OPEN ACCESS

Journal of Plant Breeding and Crop Science

May 2019
ISSN 2006-9758
DOI: 10.5897/JPBCS
www.academicjournals.org

ACADEMIC JOURNALS
expand your knowledge

ABOUT JPBCS

The **Journal of Plant Breeding and Crop Science (JPBCS)** is published monthly (one volume per year) by Academic Journals.

The Journal of Plant Breeding and Crop Science (JPBCS) (ISSN: 2006-9758) is an open access journal that provides rapid publication (monthly) of articles in all areas of the subject such as Sustainable use of plant protection products, Agronomic and molecular evaluation of recombinant inbred lines (RILs) of lentil, Pollen behaviour and fertilization impairment in plants, Development of a fast and reliable ozone screening method in rice etc.

The Journal welcomes the submission of manuscripts that meet the general criteria of significance and scientific excellence. Papers will be published shortly after acceptance. All articles published in JPBCS are peer-reviewed.

Contact Us

Editorial Office: jpbcs@academicjournals.org

Help Desk: helpdesk@academicjournals.org

Website: http://www.academicjournals.org/journal/JPBCS

Submit manuscript online http://ms.academicjournals.me/

Journal of Plant Breeding and Crop Science

Table of Contents: Volume 11 Number 5 May 2019

ARTICLES

Vol. 11(5), pp. 137-143, May 2019
DOI: 10.5897/JPBCS2018.0788
Article Number: 082377060791
ISSN 2006-9758

http://www.academicjournals.org/JPBCS

Journal of Plant Breeding and Crop Science

Full Length Research Paper

Genetic relationships among regenerated tall coconut (*Cocos nucifera* L.) accessions from multivariate analyses using reliable short list of morphological descriptors in Côte d'Ivoire.

Yao Saraka Didier Martial[1*], Diarrassouba Nafan[1], Dago Dougba Noël[1], Koffi Eric Blanchard Zadjehi[1], Fofana Inza Jesus[1], Konan K. Jean-Noel[2], Konan Konan Jean Louis[3], Bourdeix Roland[4], Sie Raoul Syvère[5] and Zoro Bi I. Arsène[5]

[1]UFR des Sciences Biologiques, Département Biochimie-Génétique, Unité Pédagogique et de Recherche (UPR) de Génétique, Peleforo Gon Coulibaly University, BP 1328 Korhogo, Côte d'Ivoire
[2]CNRA, Biotechnology Research Station of La Mé, 13 BP 989 Abidjan 13, Côte d'Ivoire
[3]CNRA, Marc Delorme Research Station of Port-Bouët, 07 BP 13 Abidjan 07, Côte d'Ivoire
[4]CIRAD, Avenue Agropolis, 34398 Montpellier Cedex 5 France.
[5]UFR Sciences de la Nature, Nangui Abrogoua University, 02 BP 801 Abidjan 02, Côte d'Ivoire

Received 6 November, 2018; Accepted 3 April, 2019

Genetic relationships among 18 regenerated tall coconut accessions from International Coconut Genebank for Africa and Indian Ocean (ICG-AIO) located at Côte d'Ivoire were studied. Analyses were achieved from 17 quantitative characters of the reliable minimal list of agro-morphological descriptors for coconut proposed by Coconut Genetic Resources Network (COGENT) in 2007. From achieved Multivariate Analyses (MVA) two geographical clusters including Afro-Indian and Far East were observed in the first generation of regenerated tall coconut accessions. In addition regenerated tall coconut accessions whose parents come from South Pacific geographical area were the more varied. This typology is similar to the one of the initial introductions previously established. Thus, creation of improved hybrids from heterosis effect searching a long time exploited in tall coconut accessions can always be pursued with regenerated accessions in Côte d'Ivoire coconut program.

Key words: Tall regenerated accessions, minimum list of coconut descriptors, morphological typology, multivariate analyses (MVA), Côte d'Ivoire.

INTRODUCTION

Coconut (*Cocos nucifera* L.), is an oleaginous, monocotyledonous plant from Arecaceae family (Teulat et al., 2000) and cultivated in wet tropical area. Coconut is used like food plant in many countries and is supplier

*Corresponding author. E-mail : didierys@yahoo.fr., Tel: (+225) 04737926.

of fatty acid to oil industry. In the Côte d'Ivoire economy, coconut palm is a very important speculation to reduce poverty at the littoral. In this area more than 20 000 families depend to coconut farming (Assa et al., 2006). In 2017, the area under coconut in Côte d'Ivoire was 103 239 ha (FAOSTAT, 2017). To sustain coconut sector, the researchers created improved coconut varieties. Coconut breeding program started by the mass selection of the best individuals from local ecotype West African Tall (WAT) (Bourdeix, 1988) that produced an average of 0.6 ton of coprah ha^{-1} $year^{-1}$. So, annual coprah output reached 1.2 ton/ha. In the worry aim to increase the genetic gain at Côte d'Ivoire, breeders opted for the widening of the genetic basis by exotic coconut population introduction in field genebank in order to landing the inbreeding depression effect (Bourdeix, 1990). Thus, 37 accessions of the tall coconut populations and 16 populations of the dwarf were introduced from inter-tropical area between 1960 and 1980 (Fremond and De Nuce, 1971). Those coconut accessions which are conserved at field became old. The inflorescences located in foliar crown of the tall coconut palms that height exceeds 12 m become inaccessible (Bourdeix et al., 2010). Consequently, from 1987 the regeneration of aging accessions is regularly undertaken by controlled pollinated method (Konan et al., 2008) to carry out seed productions.

Today, agro-morphological diversity of the first generation cycle of regenerated accession of tall coconut palms planted in ICG-AIO located at Côte d'Ivoire is unknown. However, the knowledge of the agro-morphological traits about these regenerated accessions is important, not only for efficient management and conservation of coconut resources but also for pursue coconut breeding program in Côte d'Ivoire. Indeed, during regeneration of old coconut accession with controlled pollination method the risk of genetic diversity erosion seems to exist. Such modifications due to the artificial selection on the parental accession of plants were reported (Johnson et al., 2002; Reddy et al., 2006). In ICG-AIO, several chronological studies about agro-morphological characterization of the tall coconut accessions initially introduced were achieved (De Nuce and Wuidart, 1979; De Nuce and Wuidart, 1981; Sangaré et al., 1984; N'Cho et al., 1993; Konan, 2008) from varied quantitative descriptors (IPGRI, 1995). Basing of the multivariate analysis approaches the works of N'Cho et al. (1993) showed significant differences among seventeen tall coconut cultivars from 24 vegetative traits. Also, important morphological variability in coconut ecotypes coming from Pacific was found. Based on observations of seventeen morphological traits, Konan (2008) was classified tall coconut accessions in ICG-AIO under two groups. The first group is composed of the accessions of african origin and the Indian ocean. The second group consists of the accessions coming from South Pacific, the extreme Orient and Latin America. However, these studies remain partial because they don't take into account the different generations of accessions in coconut field genebank. However, little information is available concerning morphological variation between and within first generation (G1) of tall coconut accessions planted in coconut genebank hosted by Marc Delorme research station in Côte d'Ivoire. Besides, during morphological diversity studies in coconut palms, the number and nature of the morphological descriptors used are varied. Considering the time that can take for the characterization of a high sample of accessions, COGENT recommended in 2007 a minimal list of 17 quantitative descriptors (www.bioversityinternational.org). Then, the reliability of this short list of agro-morphological descriptors for coconut diversity studies was proved in agro-climatic conditions of Côte d'Ivoire for survey about morphological diversity of coconut accessions hosted by Marc Delorme Research station of the Centre National de Recherche Agronomique (CNRA) (Yao et al., 2015).

The objective of the present study was to assess from this reliable short list for coconut descriptors established by the COGENT the relationships of morphological similarity among regenerated tall coconut accessions in ICG-AIO.

MATERIALS AND METHODS

Plant material

The analyses were done using the first cycle of 18 tall coconut accessions (Table 1) regenerated by controlled pollination method according to Konan et al. (2008). The regenerated WAT G1 accession used as control and planted in three experimental plots No. 043 (Latitude (5°15.725' N), Longitude (3°50.236' W) and Altitude (12 m)), No. 081 (Latitude (5°16.245' N), Longitude (3°50.746' W) and Altitude (14 m) and No. 091 (Latitude (5°16.373' N), Longitude (3°50.758' W) and Altitude (19 m)) was counted only one time because the different populations which compose it are similar at genetic level (Lebrun et al., 1998; Konan, 2008). All regenerated accessions were planted in ICG-AIO hosted by Marc Delorme research station of CNRA located at Côte d'Ivoire. The climate is Sudano-Guinean type and characterized by two dry seasons (January to April and August to September) and two rainy seasons (May to July and October to November). During the decade from 2000 to 2010 the annual total rainfall and sunniness were respectively 1827.9 mm and 2281.85 h onto Marc Delorme research station. Monthly averages during this same decade of the temperature and hygrometry were 26.29°C and 86.72%, respectively.

Experimental designs and assessment of the agro-morphological characters

The study was conducted on three plots for coconut genetic resources conservation. Coconut palms were planted with density of 143 trees ha^{-1}. The experimental plots, No. 81 and No. 91, were conceived in Fisher blocks with 6 repetitions of 24 trees (4 rows of 6 trees). For these two plots, 5 healthy plants were selected randomly in each elementary plot, either a total of 30 trees per accession. The third plots No. 43 was planted in alternated rows design and the number of individuals sampled was varied from 8 to 20. In all

Table 1. Characteristics of first cycle of 18 regenerated accessions (G1) studied in tall coconut genebank in Côte d'Ivoire. WAT G1 regenerated accession used as control was counted only one time.

Accession	Code	Parental accession origins (Geographical group)	Sample size
West African Tall (Control)	WAT G1	Côte d'Ivoire (Africa)	20
Grand Cambodge Kopal Tani	KAT4 G1	Cambodia (Far East)	8
Grand Cambodge Feu Kompong Trach	KAT5 G1	Cambodia (Far East)	20
West African Tall (Control)	WAT G1	Côte d'Ivoire (Africa)	30
Sri Lanka Tall	SLT G1	Sri Lanka (Indian Ocean)	30
Rotuma Tall	RTT G1	Fidji Island (South Pacific)	30
Tonga Tall	TONT G1	Tonga Island ((South Pacific)	30
Vanuatu Tall	VTT G1	Vanuatu (South Pacific)	30
Tagnanan Tall	TGT G1	Philippines (Far East)	30
West African Tall (Control)	WAT G1	Côte d'Ivoire (Africa)	30
Cambodia Ream Tall	KAT07 G1	Cambodia (Far East)	30
Cambodia Sre Cham Tall	KAT08 G1	Cambodia (Far East)	30
Cambodia Battambang Tall	KAT09 G1	Cambodia (Far East)	30
Cambodia Koh Rang Tall	KAT10 G1	Cambodia (Far East)	30
Tahiland Sawi Tall	THT1 G1	Thaïland (Far East)	30
Tahiland TaKo Samui Tall	THT4 G1	Thaïland (Far East)	30
Tahitian Tall	TAT G1	Polynesia (South Pacific)	30
Rangiroa Tall	RGT G1	Polynesia (South Pacific)	30
Rennel Island Tall	RIT G1	Solomon Island (South Pacific)	30
Solomon Island Tall	SIT G1	Solomon Island (South Pacific)	30
Total	18	9 (4)	558

G1: 1st regenerated accession cycle obtained by controlled pollination method

plots, a total of 558 individuals were observed (Table 1). All observations were done from quantitative characters of the minimal list of coconut descriptors proposed by the COGENT (www.bioversityinternational.org) described in detail by Nuce and Wuidart (1982) and Yao et al. (2015). The morphological traits observed were 17 with breakdown of 4 stem, 2 floral, and 11 fruit traits.

Stem traits

Stem height (cm), bulb girth at 20 cm above soil level (cm), stem girth at 1.5 cm heigh and Height between 11 leaf scars (cm) were observed on the stem.

Floral traits

Number of female flowers and number of spikelets were counted on inflorescence of rank n.10.

Fruits traits

Fruit weight (g), husked nut weight (g), shell weight (g), endosperm thickness (mm), husk weight (g), water weight (g), endosperm weight (g), copra weight per nut (g), dry meat oil content (%), number of bunches per palm per year and number of fruits harvested per palm per year were assessed.

Data analysis

The relationships between regenerated tall coconut accessions were carried out by fours Multivariate analyses (MVA) methods (Karsai et al., 2000) using Statistica version 7.1 software (StatSoft France, 2005). Principal components analysis (PCA) was performed from the first two principal components were obtained. PCA is a data reduction method used to reduce the number of characters and to detect structure in the relationships between these characters. Cluster analysis (CA) was performed using Euclidean distance and an average fusion strategy (UPGMA) as indicators of similarity and aggregation procedure, respectively. The clusters were then represented in a dendrogram. The differences between groups established from CA were tested with Multivariate Analysis of Variance (MANOVA) at 5% threshold of likelihood. Discriminant analysis (DA) was done to determine morphological distances like Mahalanobis distances between defined clusters (Ivandro et al., 2014).

All the previously stated analyses were done on matrix of weighted mean values of each of the 17 agro-morphological characters per accession obtained from the mean value of the WAT G1 accession used as control and planted in each experimental plot. Weighting method permitted to minimize the environmental effects on agro-morphological characters expression at the accessions planted onto different experimental plots. The raw of

Table 2. Agro-morphological factors implied in variability of the regenerated accessions of tall coconut palms studied from PCA analysis.

Identified factor	Variance (%)	Total accrued variance (%)	Character (correlation value between Character-Factor)
Fruit components	38.91	38.91	NW (0.93), HNW (0.98), SW (0.90), WW (0.92), EW (0.95), CWN (0.85).
Vegetative growth	21.08	59.99	SH (-0.76), H11LS (-0.85), NFF (0.74).
Bunch yield	10.48	70.47	NBPY (0.73)

Fruit weight (FW); Husked nut weight (NW); Shell weight (SW); Water weight (WW); Endosperm weight (EW); Copra weight per nut (CWN); Stem height (SH); Height between 11 leaf scars (H11LS)**;** Number of female flowers (NFF); Number of bunches per palm per year (NBPY).

mean data collected for each agro-morphological descriptor per accession on three distinct experimental plots were weighted from relation:

$$\bar{X}_{\text{i weighted}} = \frac{\left(\bar{X}_{\text{Ci x}}\, \bar{X}_{\text{ij}}\right)}{\bar{X}_{\text{Cij}}}$$

with $\bar{X}_{\text{i weighted}}$ the weighted mean of the descriptor i, $\bar{X}_{\text{Ci}}$ the mean of the WAT G1 control on all the plots studied for the descriptor i, $\bar{X}_{\text{ij}}$ the raw mean of the descriptor i in the plot j and $\bar{X}_{\text{Cij}}$ the mean average of the descriptor i for the WAT G1 control in plot j.

RESULTS

Agro-morphological variation and dendrogram

KMO (Kaiser-Meyer-Olkin) index that was superior to 0.7 indicates that the factorization of the 17 studied characters is a statistically acceptable solution. In the same way the Bartlett sphericity test on all characters showed that the factorial model is appropriated (Chi-square = 478.89, p<0,001). So, the first three principal factors that presented an eight value superior to 1 following Kaizer method accounted for 70.48% of variation were implied in variability of the regenerated accessions of tall coconut palms (Table 2).

The factor 1 expressed 38.91% of the variation. It presented a positive correlation with FW, HNW, SW, WW, EW and CWN. The component 1 can be defined as factor characterized by fruit components. The factor 2 accounted 21.08% of the total variation. It was explained by the variables, SH and L11LS that there are correlated negatively and the variable NFF that there is correlated positively. The component 2 can be defined as vegetative growth factor. The character NBPY contributed to the formation of the component 3 accounted 10.48% of the total variation (Table 2).

Dendrogram showed two morphological clusters within regenerated tall coconut accessions studied (Figure 1). The two geographical clusters, Afro-Indian and Far East, were distinguished at 600 Euclidean distances. The dendrogram showed that South Pacific accessions were met in both two clusters.

Differences between two geographical clusters “Afro-Indian” and Far East”

The difference between two majors groups according to agro-morphological characters used was significant following the multiple analysis of variance (MANOVA) at 5% likelihood (F = 8.08, p = 0.027). Data exam showed that this difference comes from 8 of the 17 characters analyzed (Table 3). These 8 characters that were essentially those describing the production such as fruit weight (FW), husked nut weight (HNW), shell weight (SW), water weight (WW), endosperm weight (EW), coprah weight per nut (CWN), dry meat oil content (DMOC) and number of fruit per palm per year (NFPY) were permitted a complete distinction of the two geographical clusters (Table 3).

Afro-Indian cluster was composed of 6 regenerated accessions that have a high yield of small fruit and oil. This group contains WAT G1, one accession coming from Indian ocean (SLT G1) and 4 accessions coming from South Pacific area (TONT G1, TAT G1, SIT G1 and VTT G1).

Far East cluster was composed of 12 regenerated accessions producing heavy fruits with high coprah content. It contains all 9 regenerated accessions coming from Far East (THT1 G1, THT4 G1, KAT4, KAT5, KAT7 G1, KAT8 G1, KAT9 G1, KAT10 G1 and RTT G1) and 3 accessions from South Pacific (RIT G1, TAGT G1 and RGT G1).

Lambda Wilks’test from discriminant analysis, associated to the hypothesis of equality of the middle vectors between two agro-morphological groups was significant at 5% likelihood (F = 0.234, p = 0.039). So the two major groups established from cluster analysis were different. Mahalanobis distance between two agro-morphological clusters (182.81 Mahalanobis units) was significant at 5%

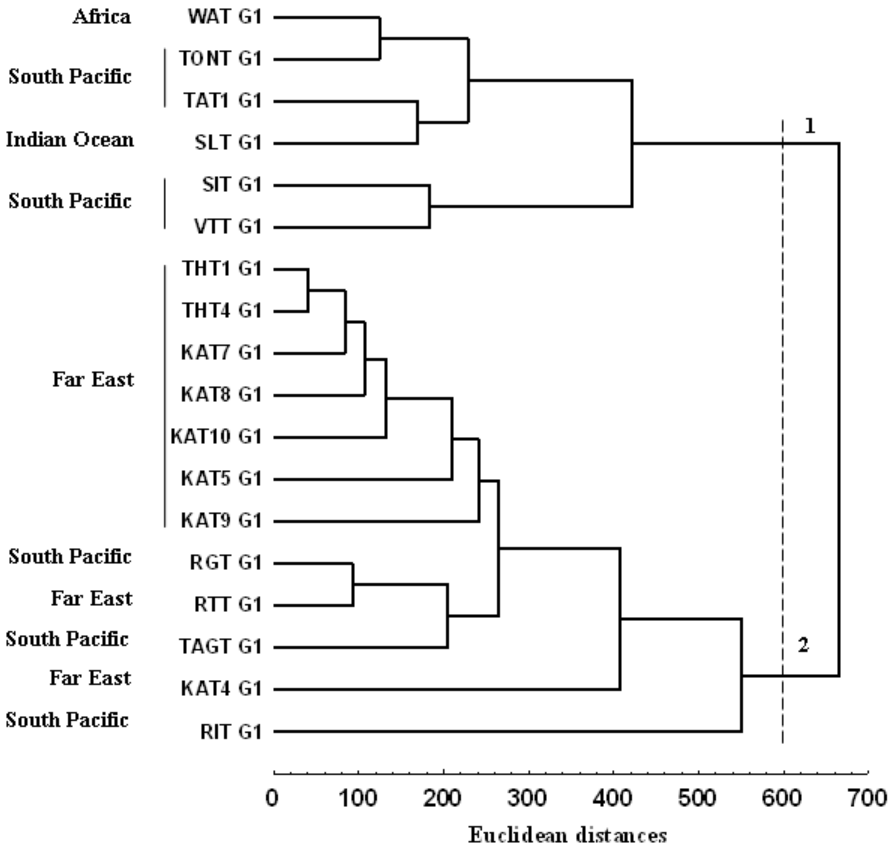

Figure 1. UPGMA dendrogram of 18 regenerated accessions in tall coconut genebank of Côte d'Ivoire. Analysis using weighted mean values from 17 quantitative characters of the minimal list for coconut descriptors. Two clusters of regenerated accessions of tall coconuts; Afro-Indian and Far East groups.

likelihood (F = 9.234, p = 0.043).

DISCUSSION

The observed differences between coconut populations with regard to agro-morphological traits are indirect or direct representations of differences at the DNA level. For this study, agro-morphological clustering of the first generation G1 of regenerated accessions of tall coconut palms was analyzed. The investigations revealed two agro-morphological clusters into these tall accessions that are Afro-Indian and Far East. This clustering could reveal two biological realities.

Firstly, the studied morphological descriptors seem to discriminate tall coconut populations with the same level like foliar polyphenols markers (Jay et al., 1989) and the genetic markers such as RFLP (Lebrun et al., 1998) and SSR (Konan, 2008). These genetic markers were permitted in some cases to group in same way coconut populations hosted by international genebank at Côte d'Ivoire. These studies oppose an Afro-Indian cluster to another compound of the accessions that come from South Pacific, Far East and Latin America. The reliability of this tall coconut populations clustering would be due to biological data provide to fruit component descriptors and the weighting method in relation to fragmented means of WAT G1 control used. Indeed, the study of N'cho et al. (1993) achieved on the same origins of coconut populations used in absence of the fruit component descriptors and no correction of raw data by weighting method was generated less clean of tall coconut clustering in nine morphotypes. Using of the weighing method of raw mean data of each descriptor assessed on tall coconut accessions planted onto different plots in relation to fragmented means of WAT G1 control is minimized environment effects on characters expression (Bourdeix, 1989). Thus, the expression of the phenotypes due to the main effects of the genes has been only revealed.

Table 3. Characteristics of two coconut geographical groups, Afro-Indian and Far East, established among first regenerated accession (G1) of Tall coconut palms from cluster analysis**.**

Short list of quantitative descriptors for coconut	Weighted means		F	p
	Afro-Indian group (N = 6)	Far East group (N = 12)		
Stem height (cm)	639.91	679.02	1.035	0.324
Bulb girth at 20 cm above soil level (cm)	155.40	146.39	0.940	0.347
Steem girth at 1.5 cm heigh (cm)	86.92	89.62	1.860	0.192
Height between 11 leaf scars (cm)	73.67	73.18	0.011	0.917
Number of female flowers	25.55	21.01	1.089	0.312
Number of spikelets	41.62	43.11	0.507	0.487
Fruit weight (g)	1023.90	1447.60	32.141	<0.001
Husked nut weight (g)	613.40	1006.50	44.095	<0.001
Shell weight (g)	139.75	204.86	33.325	<0.001
Endosperm thickness (mm)	11.48	11.11	1.091	0.312
Husk weight (g)	415.37	457.58	1.171	0.295
Water weight (g)	146.02	342.15	42.390	<0.001
Endosperm weight (g)	328.38	464.17	21.404	<0.001
Copra weight per nut (g)	201	265.72	13.022	0.002
Dry meat oil content (%)	70.13	65.91	9.270	0.008
Number of bunches per palm per year	6.36	6.03	0.744	0.401
Number of fruits harvested per palm per year	33.78	26.75	4.996	0.040

Secondly, the morphological clustering of the first cycle (G1) of tall coconut accessions regenerated by controlled pollination method with the one of the initial introductions (G0) was conform (Konan, 2008). Indeed, the sexual reproduction involves by control pollinations between male and female individuals chosen as parents would protect the organisms against eventual mistakes of DNA replication (Guetet et al., 2008). That conferred to the regenerated accessions (G1) an adaptation to climatic change and modifications concerning soil chemical properties. According to Ivandro et al. (2014), genetic distance measures based on phenotypic characters are one of the main multivariate techniques used to provide criteria for choosing parents. Thus, the parental tall coconut accessions to choose in the crossings should belong to the two revealed groups. There is a high probability of selecting transgressive genotypes due to the occurrence of heterosis and the action of complementary dominant genes (Ivandro et al., 2014). Also, the morphological structure of the regenerated accessions was revealed that those whose parents come from South Pacific are the more varied as one reported by N'cho et al. (1993) and Sugimura et al. (1997) in coconut genebank of Côte d'Ivoire and Philippines respectively.

Conclusion

This survey was initiated to evaluate regenerated tall coconut diversity using reliable short list of agro-morphological descriptors. The results revealed two genetically pools into regenerated Tall coconut accessions in ICG-AO, Afro-Indian and Far East. Also, it appears from analysis of the present results in relation to the findings of the previous research works that the agro-morphological clustering of the regenerated Tall coconut accessions (G1) was conform to the one of the parental accessions (G0) previously established in ICG-AO. Until further DNA study at large scale including all regenerated Tall coconut accessions planted in ICG-AO, if the morphological distances between these two groups of regenerated accessions reflect in fact the genetic distances, creation of improved coconut hybrids from heterosis effect searching a long time exploited in Tall coconut accessions can be pursued in coconut breeding program of Côte d'Ivoire

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

ABBREVIATIONS:

COGENT: Coconut Genetic Resources Network; **ICG-AIO:** International Coconut Genebank for Africa and Indian Ocean; **MVA:** Multivariate Analyses.

REFERENCES

Assa R. Konan K, Nemlin J, Prades A, Agbo N. Sie R (2006). Diagnostic de la cocoteraie paysanne du littoral ivoirien. Sciences et Nature. Série A, Biosciences Agronomie Environnement Biotechnologie 3(2):113-120.

Bourdeix R (1988). Efficacité de la sélection massale sur les composantes du rendement chez le cocotier. Oléagineux 43(7):283-290.

Bourdeix R (1989). La sélection du cocotier (Cocos nucifera L.). Etude théorique et pratique. Optimisation des stratégies d'une amélioration génétique. Thèse de Doctorat, Université de Paris Sud, Centre d'Orsay (France), 194 p.

Bourdeix R, Konan J, Saraka D, Allou K (2010). Regeneration of old coconut accessions in the International Genebank for Africa and the Indian Ocean. In: Rival Alain (ed.). Palms 2010, Biology of the palm family (Abstracts books): International Symposium 5-7 May 2010, Montpellier, France P 55.

De Nuce L, Wuidart W (1979). Les cocotiers grands de port Bouët (Côte d'Ivoire). 1- Grand Ouest Africain, Grand de Mozambique, Grand de Polynésie, Grand de Malaisie. Oléagineux 34(7):339-349.

De Nuce L, Wuidart W (1981). Les cocotiers Grands à Port-Bouët (Côte d'Ivoire). 2- Grand Rennell, Grand Salomon, Grand Thaïlande, Grand Nouvelles-Hébrides. Oléagineux 36(7):353-362.

De Nuce L, Wuidart W (1982). L'observation des caractéristiques de développement végétatif, de floraison et de production chez le cocotier. Oléagineux 37(6):291-297.

FAOSTAT (2017). [January, 31th 2019].Available online http://www.fao.org/faostat/en/#data/QC

Fremond Y, De Nuce L (1971). Le bloc d'amélioration du cocotier de Port Bouët. Oléagineux 2(1):71-82.

Guetet A, Boussaid M, Neffati M (2008). Etude de la vigueur reproductive de populations naturelles d'Allium roseum en Tunisie. Plant Genetic Resources Newsletter 153:28-35.

IPGRI (1995). Descriptors for coconut (*Cocos nucifera* L.). International Plant Genetic Resources Institute (IPGRI), Rome (Italy) P 61.

Ivandro B, Fernando I, Antonio C (2014). Parental Selection Strategies in Plant Breeding Programs. Journal of Crop Science and Biotechnology 10(4):211-222.

Jay M, Bourdeix R, Potier F, Sanlaville C (1989). Premiers résultats de l'étude des polyphénols foliaires du cocotier. Oléagineux 44:151-161.

Johnson R, Bradley L, Evans A (2002). Effective population size during grass germplasm seed regeneration. Crop Science 42:286-290.

Karsai I, Meszaros K, Lang L, Hayes P, Bedo Z (2000). Multivariate analysis of trait determining adaptation in cultivated barley. Plant Breeding 120:21-22

Konan J, Bourdeix R, George M (2008). Directives pour la régénération: cocotier. In: Dulloo M, Thormann I, Jorge M, Hanson J editors. Crop specific regeneration guidelines [CD-ROM]. System-wide Genetic Resource Programme, Rome, Italy.

Konan J (2008). Evaluation de la diversité agromorphologique et moléculaire de la collection internationale de cocotier (*Cocos nucifera* L.) en Côte d'Ivoire. PhD thesis, University of Cocody, Côte d'Ivoire, 150 p.

Lebrun P, N'cho Y, Seguin M, Grivet L, Baudouin L (1998). Genetic diversity in coconut (*Cocos nucifera* L.) revealed by restriction fragment length polymorphism (RFLP) markers. Euphytica 101:103-108.

N'cho Y, Sangaré A, Bourdeix R, Bonnot F, Baudouin L (1993). Evaluation de quelques écotypes de cocotier par une approche biométrique. 1. Etude des populations de grands. Oléagineux 48(3):121-132.

Reddy K, Upadhyaya H, Reddy L, Gowda C (2006). Evaluation of Pollination Control Methods for Pigeonpea (*Cajanus cajan* (L.) Millsp.) Germplasm Regeneration. SAT eJournal, ejournal.icrisat.org 2(1).

Sangaré A, Le Saint J, De Nuce L (1984). Les cocotiers Grands à Port-Bouet (Côte d'Ivoire). 3- Grand Cambodge, Grand Tonga, Grand Rotuma. Oléagineux 39(4):205-213.

Sugimura Y, Itano M, Salud C, Otsuji K, Yamaguchi H (1997). Biometric analysis on diversity of coconut palm: cultivar classification by botanical and agronomical traits. Euphytica 98:29-35.

Teulat B, Aldam C, Trehim P, Lebrun P, Barker J, Arnold G, Karp A, Baudouin L, Rognon F (2000). An analysis of genetic diversity in coconut (*Cocos nucifera* L.) population from across the geographical range using sequence tagged microsatellites (SSRs) and (AFLPs). Theoretical applied Genetic 100:764-771.

Yao S, Konan J, Sie R, Diarrassouba N, Lekadou T, Koffi E, Yoboue K, Bourdeix R, Issali A, Doh F, Allou K, Zoro Bi I (2015). Fiabilité d'une liste minimale de descripteurs agromorphologiques recommandée par le COGENT dans l'étude de la diversité génétique du cocotier (*Cocos nucifera* L.). Journal of Animal and Plant Sciences 26(1):4006-4022. http://www.m.elewa.org/JAPS

Vol. 11(5), pp. 144-157, May 2019
DOI: 10.5897/JPBCS2018.0800
Article Number: 91052C760793
ISSN 2006-9758

http://www.academicjournals.org/JPBCS

Journal of Plant Breeding and Crop Science

Full Length Research Paper

Evaluation of genetic variability, heritability, genetic advance and correlation for agronomic and yield components in common bean landraces from South western Kenya

Henry N. Anunda[1*], Evans N. Nyaboga[2] and Nelson O. Amugune[1]

[1]School of Biological Sciences, University of Nairobi, P. O. Box, 30197 – 00100, Nairobi, Kenya.
[2]Department of Biochemistry, University of Nairobi, P. O. Box, 30197 – 00100, Nairobi, Kenya.

Received 27 December, 2018; Accepted 3 April, 2019

The present study was conducted to estimate the genetic variability, heritability, genetic advance and association among selected agronomic traits of common bean landraces from South western Kenya. The field experiment was conducted using 52 common bean landraces at the Kenya Agricultural and Livestock Research Organization (KALRO), Kisii Research Center during 2015 and 2016 main cropping seasons. The experimental design was randomized complete block (RCBD) with three replications. Analysis of variance revealed significant differences indicating the existence of genetic variability among the 52 landraces for 14 quantitative traits studied. The genotypic coefficient of variation ranged from 1.00% for biological yield to 84.69% for pod width, while the phenotypic coefficient of variation ranged from 2.34% for biological yield to 84.40% for number of branches. The estimated broad sense heritability ranged from 60.20% for seeds per plant to 87.57% for days to emergence. Estimates of genetic advance as percent of mean ranged from 10.15% for biological yield to 97.45% for number of branches. Positive and highly significant association of plant height, days from planting to 50% flowering, number of pods per plant and biological yield was observed with seed yield per plant, hence these traits may be directly attributed for the improvement of seed yield. High hereditability and genetic advance was obtained for plant height, 100 seed weight, pod width and number of branches, indicating additive gene effects in controlling the traits and these traits could be used as suitable criteria for selection and improvement of common bean in breeding programs.

Key words: *Phaseolus vulgaris*, phenotypic variability, genotypic variability, quantitative traits, heritability, genetic advance, breeding.

INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) is the most important grain legume, second to maize as a stable food crop in Kenya. Africa produces 17% of the world total production, of which 70% is from Eastern Africa. Kenya

*Corresponding author. E-mail: hnranunda42@gmail.com.

produces 400-1200 kg/ha, mainly from intercropping with maize by small-scale farmers. Common bean is an important source of protein and minerals especially iron and zinc. It is a dual-purpose crop producing grains as well as fodder for livestock. Consumption of beans confers humans with various health benefits including reduction of cholesterol level, reduction of coronary heart diseases and decreases diabetes and obesity (Broughton et al., 2003; Pereira et al., 2015). Common beans also play a very important role in sustaining soil fertility by adding atmospheric nitrogen and organic matter to the soil. As a cover crop it is efficient in suppressing weeds and prevents soil erosion (Geil and Anderson, 2014).

Production of common bean in South western Kenya is constrained by various abiotic and biotic stresses. Diseases caused by fungi, bacteria and viruses are considered to be the second biggest constraint to bean production after low soil fertility, causing over 90% or total crop loss (IBPGR, 1982). Insect pests especially pod borers and weevils may also cause yield loss of up to 80%. In many bean producing areas of Kenya, there is lack of clean seed planting materials and varieties grown are often low yielding (Bennick, 2005). There is also a problem of lack of cultivars with market qualities and consumer quality attributes such as fast cooking. These factors have reduced the germplasm sources used in hybridization and have limited the genetic variability available for breeding programs. Development of high yielding cultivars with resistance to major bean diseases is an important breeding priority to reduce impact of diseases and increase common bean production in South- western Kenya. Characterization of plant germplasm using agronomic traits has been used for various purposes including identification of duplicates, correlation with characteristics of agronomic importance and identification of genotypes resistant to pests and diseases (Smartt, 1988a, b).

The selection of desirable genotypes is usually based on the genetic variation of agronomic or quantitative traits such as yield and its components. It is therefore necessary to study the relationship between genotype variability and yield components for efficient utilization of common bean genetic resources in improvement programs. Heritability is the degree of genetic control associated with certain heritable important traits (Addissu, 2011). It indicates how much of the genetic variability has a genetic origin and gives necessary information for the selection process (Falconer, 1981). The selection of superior genotypes is proportional to the amount of genetic variability present and the extent to which the characters are inherited (Scarano et al., 2014). Therefore, adequate information on the magnitude and type of genetic variability and their corresponding heritability is important in the improvement of grain yield potential of crops in breeding programs.

Yield improvement is an important breeding objective of most crop improvement programs (More and Borkar). Similar to other crops, yield in common bean is a complex trait comprising of many morphological, physiological and agronomic traits. Seed yield is affected by genotype and environmental factors because of its quantitative properties. Effectiveness of selection is dependent upon the availability of large genetic variability present in the breeding material for the target character and the extent to which it is heritable (Atta et al.,, 2008). It also depends on the direction and magnitude of association between the traits to be improved (More and Borkar, 2016). However, limited attention has been given to studies on genetic variability, heritability and genetic advance of yield and associated traits in common bean landraces to improve the seed yield in south Western Kenya. Therefore, the present study was carried out to assess the extent of genetic variability, heritability and genetic advance among common bean landraces for yield and related traits and examine their correlation with seed yield for efficient design of common bean breeding schemes.

MATERIALS AND METHODS

Plant materials

A total of 52 common bean landraces were used in this study. Seeds of 26 common bean landraces were collected from farmers' fields in different agro-climatic zones and market centers of Kisii County, South western Kenya. The accessions were collected according to the procedure of Plant Genetic Resources International Institute (IBPGR, 1991). Seeds of 26 accessions were obtained from the National Genebank of Kenya, Muguga, Kiambu. The germplasm from the Genebank were collected from farmers' fields in South western Kenya in 1980 and preserved (Table 1).

Description of the study site

Fifty two common bean landraces were planted at the Kenya Agricultural and Livestock Organization (KALRO), Kisii County, South western Kenya (situated at about 0.68° South latitude, 34.77° East longitude, at an elevation of between 1450-2210 m above sea level). The site falls in the Lower Highlands one and two (LH1 and LH2), Upper Midland one (UM1), Lower Midland one and two (LM1 and LM2) Agro-Ecological Zones (AEZs). The soil type was deep, fertile, well-drained red volcanic (nitosols). The county has climatic conditions of average rainfall ranging from 1,400 - 2,600 mm per annum and mean annual temperature ranging from 15-28°C (FA0, 2015).

Experimental design and establishment of plants in the field

The genotypes were evaluated in two consecutive planting seasons namely between March and July, 2015 and repeated in the same period in 2016. The experiment consisted of a randomized complete block design (RCBD) with three plot replications for each landrace. The cultivars were grown in plots measuring 3 m × 4 m with distance between rows of 50 cm. Seeds were sown on raised beds with 40 cm row to row spacing and 15 cm plant to plant spacing at a depth of 5 cm. One teaspoonful of Diammonium phosphate (DAP) was added to each hole at planting. Normal crop.

Table 1. Origin, codes and local names of germplasm.

Entry	Genotype Code	Local name	Source of genotype
S1	LRC 006	Esaitoti	Daraja mbili mkt
S2	LRC 008	Cinchae	Kisii mnp mkt
S3	LRC 018	Richore	Marani
S4	GK030171	NNP	Gene bank
S5	GK030217	NNP	Gene bank
S6	GK030178	NNP	Gene bank
S7	GK030185	NNP	Gene bank
S8	GK036526	NNP	Gene bank
S9	GK030261	NNP	Gene bank
S10	GK030200	NNP	Gene bank
S11	GK030204	NNP	Gene bank
S12	GK030210	NNP	Gene bank
S13	GK030246	NNP	Gene bank
S14	GK036524	NNP	Gene bank
S15	GK030211	NNP	Gene bank
S16	GK030249	NNP	Gene bank
S17	LRC 001	Ekenagwa	Kisii Mn Mkt
S18	LRC005	Egirini	Kisii Mn Mkt
S19	LRC010	Bunda entambe	Daraja mbili mkt
S20	LRC016	Manoa emwamu	Kisii Mn Mkt
S21	LRC015	Ekoko enyenge	Suneka
S22	LRC026	Nyaibu/Bunda enetu	Daraja mbili mkt
S23	LRC011	Ekebure	Daraja mbili mkt
S24	LRC012	Enyamatobu	Kisii Mn Mkt
S25	LRC021	Morogi	Nyacheki
S26	LRC024	Ekoko entambe	Keumbu
S27	LRC019	Manoa endabu	Kisii Mn Mkt
S28	LRC022	Enyamwam**u**	Daraja mbili mkt
S29	GK030194	NNP	Gene bank
S30	GK030227	NNP	Gene bank
S31	GK030239	NNP	Gene bank
S32	GK036530	NNP	Gene bank
S33	LRC 023	Eosama	Nyamarambe
S34	LRC 009	Eroyoo	Kenyenya
S35	LRC025	Amaika inse	Kisii Mn Mkt
S36	LRC020	Ritinge	Daraja mbili mkt
S37	LRC 007	Eamini	Nyamache
S38	LRC 014	Esaire	Daraja mbili mkt
S39	LRC 017	MASAKU	Marani
S40	GK 030244	NNP	Gene bank
S41	GK 036527	NNP	Gene bank
S42	LRC 004	Emwetemania	Masimba
S43	LRC 013	Onyoro	Daraja mbili mkt
S44	GK036523	NNP	Gene bank
S45	GK030257	NNP	Gene bank
S46	GK036522	NNP	Gene bank
S47	GK030260	NNP	Gene bank
S48	GK030198	NNP	Gene bank
S49	GK030259	NNP	Gene bank
S50	GK030167	NNP	Gene bank
S51	LRC003	Enchano	Daraja mbili mkt
S52	LRC002	Egiero	Kisii Mn Mkt

management practices were carried out as recommended including weeding, pest/disease checks and top dressing

Agronomic data collection

Fourteen descriptors were surveyed for each common bean landrace at appropriate growth stage. The descriptors developed for *Phaseolus spp.* were used with some modifications (IBPGR, 2013). Data were recorded on a plot basis using ten individual plants selected randomly from the two central rows of each plot. Measurement unit and measurement procedure of each trait are given in Table 2.

Statistical analysis

Analysis of variance

The data collected on all the agronomic traits studied were subjected to analysis of variance (ANOVA) for the randomized complete block design (RCBD). The treatment means were clustered by Scott-Knott test at 5% probability levels for significance

Phenotypic and genotypic coefficient of variation

The estimates of phenotypic and genotypic coefficient of variation were calculated as described by Singh and Chaudhary (1979):

$$PCV\ (\%) = \frac{\sqrt{Vp}}{Mean}\ X100$$

$$GCV(\%) = \frac{\sqrt{Vg}}{mean}\ X\ 100$$

$$\mathrm{GCV(\%)} = \frac{\sqrt{\mathrm{Vg}}}{\mathrm{mean}}\mathrm{Xd}$$

where PCV is phenotypic coefficient of variance, VP is phenotypic variance, GCV is genotypic coefficient of variance, and Vg is genotypic variance. GCV and PCV values were categorized as low (0-10%), moderate (10-20%), and high (20% and above) as indicated by Subramanian and Menon (1973) and Cherian (2000).

Heritability

It was estimated as the ratio of total genotypic variance to the phenotypic variance according to Falconer (1981):

$$H^2\ = \frac{Vg}{vP}\ X\ 100$$

where H^2 = % Broad sense heritability. The heritability percentage was categorized as low (0- 30%), moderate (30 – 60%), and high ≥ 60% as described by Johnson et al. (1955).

Genetic advance

The extent of genetic advance expected through selection for the character was calculated as described by Addissu (2011):

Genetic Advance (GA): $H \times P \times K$

where H is heritability, P is phenotypic standard deviation, and K is selection deferential (2.06 at 5%).

Genetic Gain (%) = GA × 100; it is categorized as low (0-10%), moderate (10-20%) and high (20% and above) as described by Johnson et al. (1955).

The genetic advance as a % of the mean (GAM) was calculated as:

$$GAM(\%) = \frac{GA}{X}\ X\ 100$$

where GA = Genetic advance and X = Grand mean of a trait.

***Clustering and principal component analysis* (PCA)**

Clustering and PCA were carried out to assess the relationships among the common bean landraces based on data from agronomic traits using NTSYS-pc software (version 2.1) (Rohlf, 1997). Data were analyzed based on Euclidian distance method and dissimilarity coefficient. Unweighted pair-group method of the arithmetic (UPGMA) mean and SAHN clustering were used to determine the genetic relationships among the common bean landraces. Principal component analysis (PCA) was calculated using EIGEN module of NTSYS-pc software.

RESULTS

Agronomic performance of the common bean landraces

There was significant variation (P<0.05) for all the studied traits which also revealed possible amount of variability among the landraces (Table 3). Yield component traits including number of pods per plant, number of seeds per pod, number of seeds per plant, 100 seed weight and grain yield were significantly varied ranging from 12 to 52 NPPP, 4 to 9 NSPPO, 65 to 320 NSPP, 20 to 113 g WHSPP and 26 to 132 for GY, respectively, excluding the outlier (Table 3). The other traits indirectly contributing to agronomic performance varied significantly (P<0.001); the number of branches varied from 1 to 17, plant length ranged from 8 to 16 cm and biological yield varied from 101 to 2296 g.

The plant height (PH) was highest in genotype LRC008 (185 cm) while the lowest was for GK030198 (40.4 cm). The number of branches (NOB) ranged from 3 (GK030167, GK030246 and LRC004) to 15 (LRC008), while the number of days to emergence (DTE) varied from 5 for cultivar LRC010 to 10 days for cultivars GK030244, GK030204 and GK0302194. The number of days from emergence (DESTF) varied from 95.5 (LRC008) to 34 (LRC019), whereas the length of time to maturity (DSM) ranged from 150 days for genotype LRC008 to 57 for genotype LRC015 (Table 3). The table shows that the highest number of pods per plant (NPPP) was obtained from accession LRC008 (238) and the lowest from LRC007 (15), but the average number of seeds per pod (NOSPP) in these genotypes ranged

Table 2. Fourteen observed common bean quantitative characters, codes, measurement units and procedures

Character	Code	Measurement unit/sampling procedure
Days from planting to emergence	DTE	Number of days from sowing to the time the plant emergence was 50% within the centre rows
Days from emergence to 50% flowering	DFSTF	Number of days from the date of emergence to the date on which 50% of the plants on a plot opened a flower
Days from sowing to 95% maturity	DSM	Number of days from sowing to the stage when 90% of the plants in a plot changed the colour of their pods from green to yellowish orange and texture hardened
Number of pods per plant	NPPP	Average number of pods counted at harvest, for 10 plants within plot centre
Number of seeds per pod	NSPPO	Determined from the average number of seeds per 10 pods per 10 sampled plants
Weight of 100 seeds per plant (gm)	WHSPP	Determined from the average 100-seeds mass at physiological maturity (12 - 14%) moisture content of the seed and expressed in grams
Number of seeds per plant	NSPPL	Determined from the average number of seeds from 10 pods per 10 sampled plants at physiological maturity
Number of branches per plant	NOB	Number of shoots arising from the main stem counted and recorded at physiological maturity.
Pod length	PL	Exterior distance of fully matured pod from the pod apex to the peduncle measured in centimeters at physiological maturity from an average of 10 plant within plot centre
Pod width	PW	Average width of 10 pods for each genotype from one end at its widest point of the central pod to the other at physiological maturity, in millimeters
Plant height	PH	The height of the plant from the ground surface to the tip of the main stem recorded in centimeters at physiological maturity
Biological yield (weight of roots, stalk and leaves)	BY	An average from 10 plants uprooted, cleaned and weighted to get the biological yield per plant in grams
Grain yield/weight of seeds per plant	GY/WSPP	Dried grain yield in grams, obtained from 10 plants within central rows of each plot were harvested, threshed separately and seeds weighted
Harvest index (%)	HI	HI = (GY/BY) × 100

Table 3. Mean performance of 52 common bean landraces evaluated for 14 agronomic traits at KALRO-Kisii Research Center field during the 2015 and 2016 cropping seasons.

Code of landrace	PH (cm)	NOB	DTE	DESTF	DSM	NPPP	NSPPO	WHSPP (gm)	NSPPL	PL (cm)	PW (cm)	GY (gm)	BY	HI
LRC001	95.20	4.00	7.70	43.60	68.40	16.60	5.50	67.50	80.10	12.00	1.40	53.60	219.00	0.25
LRC002	130.00	4.00	7.40	42.00	65.80	21.70	7.00	68.50	147.00	12.00	1.20	99.96	252.10	0.39
LRC003	50.50	5.00	8.70	34.50	55.60	17.30	6.00	46.60	102.80	13.00	1.50	47.38	217.50	0.22
LRC004	102.70	3.00	8.50	40.00	62.00	23.00	6.00	43.00	138.60	12.00	1.50	58.91	223.00	0.26
LRC005	93.40	4.00	7.00	36.60	58.00	21.00	4.20	42.00	84.40	10.00	1.50	35.28	235.50	0.15
LRC006	45.00	6.00	8.00	35.00	60.90	19.50	4.70	73.70	76.20	10.00	1.50	56.24	234.00	0.24
LRC007	37.00	15.00	7.90	35.70	60.00	15.00	6.00	69.00	90.00	13.50	1.60	62.10	218.00	0.28
LRC008	185.00	7.00	6.00	95.50	150.00	238.00	5.00	46.90	690.00	12.00	1.50	324.30	2300.00	0.10
LRC009	79.80	6.00	6.30	37.00	62.7.00	16.00	7.60	27.80	112.00	8.00	1.00	31.36	220.20	0.14
LRC010	66.00	5.00	5.00	48.40	72.00	32.00	7.00	36.70	224.00	11.00	1.30	82.88	251.40	0.33

Table 3. Contd.

LRC011	50.30	5.00	8.40	45.00	74.80	35.10	9.40	28.50	315.50	11.00	1.30	88.20	230.00	0.38
LRC012	43.00	5.00	7.00	35.00	60.00	21.20	5.70	72.40	147.00	15.00	1.80	105.84	240.00	0.44
LRC013	148.00	4.00	6.70	40.50	63.00	15.00	7.80	29.50	105.40	13.00	1.40	30.74	220.00	0.14
LRC014	95.50	6.00	6.00	40.60	65.50	38.30	6.00	21.00	228.00	11.00	1.30	47.88	253.70	0.19
LRC015	74.70	4.00	5.30	38.00	57.00	22.80	5.50	56.80	110.00	10.50	1.50	62.70	234.40	0.27
LRC016	118.00	6.00	9.40	35.00	59.90	23.00	4.00	107.00	92.80	14.00	2.50	99.51	300.00	0.33
LRC017	81.10	5.00	6.70	35.00	61.80	17.00	4.00	66.00	68.40	11.00	1.40	44.88	230.00	0.19
LRC018	50.00	6.00	7.00	43.80	69.00	24.00	4.80	62.40	96.00	12.50	1.50	59.52	235.80	0.25
LRC019	120.00	7.00	6.00	34.00	61.00	25.00	3.60	103.00	75.00	13.00	2.50	77.25	334.20	0.23
LRC020	64.60	4.00	5.80	36.30	62.00	24.00	6.00	64.80	144.00	14.00	1.50	93.60	218.30	0.43
LRC021	56.90	6.00	5.70	42.90	73.60	33.00	6.00	31.50	198.60	10.00	1.40	63.36	219.00	0.29
LRC022	100.00	6.00	5.50	40.00	70.00	36.00	7.00	27.00	252.00	11.50	1.40	68.04	194.00	0.35
LRC023	91.80	5.00	9.00	36.00	68.70	38.00	6.80	32.00	246.00	10.00	1.30	78.72	196.70	0.40
LRC024	56.50	7.00	8.00	40.00	70.10	19.00	4.00	57.70	76.60	12.00	1.50	44.08	240.00	0.18
LRC025	84.80	4.00	7.10	42.50	70.00	17.10	6.00	62.00	102.40	12.00	2.00	63.24	270.00	0.23
LRC026	52.00	5.00	8.00	37.70	63.00	21.70	6.00	64.00	126.00	13.50	1.50	80.64	260.00	0.30
GK036527	97.30	6.00	9.30	43.80	68.40	28.00	6.30	57.80	168.60	14.00	1.50	97.00	198.40	0.49
GK036528	86.40	6.00	6.70	41.40	65.00	25.60	6.70	48.00	150.50	12.40	1.20	72.00	297.00	0.24
GK036530	75.20	7.00	6.40	40.30	63.90	36.00	6.80	42.00	216.60	10.00	1.30	91.00	291.00	0.31
GK036524	121.10	6.00	7.00	38.90	62.30	37.80	8.70	43.70	296.00	9.40	1.00	130.00	295.00	0.44
GK030260	60.50	4.00	9.00	36.00	60.20	36.50	4.00	46.50	144.00	10.00	1.50	67.00	231.00	0.29
GK030261	123.00	5.00	7.40	41.90	68.80	33.00	7.80	44.40	231.00	11.00	1.40	102.00	278.60	0.36
GK036522	119.00	6.00	8.00	40.20	72.00	33.00	6.60	58.50	198.20	14.00	1.50	117.00	290.40	0.40
GK030211	98.3.00	7.00	7.00	40.80	71.70	40.40	8.00	41.00	320.20	11.00	1.50	131.00	271.00	0.48
GK030227	65.00	5.00	8.50	44.70	73.80	30.60	6.00	58.60	180.40	12.50	1.50	106.00	269.50	0.39
GK030239	40.40	7.00	9.00	38.00	65.60	15.40	5.00	42.10	75.00	11.50	1.40	32.00	216.00	0.15
GK030244	67.40	6.00	10.00	37.60	66.10	27.50	5.60	46.00	135.00	10.50	1.50	62.00	263.00	0.23
GK030180	78.00	6.00	5.60	36.500	65.00	32.00	6.70	52.00	192.70	14.00	1.50	100.00	248.40	0.40
GK030194	65.30	4.00	10.00	43.00	71.00	32.00	5.00	53.00	160.00	10.50	1.50	84.00	251.00	0.33
GK030198	40.20	4.00	9.40	37.00	63.20	17.70	6.00	42.00	102.20	12.50	1.50	43.00	233.90	0.18
GK030200	61.00	5.00	9.00	40.60	70.20	35.50	4.00	48.50	140.70	10.40	1.40	67.00	260.00	0.26
GK030204	82.50	7.00	10,00	41.70	73.30	34.70	6.00	65.00	204.00	15.00	1.50	132.00	238.00	0.55
GK030210	58.60	4.00	7.30	35.00	60.00	16.30	5.80	38.70	80.60	10.50	1.50	31.00	263.00	0.12
GK030167	110.00	3.00	7.80	40.00	68.30	33.00	7.00	43.00	231.80	11.00	1.30	98.00	282.00	0.35
GK030171	46.20	5.00	6.20	38.00	68.40	23.30	7.00	54.00	161.90	10.00	1.30	87.00	216.00	0.40
GK030178	116.00	5.00	6.0	42.80	73.00	34.00	7.70	42.00	238.60	10.50	1.30	100.00	236.50	0.42
GK036523	78.80	6.00	7.60	36.0	67.80	24.00	6.70	38.50	144.00	11.00	1.50	56.00	239.80	0.23
GK036526	64.20	7.00	9.70	35.40	63.00	52.00	5.40	41.00	260.00	14.50	1.80	106.00	305.00	0.35
GK030246	126.	3.00	8.00	40.70	73.00	22.6.00	8.00	43.00	176.00	11.50	1.40	76.00	273.70	0.28

Table 3. Contd.

GK030249	121	08	8.3	40.50	70.70	35.00	6.60	37.00	210.00	10.00	1.20	78.00	255.00	0.30
GK030257	98.1	05	7.4	36.00	68.40	25.00	6.00	42.00	150.50	10.00	1.40	63.00	267.20	0.23
GK030259	58	05	7.4	37.00	63.00	37.10	5.00	48.00	185.10	10.50	1.40	89.00	236.30	0.38
Mean	83.26	5.50	7.55	40.23	63.00	31.31	6.08	50.45	170.82	11.65	1.47	80.33	247.76	0.30
CV (%)	37.88	32.71	17.71	21.04	20.04	97.09	21.16	33.41	57.82	13.70	18.04	54.18	12.18	35.00
LSD (0.05)	0.11	0.10	0.05	0.06	0.06	0.30	0.06	0.10	0.16	0.04	0.05	0.15	0.03	0.10

LRC - Landrace; DTE - Days from planting to emergency; DFSTF - Days from sowing to 50% flowering; DSM - Days from sowing to maturity; NOPPP - Number of pods per plant; NOSPP - Number of seeds per pod; WOSPP - Weight of seeds per pod; NSPP - Number of seeds per plant; PWPP - Pod weight per plant; SSZ - Seed size; GH - Growth habit; PH - Plant height; NOB - Number of branches per plant; PL - Pod length; PW - Pod width; PS - Plant size; BY - Biological yield; HI - harvest index (%); GY/WSPP - Grain yield/weight of seeds per plant; NA - Not available; GK - Genebank of Kenya.

from 4.2 in LRC 005 to 9.7 for LRC011. Accessions LRC016 and LRC 019 recorded the highest weight of hundred seeds per plant (WHSPP) (107 and 103 gm, respectively), compared to genotype LRC 014 which recorded the lowest (21). There was wide variation in the number of seeds per plant (NSPPL) ranging from 320 (GK320211) to 68 (LRC017) not considering the outlier (LRC 008). Pod length (PL) and pod width (PW) varied from 8.0 cm and 1.2 cm for cultivars LRC009 and GK030249 and GK 036528 as lowest values; while highest values were recorded for landraces LRC016 (14 for PL and 2.5 for PW). The highest biological yield (BY) and grain yield (GY) was 334 and 132 for accessions LRC 019 and GK 030204 respectively, disregarding the outlier. The harvest index ranged from 0.48 to 0.10 of which landraces GK036527 and LRC008 recorded the highest and lowest, respectively (Table 3).

Variation in agronomic characteristics of the common bean landraces

The analysis of variance in the present study showed that there were highly significant (P≤0.001) differences among the common bean landraces for all the 14 agronomic traits (Table 4). The coefficients of variation were generally low except for biological yield (60.66). The range and mean values for the 14 traits are presented in Table 4.

Phenotypic and genotypic variability and estimation of genotypic and phenotypic coefficient of variation

The extent of variability in respect of phenotypic and genotypic variances and phenotypic and genotypic coefficients of variance (PCV and GCV) for the yield determining quantitative characters studied is represented in Table 5. In the present study, the highest genotypic variance were observed for days to maturity (59.44) and number of seeds per plant (31.13) while the lowest genotypic variance was found for pod length (2.57), pods per plant (2.14) and pod width (1.55). The highest phenotypic variances were for days to maturity (76.34) followed by seeds per plant (51.73) while the lowest were for pod length (3.17) and pod width (2.02). The genotypic coefficients of variation (GCV) ranged from 1.00% for biological yield to 84.69% for pod width, while phenotypic coefficients of variation (PCV) ranged from 2.34% for biological yield to 96.68 for pod width. Moreover, moderate GCV and PCV were observed (>10%) in the traits for yield. Moderate (29.46) and high (75) GCV were also recorded for number of seeds per pod and number of branches respectively, while PCV values were 35.12 and 84.40 for number of seeds per pod and number of branches respectively. The lowest GCV was recorded for biological yield (1.00) and grain yield (2.21) while PCV values were 2.34 and 2.72 for the same variables respectively (Table 5).

Heritability and genetic advance

Broad sense heritability and genetic advance values are presented in Table 4. Heritability in broad sense estimates of the 13 quantitative traits ranged from 60.20% for number of seeds per plant to 87.57 for days to emergency. Genetic advance varied from 1.78 for number of seeds per pod to 92.71 for number of seeds per plant. All the traits showed a relatively high heritability values (>60%). However, almost all variables recorded moderate to low genetic advance (<60%) except values for plant height (78.13) and number of seeds per plant (92.71), (Table 5).

Table 4. Mean values, coefficients of variation, ranges and mean squares from a combined analysis of variance for 14 agronomic traits of 52 common bean landraces.

Trait	Mean square	Error	Range		Mean	CV (%)
			Minimum	Maximum		
PH (cm)	2983.23**	1441.3	36	186	83.26	4.51
NOB	9.71**	414.04	3	17	5.5	36.63
DTE	5.35**	121.65	4.6	13.1	7.55	14.48
DFETF	215.63**	851.84	32	102	40.23	7.17
DSM	478.41**	2018.51	50	154	63	6.57
NPPP	2772.44**	793.64	12	244	31.31	8.91
NSPPO	4.95**	287.72	0.8	11	6.08	27.64
WHSPP	852.66**	893.72	20	113	50.45	5.86
NSPPL	29264.55**	3755.96	65	698	170.82	3.55
PL	7.63**	150.18	8	16	11.65	10.42
PW	0.21**	1.85	0.8	2.7	1.47	9.15
GY	5683.92**	1645.86	26	329	80.33	5
BY	109105.3**	2822475	101	2296	274.76	60.66
HI	0.03**	0.36	0.1	0.586	0.3	19.82

** Highly significant at (P≤0.001); PH - Plant height; NOB - number of branches per plant; PL - Pod length; PW - Pod width; PS - Plant size; BY - biological yield; GY Grain yield; HI - Harvest index; NSPPL - Number of seeds per plant; WHSPP - Weight of 100 seeds per plant; NSPPO - Number of seeds per pod; DFETF - Days from emergence to flowering; DSM - Number of days from sowing to maturity; NPPP - Number of pods per plant.

Association among the agronomic trait components

The genotypic or phenotypic correlation coefficients were significant (Table 6). The highest positive correlation (highly significant P≤0.01) was between number of pods per plant (r=0.97) and days from emergency to flowering, closely followed by biological yield (r = 0.96) and days from emergency to flowering. Seed yield per plant showed significant (P≤0.01) positive correlation with plant height (r = 0.68), days from planting to 50% flowering (r=0.68), number of pods per plant (r=0.67), and biological yield (r=0.68). Plant height was observed to have a highly significant (P≤0.01) and positive correlations with days from sowing to flowering (r = 0.68), number of pods per plant (r = 0.67), grain/seed yield (r = 0.68) and biological yield (r = 0.68) but low and non - significant correlation with days to emergence (r = 0.22), weight of hundred seeds per plant (r = 0.34), pod length (r = 0. .35) and pod width (r = 0.36) as estimated from the pooled analysis. Number of branches per plant revealed a fairly low to medium correlation with all traits ranging from r = 0.31 for number of seeds per pod to r = 0.47 for pod length. Harvest index expressed significant (P≤0.01) and positive correlation with number of seeds per pod (r = 0.61) but had low and non- significant correlation with days from emergency to flowering (r = 0.26) and biological yield (r = 0.18).

Cluster analysis

Cluster analysis based on the 14 agronomic traits grouped the 52 common bean landraces into four distinct clusters (Figure 1 and Table 6). Cluster I was the largest constituting 36.5% of the total landraces. This cluster consists of landraces with the smallest number of branches and had the minimum number of days to emergence, flowering and maturity. The landraces in cluster I were also characterized by fewer numbers of pods and seeds per plant which resulted in low grain yield compared to other clusters. Clusters II and III constituted 34.6 and 15.38% of the landraces, respectively. The landraces in clusters II and III were characterized by intermediate number of pods per plant and a relatively large number of seeds per pod. However, landraces in cluster II had a higher biological yield and produced more seeds per plant than cluster III (Table 7). Landraces with the large seeds, seed weight, pod length and width but a low number of pods per plant were grouped in cluster IV which constituted 11.5% of the total number (Table 7). Landrace LRC008 was clustered as an out group and was characterized with tall and large plants which recorded a higher number of pods per plant and medium seed size but a lower number of seeds per pod. The landrace had the longest period from planting to maturity as well as the largest biomass, although the harvest index (HI) was low (Table 7).

Principal component analysis (PCA)

Principal component analysis (PCA) of the quantitative data was performed to determine the importance of different traits in explaining the variations among the

Table 5. Estimation of genetic variables of the 14 agronomic traits of 52 common bean landraces evaluated.

Trait	GM	GV	PV	GCV (%)	PCV (%)	H^2 (%)	GA	GAM
PH	83.25	20.34	24.56	5.41	59.52	81.97	78.13	93.84
NOB	5.5	17.02	21.55	75	84.4	78.97	5.36	97.45
DTE	7.54	16.43	18.76	53.75	57.44	87.57	6.78	89.92
DETF	40.27	12.46	16	8.76	10	77.87	5.94	14.75
DTM	67.71	59.44	76.34	11.38	13	77.86	13.84	20.44
NPPP	31.31	2.14	3.21	4.67	5.72	66.66	16.02	51.16
NSPPO	6.1	3.23	4.59	29.46	35.12	70.37	1.78	29.2
WHSPP	50.45	5.44	6.31	4.62	5	86.21	39.16	77.62
NSPPL	170.81	31.13	51.73	3.26	4.21	60.2	92.71	54.27
PL	11.64	2.57	3.17	14	15.29	81.07	2.51	21.56
PW	1.47	1.55	2.02	84.69	96.68	84.43	1.22	83
GY	80.33	3.18	4.79	2.21	2.72	66.38	25.37	31.6
BY	274.22	7.43	9.45	1	2.34	78.62	27.84	10.15

GM – Mean of traits; GV – Genotypic variance; PV – Phenotypic variance; GCV – Genotypic coefficient of variation (%); PCV – Phenotypic coefficient of variation (%); H^2 – Heritability (%); Genetic advance; GAM – Genetic advance as percentage of mean; PH - Plant height; NOB - Number of branches per plant; PL - Pod length; PW - pod width; PS - Plant size; BY - Biological yield; GY grain yield; HI - Harvest index; NSPPL - Number of seeds per plant; WHSPP - Weight of 100 seeds per plant; NSPPO - Number of seeds per pod; DFETF - Days from emergence to flowering; DSM - Number of days from sowing to maturity; NPPP - Number of pods per plant.

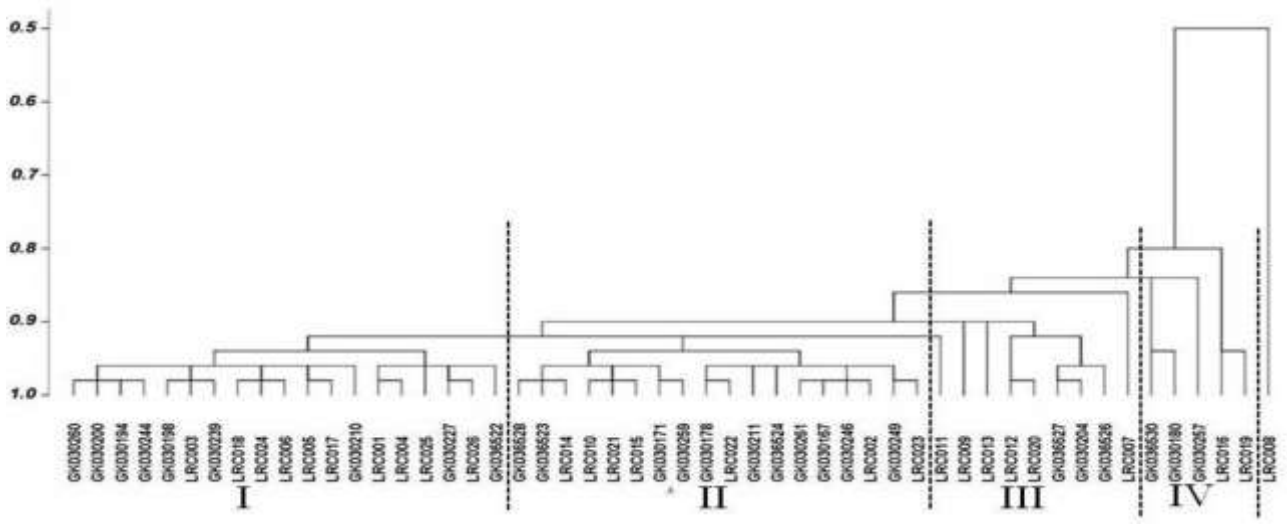

Figure 1. Dendrogram showing relationship among 52 common bean landraces based on 14 agronomic traits using UPGMA method.

landraces (Figures 2 and 3). In the principal components analyses of the 52 common bean landraces performed using 14 agronomic traits, the first principal component (F1) and the second principal component (F2) accounted for 29.33 and 19.27%, respectively of the total variation (48.60%). Trait eigenvectors indicated that F1 was mainly a positive indicator of biological yield, grain yield, number of pods per plant, and of characteristics contributing to high to medium-term biological yield and high seed yield (Figure 2) F2 was mainly a positive indicator of earlier days to emergency and maturity and characteristics with low harvest index. Accordingly, the first two principal components revealed that the landraces were scattered in all the quarters (Figure 3), which showed the high level of genetic diversity in the evaluated genotypes.

DISCUSSION

Breeding programs aimed at crop improvement requires heritable variation in important agronomic traits of the crop. The efficacy of selection depends upon the

Table 6. Summary of the main characteristics of the genotypes clusters of common been evaluated.

Cluster number	Number of landraces (percentage)	Landraces	Unique agronomic traits of the landraces
I	19 (36.5%)	LCR003, LCR018, LCR024, LRC006, LCR005, LCR017, LCR001, LRC004, LRC025, LCR 026, GK030260, GK030200, GK030194, GK030244, GK030198, GK030239, GK030210, GK030227, and GK036522	Fewer number of branches, pods, seeds; earlier emergence, flowering and maturity; low yield
II	18 (34.6%)	LCR014, LCR010, LCR021, LCR015, LCR022, LCR002, LCR023, LCR011, GK036528, GK030171, GK030259, GK030178, GK030211, GK036524, GK030261, GK030167, GK030246 and GK030249	Intermediate number of pods per plant; a relatively large number of seeds per pod; high biological yield; a higher number of seeds per plant
III	8 (15.38%)	LCR011, LCR009, LCR013, LRC012, LRC020, GK036527, GK030204 and GK036526	Medium number of pods per plant and a large number of seeds per pod
IV	6 (11.5%)	LRC007, LRC016, LRCO19, GK036530, GK030180 and GK030257	Large sized seeds, seed weight, pod length and width but low number of pods per plant
Outgroup		LRC 008	Long period from planting to maturity, large biomass, high yield, many pods and branches.

Table 7. Cluster means for fourteen different agronomic traits in 52 common bean landraces

Traits		Means of clusters			
		I	II	III	IV
Plant height	PH	67.82	94.43	78.71	87.71
Number of branches	NOB	4.63	5.23	5.5	7.66
Days to emergence	DTE	8.25	6.85	7.9	7.11
Days from sowing to 50% flowering	DESTF	38.98	40.32	39.33	36.25
Days from sowing to maturity	DSM	65.31	68.03	65.9	65.63
Number of pods per plant	NOPPP	23.19	31.53	28.25	26
Number of seeds per pod	NOSPP	5.22	6.91	6.77	5.52
100 seed weight	WHSPP	53.62	42	48.35	69.16
Seeds per plant	NSPPL	114.08	208.37	182.06	136.26
Pod length	PL	11.6	10.79	13.06	21.41
Pod width	PW	1.5	1.32	1.47	1.8
Grain yield	GY	60.67	84.58	85.59	82.14
Biological yield	BY	244.34	249.01	233.73	276.46
Harvest index	HI	0.24	0.34	0.36	0.29

magnitude of genetic variability for yield and yield contributing traits in the breeding material. The knowledge of heritability and genetic advance guides the breeder to select superior parents to initiate an effective and successful crossing program (Johnson et al., 1955). Therefore, the available genetic variation, heritability and expected genetic gain in important agronomic characters are useful to design better and effective breeding strategies in common bean landraces. In the present study, all the fourteen agronomic traits showed highly significant ($P<0.05$) variations indicating the presence of sufficient amount of genetic variability among the landraces for all the studied traits. In common bean genotypes, significant variations have been previously reported for various agronomic traits (Amanulla et al., 2016; Salehi et al., 2008a, b; Nechifor et al., 2015; Fivano and Msolla, 2011).

Knowledge about the variability using parameters like genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) is of paramount importance

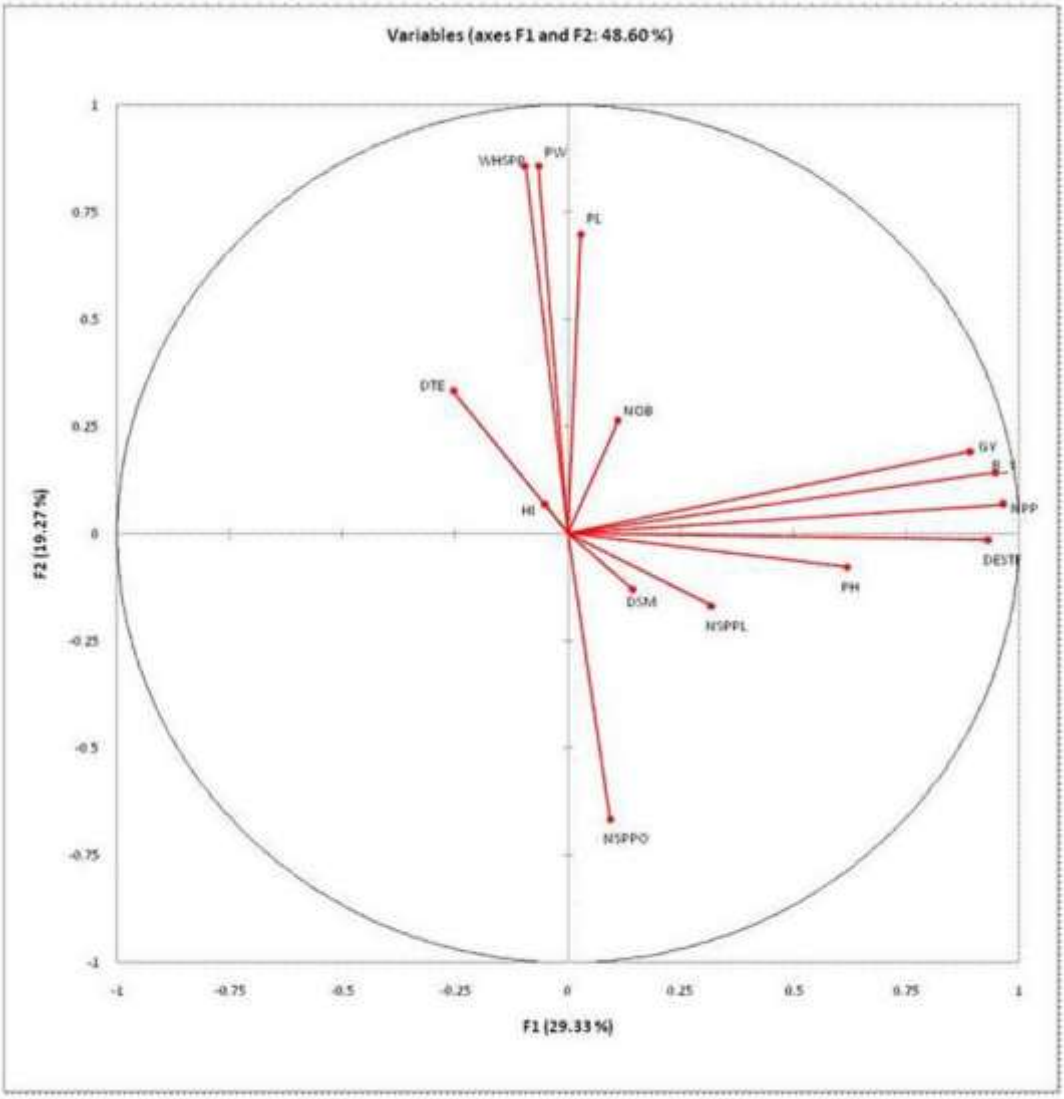

Figure 2. Two dimensional ordination of 14 agronomic traits in common bean landraces on principal component analysis. PH - plant height; NOB - number of branches per plant; PL - pod length; PW - pod width; PS - plant size; BY - biological yield; GY - grain yield; HI - harvest index; NSPPL - number of seeds per plant; WHSPP - weight of 100 seeds per plant; NSPPO - number of seeds per pod; DFETF - days from emergence to flowering; DSM - number of days from sowing to maturity; NPPP - number of pods per plant. F1 and F2 = Principal component 1 and 2, respectively.

for an effective breeding program in crops like common bean. According to Miklas et al. (2006), genotypic and phenotypic coefficients of variation values are categorized as low (<10%), moderate (10-20%), and high (>20%). In this study, based on the classification, high and close values of PCV and GCV were recorded for pods per plant, seeds per pod, 100 seed weight, seeds per plant, grain yield and biomass yield, which suggest the potential variability available in the landraces for these traits for effective selection and improvement as there was minimal influence of environment. Similar results were also reported by Stoilova et al. *(*2004) for clusters per plant, seed yield per plant, and biological yield per plant. Aghamdi (2015) also reported high GCV and PCV for plant height, primary number of branches per plant, days to maturity indicating the predominance of additive gene action. Nechifor et al. (2015) also reported high genetic variability for numbers of pod per plant and weight of pods per plant in common beans. Stoilova et al. (2015) performed a field trial of 42 germplasm of exotic beans at the valley of Kashmir in order to obtain superior genotype of beans under temperate condition and the findings from their study showed medium genetic variability for days of flowering and days of harvesting and low genetic variability for early flowering and early maturity.

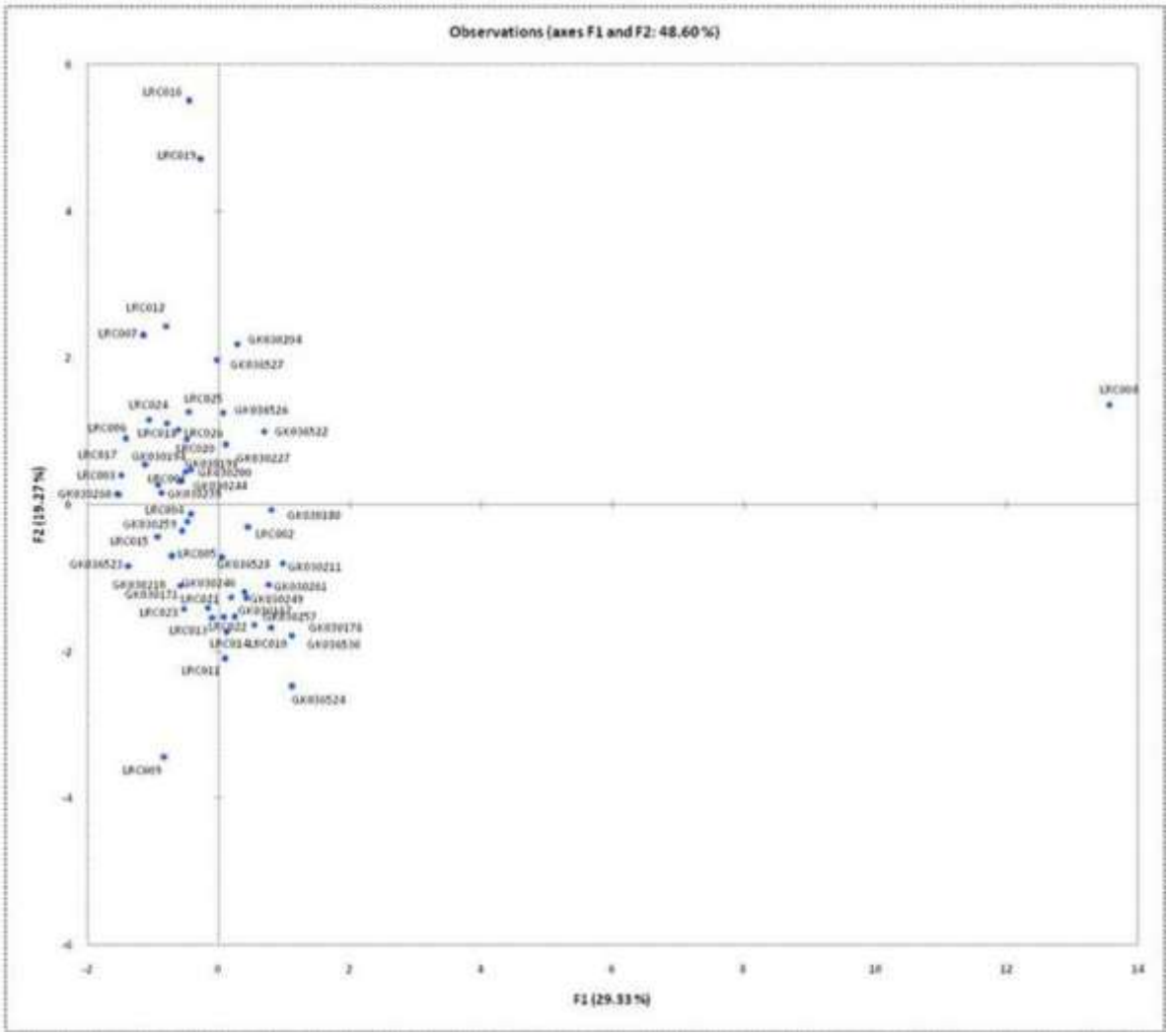

Figure 3. Biplot of first and second principal components in common bean landraces.

In the present study, the phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the traits. This would be due to the fact the variation at the phenotypic level was due to the effect of genotypes and influence of environment as reported by Singh (1999). Moderate values of GCV and PCV were observed in the present study for some traits including plant height and number of branches. Low GCV and PCV were observed for days to 50% flowering, days to maturity. Phenotypic coefficient of variation was higher than the corresponding genotypic coefficient of variation for all the traits except days to emergence and 100 seed weight. However, the differences between PCV and GCV were small. The narrow differences between PCV and GCV for most of the traits indicate low effect of environmental influence on the expression of these traits. These findings are in agreement with Salehi et al. (2008) who reported narrow differences between PCV and GCV on the study of interrelationship between different traits in common bean.

The heritability estimates help the breeders in selection based on the basis of phenotypic performance. According to Robinson et al. (1949), heritability can be classified as low (0-30%), moderate (30-60%) and high (>60%). Most traits showed a high heritability values (>60%) except number of pods per plant and biological yield which were moderate. Similar findings were also reported by Singh et al. (2015) in pea crop. Salehi et al. (2008) and Duarte and Adams (1972) also reported similar results for yield component traits which included number of pods per plant, 100-seed weight and number of seeds per pod in common bean.

However, when heritability is coupled with genetic advance (GA) together with GCV provides the best prediction of expected gain through phenotypic selection than heritability alone. Estimates of all these parameters help to understand the type of gene action involved in the expression of traits especially for polygenic traits.

Johnson et al. (1955) suggested genetic advance as percent mean can be categorized as 0-10% for low, 10-20% for moderate and >20% for high. In the present study, the genetic advance as percent of mean ranged from 10.15% for biological yield to 97.45% for number of branches. High heritability coupled with high genotypic coefficients of variation (GCV) and high genetic advance as percentage of mean were recorded by plant height followed by number of branches and days to emergence which indicates that the traits were simply inherited in nature and possessed additive gene effects. These traits can be considered as favorable for common bean improvement through effective phenotypic selection of these traits and high expected genetic gain from selection for these characters can be achieved. Similar results were reported by Dursum (2007) who tested the variability, heritability and co-relation studies of 40 common bean genotypes. However, high heritability and GA (%) along with low GCV for days to flowering and maturity indicates that expression of these traits is under the involvement of non-additive gene action and phenotypic selection of these traits might not be effective. Grain yield is a complex character which is as a result of many yield contributing traits, which are in turn influenced by the environment and genotype. Consequently, the direct evaluation and improvement of grain yield itself may be misleading due to involvement of environmental component. Therefore, to assess the magnitude of correlations for various traits with yield would be immense help in the indirect selection for the improvement of yield. The correlation coefficients of yield and its components determined in the present study indicated that most of the traits studied were positively and significantly correlated with yield. Significant and positive correlation of seed yield/plant was found with plant height, days from sowing to 50% flowering, number of pods/plant and biological yield. These findings are in agreement with previous study in common beans by Dursun (2007) who reported positive and significant correlation of seed yield/plant with number of pods/plant. Valenciano et al. (2006) also reported significant positive correlation of pod weight with seed yield and length of pods, number of pods with seed weight/plant, number of pods/plant with number of pod bearing nodes. This study also showed that plant height at maturity was positively and significantly correlated with days from sowing to flowering, number of seeds/plant, seed yield and biological yield. This is in agreement with the findings of Pereira et al. (2015) who reported significant positive correlation of plant height with seeds/plant. However, our results contradict reports by Stoilova et al. (2015) and Singh et al. (1979) who found negative correlation of plant height with seed yield. This deviation may be attributed to the differences in genotypes and effect of the experimental conditions (Pereira et al., 2005).

Cluster analysis based on fourteen agronomic traits grouped 52 common bean landraces into four different clusters indicating that the landraces exhibited notable genetic divergence in terms of agronomic traits. Formation of different clusters using agronomic characters in diverse common bean genotypes has also been reported (Nechifor et al., 2015). The maximum inter-cluster distance was recorded between cluster I and the out-group (LCR 008) followed by cluster II and the out-group, suggesting wide diversity among these groups. On the other hand, the minimum distance between cluster IV and the out-group and cluster I and II indicates their close relationship. Essentially, crossing of genotypes belonging to the same cluster is not expected to generate superior hybrids or segregants, because genotypes grouped in the same cluster diverge little from one another. However, the larger the divergence between the genotypes, the higher will be the amount of heterosis in F1 progeny and subsequent generations. It may be useful to produce crosses between genotypes belonging to the clusters separated by large estimated genetic distances (Negri and Tosti, 2002). Success might therefore be expected through making crosses between the genotypes from cluster II and cluster III, followed by the one between cluster IV and the outgroup. Genotypes from these clusters can be selected for hybridization program that can evolve high heterotic crosses, which might prove potential in isolating superior hybrids. The PCA grouped the accessions into groups over the four quadrants based on the quantitative traits. The accessions remained scattered in all four quadrants, showing large genetic variability for the traits studied.

Conclusion

The present study revealed significant levels of genetic variability among the 52 common bean landraces for all the agronomic traits. High values of genotypic coefficient of variation, broad sense heritability and genetic advance were recorded for pod width, plant height, number of branches and days to emergence and therefore these traits are favorable attributes for common bean improvement through simple selection and high expected genetic gain can be achieved for these characters. Cluster analysis using the fourteen different traits classified the common bean landraces into four separate clusters, exhibiting that hybridization of landraces across clusters could lead to an increase in heterosis in progenies.

ACKNOWLEDGEMENT

Special thanks go to The National Research Fund (Kenya) for financing the research work. The authors are also grateful to the Kenya Agricultural and Livestock Research Organization (KALRO), Kisii station for providing land for the research.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

REFERENCES

Adams MW (1972). Plant architecture and yield breeding. Iowa State Journal of Research 56:225-254.

Addissu AG (2011). Heritability and genetic advance in recombinant inbred lines for drought tolerance and other related traits in sorghum (*Sorghum bicolor*). Continental Journal of Agricultural Science 5(1):1-9.

Amanullah A, Khan A, Nawab K,Sohail Q (2016). Performance of promising common bean (*Phaseolus vulgaris* L.) germplasm at Kalam-Sawat. Pakistan Journal of Biological Sciences 9:2642-2646.

Atta BM, Haq MA, Shah TM (2008). Variation and inter relationships of quantitative traits in chickpea (Cicer arietinum L.). Pakistan Journal of Botany 40:637-647.

Bennick M (2005). Eat beans for good health. Annual Report of the Bean Improvement Cooperative 48:1-5.

Broughton WJ, Hernández G, Blair M, Beebe S, Gepts P (2003). Beans (*Phaseolus spp*.) Model food legumes. Plant and Soil 252(1):55-128.

Cherian E (2000). Genetic variability in Capsicum chinense jacq [M.S. thesis]. Kerala Agricultural University.

Dursun A (2007). Variablity, heritability and co-relation studies in bean genotypes. World Journal of Agricultural Science 3:12-16.

Falconer DS (1981). Introduction to quantitative genetics, Longman.

Fivano NC, Msolla SN (2011). The diversity of common bean landraces in Tanzania. Tanzanian Journal of Natural and Applied Sciences 2(1):1821-7249.

Geil PB, Anderson JW (2014). Nutrition and health implications of dry beans: a review. Journal of the American College of Nutrition 13:549-558.

IBPGR (2013). Descriptors for *Phaseolus vulgaris*. International Board of Plant Genetic Resources Institute, Rome, Italy.

Johnson HW, Robinson H, Comstock R (1955). Estimates of genetic and environmental variability in soybeans. Agronomy Journal 47(7):314-318.

Miklas NP, Kelly JD, Beebe SE, Blair MW (2006). Common bean breeding for resistance against biotic and abiotic stresses: From classical to marker assisted selection breeding. Euphytica 147(1-2):105-131.

More AD, Borkar AT (2016). Analysis of genetic variability, heritability and genetic advance in *Phaseolus vulgaris* L. International Journal of Current Microbiology and Applied Science 5:494-503.

Nechifor O, Filimon O, Szilagyi L. (2015). Genetic variability, heritability and expected genetic advance as indices for yield and yield components selection in common bean (*Phaseolusvulgaris* L.). Scientific Papers, UASVM Bucharest, Series A 1222-5339.

Negri V, Tosti N (2002). *Phaseolus* genetic diversity maintained on-farm in Central Italy. Genetic Resources and Crop Evolution 49:511-520.

Pereira G, Mihov M, Atanassova D, Costa R, Stoilova T, Tavares-de-Sousa MM (2015). Study of plant variability in a pea collection. Melhoramento 42:56.

Pereira T., Coelho CMM, Bogo A, Guidolin AF, Miquelluti DJ (2005). Diversity in common bean landraces from south Brazil. Acta Botanica Croatica 68:79-92.

Rohlf JF (1997). NTSYS-pc: Numerical Taxonomy and Mul-tivariate Analysis System, Version 2.1e. Exeter Soft-ware. New York, USA.

Salehi M, Tajik M, Ebadi A (2008a). The study of interrelationship between different traits in common bean using multivariate analysis. American-Eurasian Journal of Agriculture and Environmental Science 3:806-809.

Salehi M, Tajik M, Ebadi AG (2008b). The study of relationship between different traits in common bean (P*haseolus vulgaris* L.) with multivariate statistical methods. American-Eurasian Journal of Agriculture and Environmental Science 3:806-809.

Scarano D, Rubio F, Ruiz JJ, Rao R, Corrado G (2014). Morphological and genetic diversity among and within common bean (*Phaseolus vulgaris* L.) landraces from the Campania region (Southern Italy). Scientia Horticulturae 180:72-78.

Singh SP (1999). Improvement of small-seeded race Mesoameriaca cultivars. In: Common bean improvement in the twenty–first century. Kluwer Academic Publishers. Dordrecht. Boston, London, pp. 255-274.

Singh RK, Chaudhary BD (1979). Biometrical methods in quantitative genetic analysis, Kalyani Publishers.

Singh SP, Gepts P, Debouck DG (2015). Races of common bean (*Phaseolus vulgaris*, Fabaceae). Economic Botany 45:379-396.

Smartt J (1988a). Morphological, physiological and biochemical changes in *Phaseolus* bean under domestication. In: Gepts P, ed. Genetic resources of *Phaseolus* bean. Dordrecht, The Netherlands: Kluwer, pp. 143-161.

Smartt J (1988b). The evolution of pulse crops. Economic Botany 32:185-198.

Stoilova T, Pereira G, Sabeva M**,** Chavdarov P (2004). Study on the phenotypic variability in landraces of dry beans (*Phaseolus vulgaris* L.). Field Crops Studies 2:226-233.

Stoilova T, Pereira G, Tavares-de-Sousa MM, Carnide V (2015). Diversity in common bean landraces (*Phaseolus vulgaris* L.) from Bulgaria and Portugal. Central European Journal of Agriculture 6(4):443-448.

Subramanian SS, Menon M (1973). Heterosis and inbreeding depression in rice. Madras Agricultural Journal 60:1139.

Valenciano JB, Casquero PA, Boto JA, Guerra M (2006). Effect of sowing techniques and seed pesticide application on dry bean yield and harvest components. Field Crops Research 96:2-12.

Vol. 11(5), pp. 158-163, May 2019
DOI: 10.5897/JPBCS2018.0797
Article Number: 4ECBD9C60922
ISSN 2006-9758

http://www.academicjournals.org/JPBCS

Journal of Plant Breeding and Crop Science

Full Length Research Paper

Field performance of *shrunken-2* super-sweet corn populations derived from tropical field maize × *shrunken-2* super-sweet corn crosses in Ibadan, Nigeria

Ayodeji Abe[1*], Oladayo Abosede Lasisi[1] and Olabisi Josephine Akinrinbola[1,2]

[1]Department of Agronomy, Faculty of Agriculture, University of Ibadan, Ibadan, Nigeria.
[2]Federal Institute of Industrial Research Oshodi, Lagos, Nigeria.

Received 26 December, 2018; Accepted 3 April, 2019

The conversion of tropical field corn genotypes into sweet corn could broaden the genetic base and improve yield and adaptation of sweet corn varieties. In this study, the performance of *shrunken-2 (sh2)* super-sweet corn populations derived from crosses between a *sh2* population and tropical field corn genotypes were evaluated in Ibadan. Experiments were conducted using randomised complete block design with three replicates. Data were collected on agronomic and fresh ear yield traits, and then subjected to analysis of variance. Significant genotypic differences were observed among the populations with most of the derived populations significantly superior to the donor population for most of the traits. Yield of marketable cobs ranged from 5.80 to 7.63 t/ha (mean = 6.84 t/ha). Six derived populations had significantly higher yield of marketable cobs than the donor population. On the average, 83.1% of the number of cobs harvested was marketable. Husk cover scores ranged from 2.8 to 6.8, with all the derived populations having significantly lower husk cover scores than the donor population. The results indicated that the conversion of the field corn genotypes into super-sweet corn was effective in the development of new super-sweet corn populations. The observed genetic differences could be exploited in further breeding programmes.

Key words: Fresh ear yield, husk cover, *shrunken-2* super-sweet corn, yield of marketable cobs

INTRODUCTION

Maize (*Zea mays* L.) is an important and highly diversified crop in the world, and a cereal food staple cultivated in every agro-ecological zone in West and Central Africa. It is made up of different types, classified by their kernel endosperm characteristics. The most common types are; flint, dent, flour, pop, pod, waxy and sweet. In West and Central Africa, the flint and dent types are the most widely cultivated (Kim et al., 1987; Kim and Ajala, 1996). These field maize types, in addition to the dry grains being consumed in different processed forms, are harvested and consumed fresh as green maize (after roasting, steaming or boiling on the cob). This contrasts with developed countries where human consumption of fresh maize is of sweet and super-sweet corn (Osayintola et al., 1992; Lee et al., 1999; Zan and Brewbaker, 1999). The widely grown field maize varieties in West and Central Africa were however not specifically developed for direct fresh human consumption (Ogunbodede, 1999).

*Corresponding author. E-mail : ayodabe@yahoo.com, Tel: +2348065019295.

Sweet corn (*Zea mays* L. var *saccharata*), is a type of maize with kernels that are sweet as a result of high sugar content which when consumed in the fresh immature stage, has high levels of total sugars than field maize, rich in fibre, minerals, certain vitamins (Tracy, 1997; Lertrat and Pulam, 2007), and significant antioxidant properties (Dewanto et al., 2002). Sweet corn has its origin from a mutation that influences carbohydrate biosynthesis in the endosperm. In the genome of sweet corn, at least one of the eight mutant genes preventing the conversion of sugars to starch is present. These genes, which include *shrunken-2* (*sh2*) on chromosome 3; brittle (*bt*), and amylose extender (*ae*) on chromosome 5; sugary enhancer (*se*), sugary (*su*), and brittle-2 (*bt2*) on chromosome 4; dull (*du*) on chromosome 10; and waxy (*wx*) on chromosome 9 (Tracy et al. 2006, Qi et al., 2009) are monogenic and recessive (Santos et al., 2014). Of all the mutant types, *sh2* (Yousef and Juvik, 2002) and *bt2* (Brewbaker, 1977) have the greatest commercial value.

The *sh2* types of sweet corn contain about 29.9% sucrose, which is about ten times that of field maize. These types of sweet corn, generally referred to as super-sweet or extra-sweet corn, have extended shelf life due to the slow conversion of sugars to starch after harvest (Tracy, 1997), but with highly reduced levels of total carbohydrate. The *sh2* gene reduces endosperm content of starch and water soluble polysaccharides which leads to a reduction in the energy content of maize kernels and the markedly collapsed physical appearance of the kernels when dry. Due to these features, *sh2* varieties generally have a significantly reduced germination, seedling emergence, seedling vigour, plant development and growth and poor stand establishment.

In Nigeria, maize is grown throughout the country from the high rainfall forest of the southeast to the low rainfall Sudan savanna of the north; and with supplemental irrigation, maize can be grown throughout the year. Nigeria produces about 40% of the maize production in West and Central Africa (FAO, 2016). Great potential therefore exists for the production of super-sweet corn in Nigeria. Sweet corn production is usually targeted at three distinct and largely independent markets, namely; fresh, canning and freezing, with the fresh market component accounting for more than 70% of the total (Lizaso et al., 2007; USDA, 2017). Imports of canned sweet corn to Nigeria have increased in recent years largely due to widening food preferences. Therefore, the development and production of super-sweet corn in large quantity and quality would impact positively on the social and economic life of Nigeria. However, sweet corn cultivars are virtually nonexistent in Nigeria, and coupled with poor adaptation to tropical environments, its cultivation and utility is limited.

To bridge the gap created by these challenges, a broad-base temperate super-sweet *sh2* corn population was introduced into the country and adapted to the prevailing tropical environmental conditions by four cycles of mass selection (Adetimirin, 2008). This was meant to serve both as an open pollinated variety, as well as basis for inbred line development and hybrid production. The performance of this *sh2* super-sweet population in the growing conditions of Nigeria could be improved. One way of achieving this is by converting tropical field maize genotypes into sweet corn through backcrossing and selection for the sweet corn trait. This strategy will lead to improvement in the yield of the super-sweet corn varieties, broaden the narrow genetic base characteristic of *sh2* (Tracy, 2001; Teixeira et al., 2013), and facilitate the development of *sh2* inbred lines and hybrids. According to Entringer et al. (2017), the backcross method of breeding is efficient for obtaining super-sweet corn populations with good agronomic performance. Previous studies Cartea et al. (1996), Malvar et al. (1997, 2001), Tracy (2001), Butrón et al. (2008) and Entringer et al. (2017) reported the use of field corn to improve the agronomic performance of sweet corn. These studies have also shown that field maize genotypes could differ in their ability to improve the agronomic performance and quality of sweet corn. Therefore, tropical normal endosperm field maize genotypes have the potential to improve the adaptation and productivity of super-sweet corn. The objective of this study was to evaluate the agronomic performance of some *sh2* super-sweet corn populations derived from crosses between a tropicalised *sh2* population and tropical normal endosperm field corn genotypes.

MATERIALS AND METHODS

Location of experimental site

The study was conducted at the experimental field of the Department of Agronomy, Faculty of Agriculture, along Parry road, University of Ibadan (7°26' N, 3°54' E), Ibadan, Nigeria.

Generation of new homozygous *sh2* super-sweet corn populations

A broad-based temperate super-sweet *sh2* maize population, which was introduced and adapted to tropical environmental conditions of Ibadan, Nigeria after four cycles of mass selection (Adetimirin, 2008), was crossed as male (using bulk pollen) to six tropical field maize inbred lines (1368, 4001, 4008, 9613, KU1409 and KU1414) and five commercial/experimental hybrids [1368/9071 (Oba super 1), 4001/KU1414 (Oba super 2), KU1409/9613, KU1409/4008 and 4001/4008], all developed at the International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria

The resulting F1 populations from each of these initial crosses were sib-mated to generate F2 populations. The F2 seeds were thereafter selected for kernels homozygous for the *sh2* phenotype. The selected homozygous *sh2* derived from each of the F2 populations were backcrossed to the recurrent (field maize) parents. The BC1 plants from each population were sib-mated to generate BC1S1 which were thereafter selected for kernels homozygous for the *sh2* phenotype. The selected homozygous *sh2* derived from each of the BC1S1 populations were then bulked to

Table 1. Codes of *sh2* populations and their corresponding field maize parent genotypes.

S/N	Code	Field maize parent
1	Pop1	KU1409
2	Pop2	1368
3	Pop3	KU1409/4008
4	Pop4	KU1414 SR
5	Pop5	KU1409/9613
6	Pop6	Oba Super 1
7	Pop7	4001/4008
8	Pop8	Oba Super 2
9	Pop9	4008
10	Pop10	9613
11	Pop11	4001
12	*sh2* donor Pop	

form new homozygous *sh2* populations as shown in Table 1.

Evaluation of *sh2* super-sweet corn populations

The eleven new homozygous derived *sh2* populations alongside the original donor *sh2* population were evaluated in replicated field trials under rain-fed conditions during the 2016 and 2017 cropping seasons. The soil at the experimental site is sandy-loam with 15.20 g kg^{-1} organic carbon, 0.98 g kg^{-1} total nitrogen, 14.79 mg kg^{-1} available P (Bray-1), 0.26 cmol kg^{-1}K and a pH(H_2O) of 6.1. The twelve *sh2* populations were arranged in a randomized complete block design with three replicates. Each plot consisted of four 5.0 m long rows, with plants spaced 0.50 m and rows 0.75 m apart. Planting was done on the flat. Plots were over-sown to ensure good plant stand (since germination failure is a common feature in super-sweet corn with the *sh2* gene) and later thinned to two plants at two weeks after planting (WAP) to give a plant population of approximately 53,333 plants per hectare. NPK 15-15-15 fertilizer was applied at the rate of 300 kg ha^{-1} at 2 WAP, which provided 45 kg N ha^{-1}, 20 kg P ha^{-1} and 36 kg K ha^{-1} and top-dressed using urea at the rate of 25 kg N ha^{-1} at 4 WAP. Plots were kept weed free by hand weeding.

Data collection

Data were collected on days to anthesis (DA) as number of days from planting to when 50% of the plants in a plot shed pollen, and days to silking (DS) as number of days from planting to when 50% of the plants in a plot have emerged silks. Anthesis-silking interval (ASI) was calculated as the difference in days between DS and DA. Plant height (PH) and ear height (EH) were measured in meters 2 weeks after silking on all plants in the two middle rows of a plot, as the average distance from the soil level to the collar of the uppermost leaf and collar of the leaf bearing the uppermost ear, respectively. Husk cover (HC) was scored on plot basis on a scale of 1 to 9 (1 = husk tightly covers ear tip and extends beyond it; 9 = poor husk cover with ear tip clearly exposed). Harvesting for yield data was carried out between stages R4 and R5 when the ears were still green and fresh, 21 days after silking using plants in the two middle rows of a plot. Yield data included: (i) number of cobs (NC) recorded as total number of ears (fresh ears with husk removed) harvested per plot expressed per hectare; (ii) yield of cobs (YC) recorded as total weight of cobs (fresh ears with husk removed) harvested per plot expressed in tonnes per hectare; (iii) number of marketable cobs (NMC) recorded as number of cobs with approximately 250 filled edible kernels per plot, expressed per hectare; (iv) yield of marketable cobs (YMC) recorded as total weight of marketable cobs per plot expressed in tonnes per hectare; (v) number of kernel rows (NKR) recorded as the average number of kernel rows of 10 top cobs; (vi) cob length (CL) measured in cm as the average length of 10 top cobs; (vii) cob diameter (CD) was measured using an electronic 6 in digital calliper (Pittsburgh®, Item #47257) as the average diameter of 10 top cobs taken at the middle portion of the cob.

Data analyses

All data were subjected to analysis of variance for a randomized complete block using the PROC. GLM procedure in SAS (SAS Institute, 2003) assuming a mixed model with genotype and the interaction between genotype and environment were considered random. The years were considered as separate environments. Significant means were separated using DMRT (p=0.05).

RESULTS

Significant genotype differences were observed for all traits, except ASI. Effect of years was only significant for YC, NC and EH. Significant interactions between genotypes and environment were also found for most of the traits except YC, NC, HC, EH and ASI. However, the contribution of the main effects of genotype to the total sum of squares was in all cases larger than that due environment or interaction of genotype and environment (Table 2). Mean performance of the 12 populations over two years is presented in Table 3. The range in YMC from the lowest value (5.80 t/ha) to the highest value (7.63 t/ha) was 26.7% of the mean YMC (6.84 t/ha). However, six of the derived populations had significantly higher YMC than the donor *sh*2 composite population. The YMC obtained in the present study was 95.5% of YC.

Table 2. Mean squares from analysis of variance on the effects of environment and genotype onagronomic and fresh ear yield traits averaged across two years of 12 *shrunken-2* super-sweet corn populations evaluated across two years in Ibadan, Nigeria.

Source of variation	df	Mean square												
		YMC (t/ha)	NMC	YC (t/ha)	NC	NKR	CL (cm)	CD (mm)	HC	PH (cm)	EH(cm)	DA	DS	ASI
Rep(Env)	4	0.43*	6.73	0.30	4.36	0.11	0.08	1.48	0.31	52.66	90.11*	0.69**	0.51	0.61
Environment	1	1.31	0.39	2.47*	33.04*	0.59	0.59	5.39	0.01	277.30	475.35**	1.13	2.35	0.22
Genotype	11	2.56**	40.07**	3.65**	61.20**	2.94**	2.14*	10.69**	7.86**	230.57**	389.72**	6.59**	5.14**	1.65
Env*Genotype	11	0.59**	9.10**	0.36	4.06	0.39**	0.55**	2.24**	0.50	78.36**	33.86	0.43*	1.01**	1.07**
Error	44	0.16	3.12	0.25	3.63	0.12	0.13	0.72	0.35	27.62	30.69	0.18	0.33	0.34

YMC: Yield of marketable cobs; NMC: Number of marketable cobs; YC: Yield of cobs; NC: Number of cobs; NKR: Number of kernel rows; CL: Cob length; CD: Cob diameter; HC: Husk cover score; PH: Plant height; EH: Ear height; DA: Days to anthesis; DS: Days to silking; ASI: Anthesis-silking interval*, **: significant respectively at 0.05, 0.01 probability levels.

Table 3. Genotypic means of agronomic and fresh ear yield traits averaged across two years of 12 *shrunken-2* super-sweet corn populations evaluated across two years in Ibadan, Nigeria.

Genotype	YMC (t/ha)	NMC (× 10^3)	YC (t/ha)	NC (× 10^3)	NKR	CL (cm)	CD (mm)	HC	PH (cm)	EH (cm)	DA	DS	ASI
Pop1	6.51^{b}	40.82^{b}	6.83^{b}	50.50^{b}	13.8^{ef}	15.0^{e}	44.3^{cd}	3.3^{ef}	2.05^{ab}	0.97^{cd}	55.8^{bc}	58.3^{abc}	2.5^{bcd}
Pop2	6.59^{b}	37.88^{cd}	6.94^{b}	46.38^{de}	15.3^{ab}	16.1^{bc}	47.3^{a}	5.8^{b}	2.07^{ab}	1.04^{b}	56.2^{abc}	58.7^{ab}	2.5^{bcd}
Pop3	7.21^{a}	43.73^{a}	7.56^{a}	53.33^{a}	13.0^{h}	15.4^{de}	43.2^{d}	3.7^{de}	1.88^{f}	0.86^{e}	55.7^{c}	58.7^{ab}	3.0^{abc}
Pop4	7.31^{a}	45.30^{a}	7.60^{a}	50.10^{b}	13.8^{ef}	15.4^{de}	45.9^{b}	3.3^{ef}	2.00^{bcd}	1.06^{b}	55.7^{c}	58.0^{bcd}	2.3^{cd}
Pop5	5.80^{c}	36.71^{d}	6.18^{cd}	43.93^{f}	14.7^{bc}	14.3^{f}	44.4^{cd}	4.0^{de}	2.00^{bcd}	1.03^{bc}	54.0^{d}	56.5^{f}	2.5^{bcd}
Pop6	7.43^{a}	39.29^{bc}	7.83^{a}	43.30^{f}	15.0^{ab}	15.8^{bcd}	46.9^{ab}	4.3^{cd}	1.95^{de}	0.94^{d}	54.0^{d}	56.3^{f}	2.3^{cd}
Pop7	7.63^{a}	41.55^{b}	8.11^{a}	49.86^{bc}	14.2^{de}	16.6^{a}	45.9^{b}	3.7^{de}	1.90^{ef}	0.97^{cd}	56.3^{ab}	57.8^{cd}	1.5^{e}
Pop8	7.53^{a}	40.63^{b}	7.79^{a}	44.45^{ef}	14.0^{def}	16.2^{b}	46.3^{ab}	3.7^{de}	2.06^{ab}	1.06^{b}	54.3^{d}	56.8^{ef}	2.5^{bcd}
Pop9	6.11^{bc}	37.76^{cd}	6.59^{bc}	49.42^{bc}	13.7^{fg}	15.9^{bcd}	43.8^{cd}	3.8^{de}	2.04^{abc}	1.08^{b}	56.0^{bc}	59.0^{a}	3.0^{abc}
Pop10	6.26^{bc}	38.14^{cd}	6.57^{bc}	47.55^{cd}	14.3^{cd}	15.6^{cd}	44.4^{cd}	2.8^{f}	2.03^{abc}	1.16^{a}	54.3^{d}	57.5^{de}	3.2^{abc}
Pop11	7.50^{a}	39.40^{bc}	8.16^{a}	51.50^{ab}	13.3^{gh}	16.1^{bc}	45.8^{b}	4.8^{c}	1.97^{cd}	0.93^{de}	56.7^{a}	58.8^{a}	2.2^{de}
sh2 donor Pop	6.27^{bc}	38.16^{cd}	5.82^{d}	46.87^{d}	15.0^{ab}	15.6^{d}	44.0^{cd}	6.8^{a}	1.95^{de}	0.98^{cd}	53.8^{d}	57.3^{de}	3.5^{a}
Mean	6.84	39.95	7.16	48.1	14.2	15.7	45.2	4.2	1.99	1.01	55.2	57.8	2.6
CV (%)	5.91	4.42	6.98	3.96	2.47	2.30	1.88	14.17	2.64	5.51	0.77	1.00	22.52

YMC: Yield of marketable cobs; NMC: Number of marketable cobs; YC: Yield of cobs; NC: Number of cobs; NKR: Number of kernel rows; CL: Cob length; CD: Cob diameter; HC: Husk cover score; PH: Plant height; EH: Ear height; DA: Days to anthesis; DS: Days to silking; ASI: Anthesis-silking interval.

The YC ranged from 5.82 to 8.16 t/ha. The range in NC and NMC were 43,290 to 53,330 and 36,710 to 45,300 cobs/ha, respectively. On the average, 83.1% of the total NC harvested was marketable. The NKR, CL and CD averaged 14.2, 15.7 cm and 45.2 mm, respectively.

One important quality attribute in fresh market sweet corn production is HC. In the present study, HC scores ranged from 2.8 to 6.8 with a mean of 4.2. All the derived *sh*2 super-sweet corn populations had significantly lower HC scores than the donor *sh*2 population, eight of which had scores lower than the mean. The PH and EH of the populations ranged from 1.9 to 2.1 m (mean = 2.0 m) and 0.9 to 1.2 m (mean = 1.0 m), respectively. On the average, ears were placed mid-way the height of the plants.

All the population including the *sh2* donor population exhibited intermediate maturity with DA and DS ranging from 53.8 to 56.7 days and 56.3 to 59.0 days, respectively. However, nine of the derived populations shed pollen significantly later than the donor *sh2* population. On the average, the derived *sh2* super-sweet corn populations flowered significantly later than the donor *sh2* population. The ASI, which is an indication of the extent of synchrony in flowering ranged from 1.5 to 3.5 days with a mean of 2.6 days. Eight of the derived *sh2* populations had significantly lower ASI that the donor *sh*2 composite population.

In this study, orthogonal comparison revealed significant differences between the derived *sh2* populations and the donor *sh2* composite population for all the traits, with the derived *sh2* populations being superior to the donor *sh2* composite (Table 3).

DISCUSSION

Sweet corn cultivars are virtually non-existent in Nigeria, have narrow genetic base and poor adaptation to tropical environments. One strategy that could be adopted to broaden its genetic base, improve its adaptation and enhance its agronomic performance under tropical conditions is to cross with tropical field maize. In this study, some *sh2* super-sweet corn populations derived from crosses between *sh2* super-sweet corn population and tropical field maize genotypes were evaluated for their agronomic performance.

The significant effects of genotype and the higher contribution of the main effects of genotype to the total sum of squares observed in this study was a manifestation of the fact that the populations varied greatly in their performance. These genetic differences could be exploited in further breeding programmes. These significant genetic differences also indicated that the conversion of the field corn genotypes into super-sweet corn was effective in the development of new sweet corn populations different from the *sh2* donor parent. This was furthermore evidenced in the superiority of most of the derived populations over the *sh2* donor parent population for most of the traits studied. In this study, yield of marketable cobs averaged 6.84 t/ha. This was higher than the average yield of marketable fresh cobs of 5.03 t/ha reported by Kim et al. (2007) and 4.72 t/ha reported by Abe and Akinrinola (2015) for open pollinated varieties of normal endosperm tropical field maize. This observed yield potential reflects the great prospects that abound for sweet corn production in Nigeria. The findings of this study confirmed previous reports (Cartea et al., 1996; Malvar et al., 1997, 2001; Tracy, 2001; Butrón et al., 2008; Santos et al., 2014; Entringer et al., 2017) on the potential of tropical field maize genotypes in the improvement of sweet corn.

Conclusion

Significant genotypic differences were observed among the populations studied. Most of the derived *sh2* populations exhibited significantly superior performance relative to the *sh2* donor population for most of the traits. The results of the present study indicated that new super-sweet corn populations different from the donor parent could be developed by converting field corn genotypes into super-sweet corn through backcrossing and selection for the sweet corn trait. The observed genetic differences could be exploited in further breeding programmes. The superior populations could be further improved and used as base populations for inbred line development.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

ACKNOWLEGEMENTS

The authors wish to thank Professor V.O. Adetimirin of the Department of Agronomy, University of Ibadan for generously providing the *sh2* donor population used in this study. The normal endosperm tropical field maize genotypes were sourced from the Maize Improvement Programme of IITA, Ibadan. This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

REFERENCES

Abe A, Akinrinola TB (2015). Green ear yield potential of tropical field maize maize at two levels of nitrogen fertiliser application in Ibadan, Nigeria. Ibadan Journal of Agricultural Research 11(1):201-209.

Adetimirin VO (2008). Stand establishment and early field vigour variation in a tropicalised shrunken-2 maize population. Field Crops Research 108:143-149.

Brewbaker JL (1977). 'Hawaiian superweet #9' corn. HortScience 12:355-356.

Butrón A, Álvarez A, Revilla P, Malvar RA, Rodriguez VM, Galarreta JIR, Ordás A (2008). Agronomic performance of sweetcorn populations derived from crosses between sweetcorn and field corn. Journal of Agricultural Research 6:378-384.

Cartea ME, Malvar RA, Revilla P, Ordás A (1996). Improvement of early vigor and adaptation of sweet corn to European Atlantic coast with open-pollinated field corn populations. Maydica 41:119-125.

Dewanto V, Wu X, Liu RH (2002). Processed sweet corn has higher antioxidant activity. Journal of Agriculture and Food Chemistry 50(14):4959-4964.
Entringer GC, Vettorazzi JCF, Crevelari JA, Durães NNL, Catarina RS, Pereira MG (2017). Super-sweet corn breeding by backcross: A new choice for the Brazilian market. Brazilian Journal of Agriculture 92(1):12-26.
FAO (2016). Food and Agriculture Organization of the United Nations statistical database, http://www.faostat.fao.org/site/567/DesktopDefault.asp?PageID=567#ancor (accessed on 26 August, 2017).
Kim SK, Ajala SO (1996). Combining ability of tropical maize germplasm in West Africa II. Tropical vs. Temperate × Tropical origins. Maydica 41:135-141.
Kim SK, Adetimirin VO, Yoon ST, Adepoju MA, Gbadamosi BA (2007). Green-maize potential of hybrid and open pollinated cultivars at varying levels of applied nitrogen: relationships with grain yield. Tropical Science 47(4):149-158.
Kim SK, Efron Y, Khadr F, Mareck J, Fajemisin J (1987). Registration of 16 maize streak virus resistant tropical maize parental inbred lines. Crop Science 27:824-825.
Lee SS, Yun SH, Kim JH (1999). Sugars, soluble solids, and flavour of sweet, super-sweet, and waxy corns during grain filling. Korean Journal of Crop Science 44(3):267-272.
Lertrat K, Pulam T (2007). Breeding for increased sweetness in sweet corn. International Journal of Plant Breeding 1(1):27-30.
Lizaso JI, Boote KJ, Cherr CM, Scholberg JMS, Casanova JJ, Judge J, Jones JW, Hoogenboom G (2007). Developing a Sweet Corn Simulation Model to Predict Fresh Market Yield and Quality of Ears. Journal of American Society of Horticultural Science 132(3):415-422.
Malvar RA, Cartea ME, Revilla P, Butrón A, Ordás A (2001). Checking performance of field corn inbreds as donors of favourable alleles to improve early vigor and adaptation of sweet corn hybrids to European conditions. Maydica 46:187-193.
Malvar RA, Revilla P, Cartea ME, Ordás A (1997). Field corn inbreds to improve sweet corn hybrids for early vigor and adaptation to European conditions. Maydica 42:247-255.
Ogunbodede BA (1999). Green maize production in Nigeria in the new millennium- Prospects and Problems. *Genetics and food security in Nigeria in the twenty-first century.* Olaoye, G. and Ladipo, D.O. Eds. Genetics Society of Nigeria special publication pp. 33-37.
Osayintola OJ, Mareck JH, Akingbala JO (1992). Effect of time of harvest and variety on the quality of boiled green field maize (*Zea mays* L.). Tropical Science 32:369-376.
Qi X, Zhao Y, Jiang L, Cui Y, Wang Y, Liu B (2009). QTL analysis of kernel soluble sugar content in super-sweet corn. African Journal of Biotechnology 8:6913-6917.
Santos PHAD, Pereira MG, Trindade RS, Silva da Cunha K, Entringer GC, Vettorazzi JCF (2014). Agronomic performance of super-sweet corn genotypes in the north of Rio de Janeiro Crop Breeding and Applied Biotechnology 14:8-14.
SAS Institute Inc. (2003). SAS/STAT user's guide, version 9.1.3. SAS Institute Inc., Cary, NC, USA.
Teixeira FF, Miranda RA, Paes MCD, Souza SM, Gama EEG (2013). Melhoramento do milho doce. Sete Lagoas: Embrapa Milho e Sorgo. 32 p
Tracy WF (1997). History, genetics, and breeding of super-sweet (*shrunken2*) sweet corn. Plant Breeding Reviews14:189-236.
Tracy WF (2001). Sweet corn. *Speciality corns*. Hallauer, A.R. Ed. 2nd ed. CRC Press, Boca Raton, Florida. pp. 155-197.
Tracy WF, Whitt SR, Buckler ES (2006). Recurrent mutation and genome evolution: example of Sugary1 and the origin of sweet maize. Crop Science 46:1-7.
U.S. Department of Agriculture (USDA) (2017). Sweet corn data. https://www.nass.usda.gov/Statistics_by_Subject/result.php?49AD4F93-5D68-3E98-BA30-EE901B111899&sector=CROPS&group=VEGETABLES&comm=SWEET%20CORN (Accessed 24 December, 2018).
Yousef GG, Juvik JA (2002). Enhancement of seedling emergence in sweet corn by marker-assisted backcrossing of beneficial QTL. Crop Science 42(1):96-104.
Zan GH, Brewbaker JL (1999). Seed quality of isogenic endosperm mutants in sweet corn. Maydica 44:271-277.

Related Journals: