective breeding strategies for cowpea improvement. The biplot containing the principal components based on eigenvalues >1 is shown in Figure 1.

The presence of agronomic traits variances among the genotypes was further validated by principal component analysis, which indicated that the overall diversity observed could be elucidated by a few eigenvectors (Fig. 2). The cumulative contribution was split into eight PCs equal to the variables in the study based on Kaiser-Guttmann rule (Guttman, 1954). The resulting three PCs with eigenvalues >1 provided a potential criteria in the selection of the critical principal components contributing to the total variation as suggested by Gerrano *et al.* (2019).The Principal Component Analysis can significantly enhance cowpea production by identifying key traits that contribute to yield variation. By focusing on these critical components, breeders can make informed decisions to optimise breeding programmes, ultimately leading to improved cowpea yields and better resources management in agriculture.

The present study has revealed three important PCs (PC1, PC2 and PC3) among the evaluated agronomic traits, contributing 36.1, 19.3 and 16.1%, respectively; totaling to 71.6% of cumulative variation (Table 8). This forms the basis for characterisation and evaluation of Kenyan dual-purpose cowpea genotypes by selection of promising and suitable genotypes for production by small-scale and commercial farmers as well as to develop breeding populations for high yield and related traits; although Gixhari *et al.* (2014) suggested that pulse crops genetic characterisation, acceptable total variation should be greater than 75%. These findings from the Principal Component Analysis (PCA) of the Kenyan dual purpose indicates that significant genetic diversity aimed at enhancing yields and resilience is crucial for breeding programmes culminating in traits selection identified through PCA that serves as a guide in selection of promising genotypes suitable for small scale farmers in sub-Saharan Africa for production optimisation and sustainability through farmers training on selecting genotypes aligning with PCA findings.

Principal Component 1 accounted for 36.1% of the total variation; mainly influenced and impacted by variation due to days to flowering, pod length, pods plant^{-1}, grain yield row^{-1}, and seed yield ha^{-1} among Kenyan dual-purpose cowpea genotypes, as the main positive contributors with eigenvalue of 3.0446 accounting for the greatest amount of variance of the original data. Genotypes with high PC1 scores could provide good genitors for enhancing diversity in cowpea breeding programme by introduction of variations into breeding lines leading to improved yields and enhance potential effectiveness of the breeding efforts. To leverage on these findings, a priority on these traits should be evaluated on field trials to assess their interactions under varying conditions, and use PCA results to identify superior genotypes for specific environments. This targeted approach can enhance productivity and resilience in cowpea cultivation, particularly in drought-prone areas of Kenya.

The rich diversity endowed within the genotypes, provides greater chance of selection in cowpea breeding programmes in Kenya. This diversity allows cowpea breeders to identify and select traits that contribute to improved yield, disease resistance and adaptability to different environmental conditions. By leveraging this genetic variation, breeding programmes can develop new cowpea varieties that meet the needs of farmers and consumers while improving overall crop resilience and productivity.

Principal Component 2 contributed 18.1% of the total variation; which accounted for the greatest variance in the residual variation that was not accounted in the first principal component (Table 8). PC 2 was negatively dominated by days to flowering and maturity; but positively associated with the pod length and grain yield plant^{-1}. The 18.1% variation in PC 2 highlights significant relationships in the dataset. Its negative correlation with days to flowering and maturity may reduce overall plant growth duration that limits time available for photosynthesis and nutrient accumulation, which is critical for seed development, potentially impacting yield by reducing grain fill. Therefore, flowering time management is essential to optimise yield potential in varying climatic conditions as previously reported by Kim and Lee (2023) and Shavrukov *et al.* (2017). Conversely, its positive association with pod length and grain yield plant^{-1} indicates that these traits are crucial in maximising productivity. These findings emphasize the trade-offs between developmental timing and yield-related traits, revealing important genetic relationships that can inform breeding strategies for improved cowpea performance.

The findings indicate a trade-off between developmental timing and yield-related traits. While faster developmental timing may lead to earlier harvests, it could potentially compromise traits like pod length and grain yield. Understanding the genetic relationships between these traits can guide breeders in selecting for desirable characteristics. By focusing on traits that positively influence yield, such as pod length, breeders can develop cowpea varieties that are both high-yielding and resilient as reported by Horn and Shimelis (2020). The insights gained from these associations can inform breeding strategies aimed at maximising productivity.

Prioritising traits that enhance pod length and grain yield while maintaining optimal developmental timing could lead to significant improvements in cowpea performance. In summary, the interplay between pod length, grain yield, and developmental timing presents both challenges and opportunities in cowpea breeding. By leveraging these genetic insights, breeders can enhance cowpea varieties to meet growing food demands effectively.

The insights derived from PC3 (Fig.1) can guide breeders in selecting genotypes that not only perform well in terms of yield but also exhibit desirable developmental traits. By understanding the genetic relationships among these traits, breeding programmes can prioritise selections that optimise both early maturation and pod production, ultimately leading to improved cowpea varieties suited for diverse agricultural environments.

In summary, the analysis of PC3's contributions underscores the inter-connectedness of flowering time, maturity, grain yield, and pod production in cowpeas. These findings are instrumental for developing effective breeding strategies aimed at enhancing cowpea productivity and resilience in changing agricultural landscapes.

In PC3, days to flowering had the greatest residual variation unaccounted for by PC2 with vector loading of 0.717indicating a strong positive correlation between days to flowering and PC3. This suggests that flowering time is a critical trait influencing the overall variation captured by this principal component. The significant residual variation associated with days to flowering in PC3 suggests that its variability may be influenced by additional factors such as genetic, environmental, or management factors not captured in the analysis. Breeders may need to consider these additional influences when selecting for early flowering varieties, as improvements in this trait could lead to enhanced adaptability and yield potential. The unaccounted variation highlights opportunities for further research into the genetic basis of flowering time. Understanding the underlying mechanisms could lead to more targeted breeding strategies that effectively reduce this residual variation and enhance flowering consistency across different environments.

The high vector loading of days to flowering in PC1, combined with its significant residual variation unaccounted for by PC2, underscores its importance as a trait in cowpea breeding. This finding emphasizes the need for comprehensive approaches that consider both direct traits and those influencing flowering time to optimise cowpea productivity and adaptability.

Variables with a vector loadings of ± 0.4 and above, had the greatest contribution to total variation (Fig. 2). These characters were grain yield row^{-1}, total seed weight, days to flowering and maturity, pod length, grain yield plant^{-1} and pods plant^{-1} being the significant contributors towards the divergence based on PCA and biplot analysis (Fig. 1). These results supports the view that grain yield components such as pod length, pods plant^{-1} along with seeds pod^{-1} and days to maturity and flowering, are key traits driving genetic divergence in cowpea. Selection for these traits can lead to development on new cowpea varieties with enhanced yield potential. Days to maturity with eigenvectors of 0.6 and above was considered as having the major effect to the variation. This indicates that the trait influences the overall genetic diversity and variation among cowpea accessions.

An eigenvector value of 0.6 or higher (Table 8), suggests strong correlation, implying that days to maturity is a key factor in determining genetic differences. This trait, likely affects other yield-related characteristics, impacting breeding strategies aimed at improving cowpea genotypes for specific growing conditions and market needs. These results, to certain extent, rhyme with the findings of Hutchinson *et al.* (2017) and Nkhoma *et al.* (2020).

PCA biplots are very effective in deciphering the existence of wider phenotypic variability, by providing the contrast among variables, and interrelationships among genotypes possessing multiple traits facilitating designation of a suitable breeding strategy (Owusu *et al.*, 2021). The biplot grouped the genotypes with characteristics explained by the first two dimensions (PC1 *vs*. PC2), based on combined data across seasons showing groupings of cowpea genotypes and agronomic traits were scattered into the four quadrants depicting wide genetic variability of characters studied (Fig. 1). All the genetically dissimilar cowpea genotypes are viable genotypes that can broaden the genetic base of the cowpea materials for population bulking and utilisation in breeding programme that would contribute to food security and nutrition.

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Hierarchical clustering. Cluster analysis for the phenotypic variables depicted a clear demarcation between the dual-purpose cowpea genotypes (Fig. 3). Based on these agronomic traits, the dendrogram classified the genotypes into three divergent main clusters; namely Cluster I which is comprised of three sub-clusters with 101 genotypes; Cluster II with two sub-clusters comprising 53 genotypes; and cluster III comprising of 70 genotypes.

Cluster I was characterised by genotypes with early flowering and maturity, high number of pods per plant, longer pod length, high number of seeds per pod, high number of grain yield per plant and high total weight per plot (Fig. 3). Cluster II grouped genotypes with high pod length, high number of seeds pod^{-1}, high number of grains pod^{-1} and high grain yield plant^{-1}. Cluster III grouped genotypes with late maturity, high number of pods plant^{-1}, low grain yield plant^{-1} and short days to 50% flowering.

Clustering of genotypes did not group them according to their geographical origin, indicating no relationship between genetic and geographic distribution; mostly due to cross-border diffusion and intermixing of germplasms by farmers and traders resulting to intermediate traits; to a lesser extent introgression of alien genes from the exotic materials (*macrosperma* germplasm) for cowpea genetic base broadening (Kumar *et al.*, 2014) owing to cowpea narrow genetic base. The proximity of the source of the germplasms and availability are a major factor precipitating this observation.

Similar findings were reported by Walle e*t al.* (2019), that clustering of genotypes did not follow patterns of geographical origin, indicating no relationship between genetic and geographic distribution as cowpea genotypes originating from the same regions entered into different clusters indicating the absence of relationships between genetic diversity and geographic origin. This could have resulted from environmental variation, exchange of

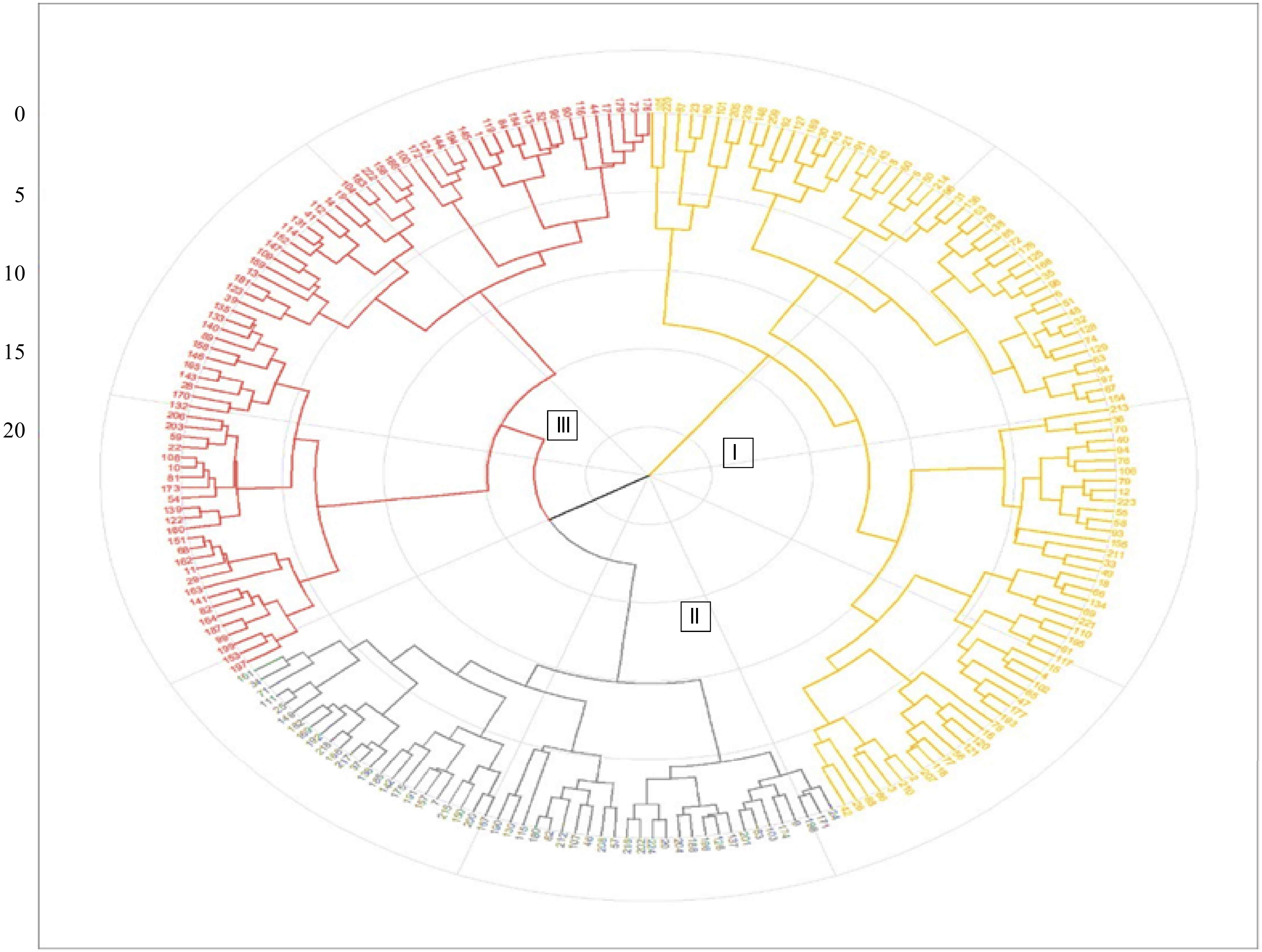

Figure 3. Hierarchical cluster analysis based on agronomic traits measured using ward.D2 method among the 224 Cowpea genotypes, using the Euclidean distance.

germplasm materials among neighboring regions, natural and artificial selection, genetic enrichment and genetic drift (Belay *et al.*, 2021). Jivani *et al.* (2013) inferred that genetic drift and selection in diverse environments, could cause greater diversity than geographic distance. Dwevedi and Lal (2009) reported no connection between geographical distribution and genetic diversity. This implies that genetic variation within cowpea does not correlate with the regions from which the genotypes were collected as factors other than geographic origin, such as breeding practices or historical selection pressures, may play a more significant role in shaping genetic diversity (Xiong *et al.*, 2016); population structure analysis often reveals that genetic differentiation occurs more within populations than between them (Dairo, 2024) and the lack of a direct connection between geographic distribution and genetic diversity highlighting the importance of broadening breeding programmes to include genotypes from various regions (Nkhoma *et al.*, 2020).

Kenyan cowpea breeders aiming at increased food security in lower Eastern regions characterised with inadequate total rainfall, erratic rainfall distribution, long dry spells and delayed onset and/or early cessation of rains that compromises its productivity can utilise the admixture with different genes for breeding cowpea with novel genes for maximum productivity and adaption to the agroecological conditions in sub-Saharan Africa where nutritional insecurity is feared to increase in near future. It is concluded that the presence of high genetic diversity in the genotypes appears to be genetic drift and selection in differing environments, rather than their geographic origin.

CONCLUSION

This study has revealed existence of a substantial level of variation among the dual-purpose cowpea genotypes present among the germplasm in Kenya. Seed yield ha^{-1} was positively and significantly correlated with grain yield row^{-1}, grain yield plant^{-1} and pods plant^{-1}. The positive correlations based on these phenotypic traits are reliable indicators for selecting high-yielding genotypes for breeding programmes aimed at enhancing yield and adaptability.

The first three principal components accounted for 71.6% of total variation with seed yield ha^{-1}, grain yield plant^{-1}, pods plant^{-1}, days to 50% flowering and maturity being the most important traits, contributing largest portion of the phenotypic diversity in parental lines towards achievement of high grain production and early maturing varieties. This information is crucial for breeders focusing on developing high-yielding and early-maturing cowpea varieties in future breeding programmes.

The dendrogram grouped the genotypes into three main clusters based on phenotypic traits and not dictated by geographic origin. These findings encourages a broader approach to selection that transcends geographic boundaries, allowing breeders to utilise diverse genetic materials from various regions.

Further study is necessary on multi-locations towards understanding the genetic basis of the observed phenotypic traits and their interactions with environmental factors to assist in breeding strategies refinement and improve cowpea resilience in changing climatic conditions in sub-Saharan Africa

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