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Full Length Research Paper

Phenotypic diversity in local coastal maize landraces in Kenya

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Crop genetic diversity is the basis of our food supply and survival. Determination of the phenotypic diversity of Kenya local coastal maize landraces (LCML) was important to understand the dynamics of maize genetic resources for the improvement and sustenance of maize productivity in the coastal region. The experiment with 30 genotypes was laid out in a randomized complete block design with three replications. Data collected included days to anthesis, days to silking, number of leaves, ear height, plant height, ears per plant, grain yield and anthesis-silking interval. Analysis of variance of morphological traits was performed using a general linear model (GLM) of SAS computer version 9.1. Pattern analysis for the relationship among genotypes was achieved through cluster analysis; dendogram were developed using a hierarchical agglomerical clustering method. Association among genotypes identified by principal component analysis were portrayed by proximity plots. Two major groups were found; Group 1- 1 consisted of the 28 coastal germplasm while group1 – 2 consisted of the two check entries being OPVs from outside the coast region (Entries 26 and 28). Group 2 - 1 had 9 entries, which include entries 7, 18, 9, 10, 17, 3, 11, 12 and 14. This group is dominated by entries from Kilifi and Lamu Counties. Group 2 – 2 had 19 entries, which include entries from Kilifi and Kwale districts. Entries from Taita Taveta and Lamu appeared only in G 2 - 1. Other checks such as PH 4, CLS-3 and KDV-3 were also in Group 2 – 2. This may indicate that these checks were developed from the local landraces from Kilifi and Kwale Counties. This study showed that LCML displayed large amounts of variation for morphological traits. The pattern of forming clusters may have some geographical implication since some clusters were formed with entries from neighboring Counties. The broad trait diversity evident among the local coastal maize landraces suggests ample opportunity for genetic improvement of the crop through selection directly from the accession and/or the development of inbred lines for future hybrid programs.

Key words: Landraces, maize, genetic diversity, coast Kenya.

INTRODUCTION

Small scale farmers in many parts of the world are confronted with complex and heterogeneous environments (Brush, 1980; Kirkby, 1973), crop diversity and good crop performance in the occurrence of growing environments characterized by differences in soils, temperature and rainfall regimens and other factors (Brush, *et al.,* 1981; Lando and Mak, 1994; Richards, 1986). Crop diversity has helped small farmers to cope with pests and pathogens, particularly in the absence of pesticides (Glass and Thurston, 1978). The natural resistance of certain crop cultivars to certain pests and diseases, which have developed through a long co-evolutionary process, has been identified as one of the key contributions of the maintenance of crop genetic diversity in plant breeding and modern agriculture (Glass and Thurston, 1978; Hawkes, 1983; NRC, 1993). The belief that traditional farming systems are unsustainable is giving way to a recognition that many small holder farmers of the tropics utilize diversity of their environments, manage a large variety of crops and genotypes, and employ a wealth of techniques both to exploit the diversity and support rural livelihoods (Reij, *et*

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al, 1996). It is, therefore, argued that traditional farming with landraces is not just a profession but a way of life (Rahul and Nellithaman, 1998). According to Altieri and Anderson (1992), the factors which account to the maintenance of landraces diversity in any region are: continuing cultivation of landraces by traditional methods; small scale farming systems; environmental diversity within the field; local adaptation to environmental and biological stresses present; and deliberate seed selections and maintenance by farmers. Other factors are; geographic fragmentation that creates isolating mechanisms conducive to rapid differentiation; seed networks and exchange among farmers within and between villages and cultural group, ethnic diversity leading to various classification, uses and management of distinct crop varieties; and tolerance of weedy relatives within and around fields promoting hybridization, ecological exchanges between the vegetation in a farmer's field and the wild vegetation surrounding the field. The conventional explanation for crop genetic erosion is that farmers increasingly specialize and replace their diverse set of landraces with a few high yielding modern varieties that provide them with higher incomes. Maize landraces are open genetic systems, which continuously incorporate traits from exotic germplasm, including improved varieties. While farmers pursue their legitimate private interest, crop genetic diversity may be lost yet it is the crop diversity which has helped small scale farmers to sustainably manage harsh environments and meet their subsistence needs in the remote rural areas (Bellon, 2003). The maintenance of crop diversity has been associated with the farmers' ability to manage these risks (Clawson, 1985; Feder, *et al*., 1985; Lipton, 1968). Clawson (1985) shows how crop varieties with different maturation periods are used by small farmer throughout the world to insure a sufficient food supply. Maize is the most important food crop at the Kenya Coast (Kega et al., 1994, Otieno et al., 1994). The former Coast Province produces only 50,279 tons of maize per year, or 20 kg per person/year (Wekesa et al., 2003). Seventy (70%) of the farmers grow local coastal maize landraces (LCML) as opposed to improved maize varieties. The average maize yields are very low being 1.0 - 1.5 t ha^{-1}, while the potential for the area is >3 t ha^{-1} (Wekesa *et al*., 2003). Farmers in the coastal region are faced with many sources of production risks and uncertainty, e.g. rainfall variability, and high temperatures. The Kenya coast has the highest level of growing traditional maize landraces (Wekesa et al., 2003). There was a need to collect study and conserve the local coastal maize landraces (CML). They form part of the primary, secondary and tertiary gene pools (Harlan and de Wet, 1971; Hawkes, 1987). The objective of this study was, therefore, to determine the phenotypic diversity of LCML for use in guiding conservation and genetic improvement.

MATERIALS AND METHODS

Experimental Site

The study was carried out at the Kenya Agricultural Research Institute (KARI) Mtwapa in coastal lowland Kenya during the December 2005 – March 2006 and April – August 2006 seasons. Mtwapa is situated 20 km north of Mombasa in Kilifi County. This falls between latitude 3^o and 4^o S and longitudes 39^o and 40^o E, at an elevation of 3 meters above sea level. Mtwapa receives 1200 mm annual rainfall has maximum temperature of 28.8^oC and minimum temperatures of 23.4^oC and has predominantly rhodic and orthic Ferralsoils (Jaetzold and Schmidt, 1983).

Experimental design

Thirty (30) maize genotypes that included landraces and OPVs (29 from the coastal region and one from the mid-altitude dry maize growing zone of Kenya were used (Table 1). The experiment was laid out in randomized complete block design (RCBD) with three replications. Due to scarcity of seeds each plot had three rows of 5 hills each with 2 seeds per hill, which constituted 44,444 plants per ha^{-1}, the recommended plant density for coast Kenya**.** Ten (10) randomly selected plants were used to record seven morphological traits.

DATA COLLECTION

Data collected included quantitative morphological traits including days to anthesis (AD), days to silking (SD), number of leaves (LN), ear height (cm) (EH), ears per plant (EPP), plant height (PH), grain yield t ha^{-1} (GY), and anthesis-silking interval (ASI).

STATISTICAL ANALYSIS

Analysis of variance of morphological traits was performed using a general linear model (GLM) of SAS computer package version 9.1. The pattern analysis for the relationship among germplasm was achieved by cluster analysis. Dendogram were developed using the hierarchical agglomerical clustering method. Associations among germplasm identified by principal component analysis (PCA) were portrayed by proximity plots.

RESULTS AND DISCUSSION

Mean and standard deviations of the 30 genotypes evaluated (Table 2) were used in cluster analysis and

Table 1. Entry and gene bank of Kenya (GBK) accession numbers of the genotypes that were evaluated at KARI Mtwapa.

Entry	GBK code	Source (County)	Name	Entry	GBK code	Source (County)	Name
1	32329	Kwale	Matsere	16	47631	Kilifi	Mungindo
2	32372	Kilifi	Matsere	17	47632	Lamu	Gonjora
3	32379	Kilifi	Mdzihana	18	47635	Kwale	Kienyeji
4	32404	Kilifi	Mingawa	19	47636	Kwale	Chitweka
5	32423	Kilifi	Tela	20	47638	Kwale	-
6	34619	Taita Taveta	-	21	47639	Kwale	-
7	34660	Taita Taveta	-	22	47641	Kwale	Kanjerenjere
8	34661	Taita Taveta	-	23	47642	Kwale	-
9	44454	Lamu	-	24	47643	Kwale	-
10	44458	Lamu	-	25	47644	Kwale	-
11	46360	Kilifi	Kanjerenjere	26	CCM	KARI-Mtwapa	CCM
12	47624	Kilifi	Mengawa	27	PH-4	KARI-Mtwapa	PH4
13	47625	Kilifi	Mdzihana	28	CLC-1	KARI-Mtwapa	CLC 1
14	47628	Kilifi	Chinga cha mosi	29	CLS-3	KARI-Mtwapa	CLS 3
15	47629	Kilifi	Mwangongo	30	KDV-3	KARI-Katumani	KDV 3

KDV 3 – Katumani drought tolerant variety 3; CLS 3 – Coastal lowland synthetic 3; PH4 – Pwani hybrid 4; CCM- Coast Composite maize

Table 2. Means and Standard deviation of the 30 genotypes evaluated at KARI Mtwapa over two seasons in 2005/2006

Entry No.	AD	SD	ASI	LN	EH	GY	Ent No.	AD	SD	ASI	LN	EH	GY
1	50	58	10	21	63	8.7	16	55	59	4	21	75	4.9
2	51	59	9	21	72	8.2	17	55	61	7	24	81	12.4
3	55	65	11	23	69	7.4	18	58	67	9	23	74	3.7
4	51	54	11	20	60	3.3	19	54	59	6	22	59	7.0
5	50	58	8	21	54	4.8	20	53	58	5	22	55	5.1
6	54	61	7	21	56	5.9	21	53	58	5	22	55	5.1
7	61	66	5	23	79	6.7	22	53	59	6	22	50	5.2
8	52	62	10	21	64	3.0	23	54	59	6	22	58	5.7
9	62	72	10	24	90	1.8	24	53	60	7	22	64	6.9
10	54	63	9	23	89	9.2	25	51	57	7	21	42	5.7
11	60	64	4	24	86	12.8	26	55	61	6	22	92	7.5
12	61	71	10	22	76	4.9	27	63	68	5	22	53	5.7
13	48	56	8	20	69	9.9	28	58	66	8	21	77	5.7
14	54	65	11	23	65	9.6	29	58	62	4	21	41	4.9
15	56	62	6	21	71	6.2	30	47	56	9	23	41	4.9
Mean	54.6	61.53	7.43	21.9	66.0	6.42	Mean	54.6	61.53	7.43	21.9	66.0	6.42
STD Dev	4.04	4.42	2.23	1.1	14.3	2.54	STD Dev	4.04	4.42	2.23	1.1	14.3	2.54

principal component analysis. Highly significant differences were observed on the entry means for LN, AD, SD and ASI. This indicates that the germplasm showed variability for these traits. There were no significant differences among means of EPP and GY (Table 3).

Results of Cluster Analysis

Cluster analysis was performed among the 30 Kenyan LCML using hierarchical agglomerical methods (Figure 1). At 62.96% similarity, there were two clusters in Figure 1. Group 1 - 1 had 28 entries from the coastal region, while, group 1 - 2 had two entries, E26 and E28. Group 1 - 2 consist of the composites from the coastal region. At 65% similarity two more clusters formed Group 1 – 1. The clusters formed were group 2 - 1 and group 2 – 2. Group 2 – 1 had 9 entries, which include entries 7, 18, 9 and 17, 3, 11, 12 and 14. This group is dominated by entries from the Kilifi and Lamu Counties. Group 2 – 2 had 19 entries, which include entries from Kilifi and Kwale Counties. Entries from Taita Taveta and Lamu appeared only appeared only in G 2 - 1. Checks such as E27, E29 and

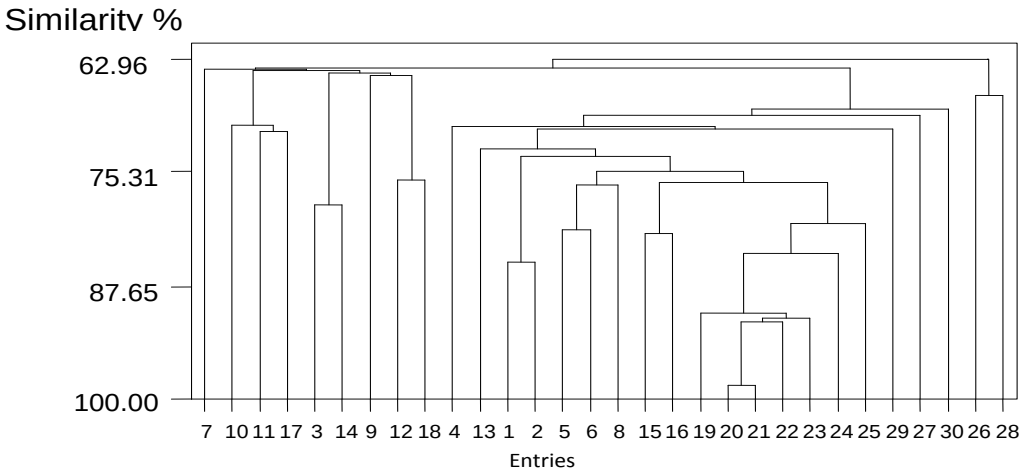
Entry	District	Local variety name	LN	AD	SD	ASI	EPP	GY
1	Kwale	Matsere	18.7 egf	73 h	74.3 ikj	2.7 ebdc	0.9 cb	0.87 edghf
2	Kilifi	Matsere	19 egdf	70.7 kj	75 ilkj	3 ebdc	1.0 cb	1.37 bac
3	Kilifi	Mdzihana	19 egdf	75.3 gf	76.3 ilhkgj	2 edc	0.8 cb	0.87 edghcf
4	Kilifi	Mingawa	19 egdf	71 ikj	73.3 lk	2.3ebdc	1.2 b	1.2 ebdacf
5	Kilifi	Tela	17.7 g	72.3 ih	78 ieflhkgj	6.3 a	1.0 cb	0.83 eghf
6	T/Taveta	T/Taveta	18.7 egf	71 ikj	75.7 ilhkj	4.7 bac	1.0 cb	0.87 edghcf
7	T/Taveta	-	21.3 ba	81.3 d	85.7 bac	4.3 bac	1.1 cb	0.8 ghf
8	T/Taveta	-	17.7 g	73.3 h	75.7 ilhkj	3.7 ebdac	1.0 cb	0.77 ghf
9	Lamu	-	20.7 bdac	83.7 c	90 a	5.0 ba	1.1 cb	0.93 edghcf
10	Lamu	-	20.3 ebdac	73 h	80.3 efhg	6.0 a	1.0 cb	1.03 ebdghcf
11	Kilifi	Kanjerenjere	22 a	85.7 b	88.7 ba	3.0 ebdc	1.0 cb	0.70 h
12	Kilifi	Mengawa	21 bac	81 d	86 bac	6.0 a	1.0 cb	0.97 edghcf
13	Kilifi	Mdzihana	18.3 gf	70.3 k	77.3 iflhkgj	6.0 a	1.0 cb	0.83 eghf
14	Kilifi	Chinga cha mosi	20 ebdfc	73 h	80 iefhg	6.0 a	1.0 cb	1.43 ba
15	Kilifi	Mwangongo	19.3 egdfc	75 g	80.3 efhg	3.7 ebdac	1.1 cb	0.9 edghf
16	Kilifi	Mungindo	18.7 egf	73.3 h	76.3 ilhkgj	4.0 bdac	1.1 cb	1.3 bdac
17	Lamu	Gonjora	20 ebdfc	76.7 f	82.3 efdc	4.3 bac	1.0 cb	1.13 ebdghcf
18	Kwale	Kienyeji	20.7 bdac	75.7 gf	82.7 edc	6.3 a	1.0 cb	0.73 ghf
19	Kwale	Chitweka	18.3 gf	72.7 h	78 ieflhkgj	4.3 bac	1.0 cb	0.77 ghf
20	Kwale	-	19.3 egdfc	79.3 e	81 efdg	2.7 ebdc	1.0 cb	1.60 a
21	Kwale	-	19 egdf	75 g	79 iefhgj	4.0 bdac	1.1 cb	1.0 edghcf
22	Kwale	Kanjerenjere	20 ebdfc	73 h	77.7 ieflhkgj	4.7 bac	1.0 cb	1.43 ba
23	Kwale	-	18.7 egf	72 ihj	75.7 ilhkj	4.3 bac	1.0 cb	1.03 ebdghcf
24	Kwale	-	19 egdf	72 ihj	75.7ilhkj	2.3 ebdc	1.1 cb	1.27 ebdac
25	Kwale	-	17.7 g	68.3 i	73 l	5.0 ba	1.0 cb	0.93 edghcf
26	Kilifi	Coast composite	18.3 gf	73 h	78.3 iefhkgj	3.7 ebdac	1.1 cb	0.83 eghf
27	Kilifi	Pwani hybrid 4	17.7 g	89 a	90 a	2.0 edc	1.3 b	0.27 ebdgcf
28	Kilifi	Coastal lowland comp 1	20 ebdfc	76 gf	78.7 iefhgj	3.0 ebdc	0.9 cb	1.17ebdghcf
29	Kilifi	Coastal lowland synth 3	19 egdf	80.7 d	79.3 iefhgj	1.3 ed	1.7 a	0.2 i
30	Makueni	-	14.7 h	59 m	61.3 m	1.0 e	0.70 c	0.7 h
		Mean	19.12	74.78	78.7	3.92	1.01	0.96
		CV	4.91	3.43	3.25	36.34	21	23.25
		DMRT	1.53	4.19	4.18	2.33	0.35	0.36

Table 3. The first two principal vectors scores from Principal Component Analysis (PCA) of the 30 genotypes

Entry	Vector 1	Vector 2	Entry	Vector 1	Vector 2
1	-1.376	1.340	16	-0.213	-0.135
2	-0.589	1.333	17	1.906	2.185
3	0.850	0.115	18	1.534	-1.257
4	-2.145	0.260	19	-0.874	0.022
5	-2.035	-0.079	20	-1.410	-0.471
6	-1.213	-0.517	21	-1.410	-0.471
7	2.287	-0.640	22	-1.461	-0.592
8	-1.194	-0.849	23	-1.034	-0.381
9	3.789	-1.931	24	-0.354	0.381
10	2.064	1.679	25	-2.584	-0.276
11	3.172	1.584	26	2.159	1.5163
12	2.183	-1.481	27	0.893	-2.211
13	-1.620	2.232	28	1.639	-0.244
14	0.711	0.720	29	-1.108	-1.695
15	0.003	-0.242	30	-2.573	0.105

**Some vectors are have positive values while others have negative values depending on how each vectors influenced the traits.*

Figure 1. Cluster analysis of 30 Kenyan local coastal maize landraces (LCML)



E30 were also in Group 2 – 2. More clusters form as the % similarity increases as indicated in Figure 1.

Discussion of cluster analysis

The fact that at 62.96% similarity two clustered formed and the forming of clusters increased with increase in % similarity indicates the diversity in LCML. Maize landraces are not static and continuously evolve due to the gene flow that farmer's favor and their selection of maize characteristics for changing conditions, preferences, individual farmer selecting own maize type over time and farmers sharing seeds. Gene flow can occur over long distances with very diverse materials, and even though some may not be appropriate for environments where they are introduced, they may constitute a source of new alleles to local populations (Bellon, 2004). Farmers have their own taste and preferences and the more diverse the farming community the more the diverse the crop will be. This has resulted in high biodiversity in LCML. The fact that the checks were in the same cluster with those from Kilifi and Kwale Counties indicates that these checks developed from landraces from these Counties. The clustering pattern indicates that phenotypic diversity of local coastal maize landraces is related to geographical diversity. The genotypes from Kilifi and Kwale Counties exhibited more phenotypic diversity than any other County in the coastal region. Equally high phenotypic diversity was observed in Kilifi and Kwale Counties. Landraces are developed and propagated by local farmers, being the Mijikenda ethnic groups in coast Kenya. The high and possibly rich genetic diversity in local coastal maize landraces can be harnessed by farmers and by maize breeders.

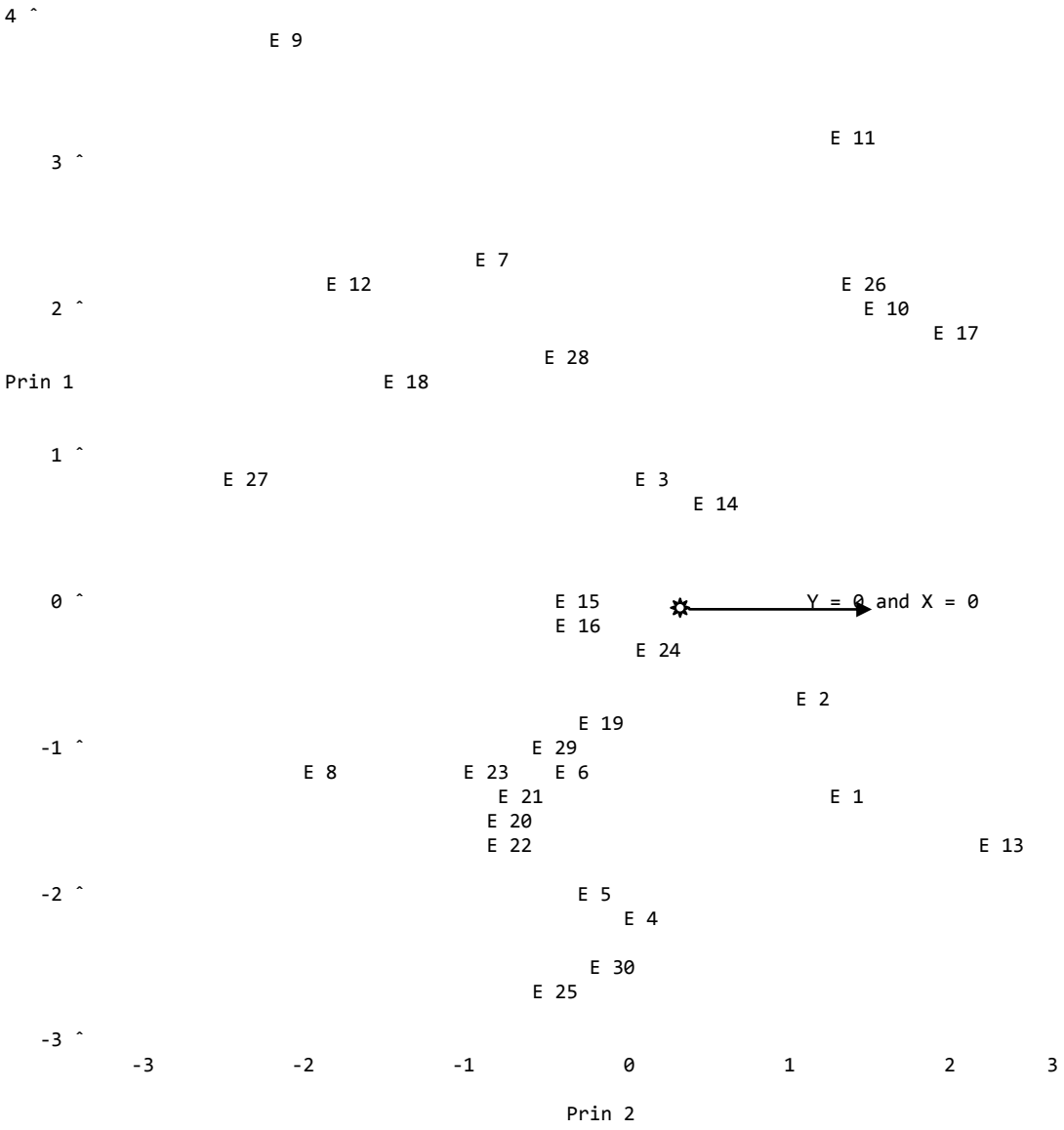


Figure 2: Proximity plot for the 30 germplasm listed in Table 1 based on the first two vectors from Principal Component Analysis (PCA). The closer the germplasm is to the principal vector 1(y) = 0 and principal vector 2 (x) = 0 point the more stable the germplasm. The figures used in making this figure are given in Table 3.

Results of proximity plot

The first two principal vectors scores of Principal Component Analysis (PCA) of the 30 local coastal maize landraces indicate the major role of these vectors in determining the grouping of local coastal maize landraces (Table 3). Associations, among entries identified by PCA were portrayed in proximity plots in Figure 2. The shaded area represent the Coast Composite and coastal lowland composite 1 which formed a cluster of their own (G 1 -2) leaving the remaining 28 entries forming the group 1 – 1.

Discussion of proximity plot

This study shows that local coastal maize landraces display large amounts of variation for morphological traits. The broad trait diversity evident among the LCMLs suggests ample opportunity for genetic improvement of the crop through selection directly from the accession and/or the development of inbred lines for future hybrid programs. Entries 3, 14, 15, 16, 19, 24, and 29 are more stable. This is because they are close to the axis y = 0 and x= 0. Grouping accessions into morphologically simi-

lar and most likely genetically similar groups (Souza and Sorrells, 1991) is helpful for selecting parents for crossing.

CONCLUSIONS

At 62.96% similarity between the two clustered forms and the forming of clusters increased which indicates the diversity in LCML. The clustering pattern indicates that phenotypic diversity of local coastal maize landraces is related to geographical diversity. The genotypes from Kilifi and Kwale Counties exhibited more phenotypic diversity than the other Counties in the coastal region. The high diversity in LCML can provide means of stabilizing reduction thus contributing to the livelihoods of local farmers. Such diversity helps farmers to cope with the high variability in the growing environments in terms of abiotic and biotic stresses. The broad trait diversity evident among the LCMLs suggests ample opportunity for genetic improvement of the crop through selection directly from the accession and/or the development of inbred lines for future hybrid programs. Entries 3 – Mdzihana, 14 (047628) –Chinga cha mosi, 15 (047629) – Mwangongo, 16 (047631) – Mungindo, 19 (047636) – Chitweka, 24 (047643) and 29 (CLC-3) – Coastal lowland synthetic- 3 are more stable. This is because they are close to the axis y = 0 and x= 0. Grouping accessions into morphologically similar and most likely genetically similar groups is helpful for selecting parents for crossing.

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