



ISSN: 0975-833X

RESEARCH ARTICLE

MORPHOLOGICAL CHARACTERIZATION OF SELECTED MAIZE (*Zea mays* L.)  
INBRED LINES UNDER ACID SOIL CONDITIONS

\*<sup>1,2</sup>Liliane N. Tandzi, <sup>2,3</sup>Eddy M. Ngonkeu, <sup>1</sup>Eric Nartey, <sup>4</sup>Martin Yeboah, <sup>1,2</sup>Hortense A. Mafouasson, <sup>2</sup>Karine Moche, <sup>3</sup>Honore Tekeu, <sup>2</sup>Jacob Ngeve and <sup>5</sup>Vernon Gracen

<sup>1</sup>Department of Agriculture, College of Basic and Applied Sciences, Univeristy of Ghana, Legon

<sup>2</sup>Institute of Agricultural Research for Development

<sup>3</sup>Plant Biology Department at the University of Yaounde I, Cameroon

<sup>4</sup>AVRDC project IITA, Yaounde, Cameroon

<sup>5</sup>Cornell University USA

ARTICLE INFO

Article History:

Received 05<sup>th</sup> February, 2015  
Received in revised form  
19<sup>th</sup> March, 2015  
Accepted 30<sup>th</sup> April, 2015  
Published online 25<sup>th</sup> May, 2015

Key words:

Inbred line,  
Genetic Diversity,  
Morphological Data,  
Performance,  
and Environment

ABSTRACT

Thirty inbred lines collected from Institute of the Agricultural Research for Development (IRAD), IITA and CIMMYT were evaluated in four environments at the Bimodal Humid Forest Zone (BHFZ) of Cameroon under acid soil condition from 2012 to 2013. An environment was made of experimental site, agricultural campaign and year. The objectives of the study were to assess the genetic diversity of parental maize inbred lines and classify them based on their performance under acid soil. Morphological data were collected as describe in the Descriptor for maize. The local inbred lines had flint and indented kernel, with a yellow color. Most of them had primary –secondary tassel type with reddish color. All the lines were divided into two major groups. The first group was subdivided into three sub-groups containing the most susceptible lines, the susceptible lines and the moderately tolerant lines. The second major group was made of tolerant lines. The diversity among the lines was not too wide.

Copyright © 2015 Liliane N. Tandzi et al. This is an open access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

INTRODUCTION

Maize (*Zea mays* L.) is cropped in a wider range of conditions than wheat and rice because of its greater adaptability (Udaykumar *et al.*, 2013). Several million people in the developing world consume maize as a staple food deriving their protein and energy requirements from it (Yadav and Singh, 2010). Concerted and intensive efforts are required to develop climate-change-resilient maize cultivars while accelerating the yield growth, without which the outcome will be hunger and food insecurity for millions of poor consumers of maize (Prasanna, 2012). Maize has enormous genetic diversity that offers incredible opportunities for genetic enhancement despite the environmental challenges. There is no lack of favorable alleles in the global maize germplasm that contribute to higher yield, abiotic stress tolerance, disease resistance or nutritional quality improvement. However, these desirable alleles are often scattered over a wide array of landraces or populations (Prasanna, 2012).

Analysis of genetic diversity and of relationships among the elite breeding materials can significantly aid in crop improvement. In maize, this information is useful in planning for hybrid and line development, assigning lines to heterotic groups and in plant variety protection (Yuan *et al.*, 2002; Yadav and Singh, 2010). In the recent past, there has been an increase in the cultivation of maize in the Bimodal Humid Forest zone (BHFZ) of Cameroon. This zone had hither to been put to tree crop cultivation due to the high rainfall. The acidic nature of the zone is, however, a limiting factor to the production of the crop as yield is always sub optimal. The soil acidity of the BHFZ is mainly due to high Aluminium (Al) content which leads to grain yield losses up to 60% (The *et al.*, 2005). To increase the livelihood of farmers in the zone and to minimize deforestation, it has become necessary to intensify the production of the crop by increasing output per unit area. This has called for breeding techniques which focus on varieties which will be adapted to the acid soils and not necessarily amending the soils to increase pH to the optimal range. There must therefore, be a concerted effort to improve on inbred lines for the Humid forest zone of Cameroon.

\*Corresponding author: Liliane N. Tandzi,  
Univeristy of Ghana, Department of Agriculture, College of Basic  
and Applied Sciences, Legon.

Morphological study of inbred lines has not yet been undertaken under acid soils of the Humid Forest Zone of country. For an effective and efficient national maize breeding program in the country, there is an urgent need to gather useful information in this regard.

The objectives of the present study were to:

- Assess maize inbred lines for variation in morphological traits
- Classify inbred lines based on their level of tolerance to soil acidity.

## MATERIALS AND METHOD

### Plant material

On station evaluation of thirty inbred lines were carried out in native acid soil at Nkoemvone from 2013 to 2014 cropping season. Fourteen of these lines came from CIMMYT, three from IITA and the other thirteen from the Institute of Agricultural Research for Development (IRAD). The origin of these lines and their respective unique characteristics are presented in Table 1.

**Table 1. Maize inbred lines used in this study**

Lines	Code	Origin	Characteristics
4001	1	IITA	Tolerant to low N
88069	2	IRAD	Good root volume
9450 (1)	3	IITA	Temperate adapted
ATP 32	4	IRAD	Acid soil tolerant
ATP 50	5	IRAD	Acid soil tolerant
ATP S5 31Y - 2	6	IRAD	Acid soil tolerant
ATP S6 20Y - 1	7	IRAD	Acid soil tolerant
ATP S6 31Y-2	8	IRAD	Acid soil tolerant
ATP S6 31Y-BB	9	IRAD	Acid soil tolerant
ATP S8 26Y - 2	10	IRAD	Acid soil tolerant
ATP S8 30Y - 2	11	IRAD	Acid soil tolerant
ATP S9 30Y - 1	12	IRAD	Acid soil tolerant
ATP S9 36Y - 1	13	IRAD	Acid soil tolerant
CI gp1 17	14	IRAD	Tolerant and P efficient
CI gp1 17 (F)	15	IRAD	/
CLA 135	16	CIMMYT	Susceptible
CLA 183	17	CIMMYT	Acid soil tolerant
CML 304	18	CIMMYT	Susceptible
CML 332	19	CIMMYT	Susceptible
CML 434	20	CIMMYT	Acid soil tolerant
CML 435	21	CIMMYT	Acid soil tolerant
CML 437	22	CIMMYT	Acid soil tolerant
CML 439	23	CIMMYT	Acid soil tolerant
CML 479	24	CIMMYT	Acid soil tolerant
CML 486	25	CIMMYT	Acid soil tolerant
CML 533	26	CIMMYT	Acid soil tolerant
CML 534	27	CIMMYT	Acid soil tolerant
CML 535	28	CIMMYT	Acid soil tolerant
D300-17	29	CIMMYT	Acid soil tolerant
KU 1414	30	IITA	Tolerant to low N

### Physiographic of experimental sites and field layout

The evaluations were carried out at one of the stations of IRAD at Nkoemvone in Ebolowa, the Southern Region of Cameroon. Nkoemvone village is located 25 km from the city of Ebolowa and, 180 km from the main research station at Yaounde.

The altitude is 615 m above sea level with geographic coordinates of 12° 24' E, 2° 40' N (The *et al.*, 2006). The average temperature is 24 °C and the annual rainfall is 1800 mm with a bimodal distribution (The *et al.*, 2001). The soil has been classified as Kandiodox with high Al toxicity (The *et al.*, 2005). At Ebolowa, soil is highly weathered and acidic with a soil pH in water of about 4.2 and saturation of 79.8%. In general, this tropical rainforest is dominated by nutrient-poor soils, in spite of the tremendous amount of forest biomass (Yemefack *et al.*, 2005). The main farming system is cocoa, maize, groundnut, cassava intercrop.

The inbred lines were evaluated at two experimental sites in two seasons per year during two years. One cropping season on an experimental site in a year was considered as an environment. After initial land preparation which involved stumping and ploughing, the genotypes were sown in the field in alpha lattice design (10 x 3). Each year, site and treatment (acid soil and control) was considered as one environment. Each genotype was planted in single row of 4 m long in two replications. Rows spacing was 0.75 m apart and the hill spacing on the same row was 0.50 m. Three seeds were planted per hill and 10 days after emergence, plants were thinned to 2 per hill for a total density of 53,333 plant/ha. Weeds were controlled by the use of herbicides. The field trial received the recommended rate of fertilizer in split application, which consist of a basal dose of 37 N, 24 P<sub>2</sub>O<sub>5</sub> and 14 K<sub>2</sub>O kg/ha applied 7 days after planting and the remaining 126 kg N/ha applied 30 days after planting (The *et al.*, 2005).

### Data collection

### Morphological characterization of inbred lines

Data were recorded on number of days to anthesis, number of days to silking, plant height (cm), and ear height. Plant aspect was scored on a scale of 1 to 5 (with 1 being very good height, good ear height and good size) and 5 (being very poor height, very low or very high ear height, poor plant size), ear aspect (rated from 1 to 5 where 5 corresponded to the very bad aspect of grain and 1 to the very good ear aspect). Seed moisture content, plant stand at harvest, number of ears at harvest and grain yield was also taken. At harvest, grain yield (GY) was measured on a whole plot basis following standard CIMMYT procedure and was adjusted to 15% moisture using the formula below  $GY (t/ha) = [Grain\ Weight (kg/plot) \times 10 \times (100-MC) / (100-15) / (Plot\ Area)]$  Where MC = Grain Moisture Content (CIMMYT, 1985); And plot area = row length \* 0.75 (4\*0.75 = 3m).

Vegetative plant data was taken outlined by the 'Descriptors for maize' (IBPGR, 1991): Rating of total leaf surface, number of leaves above the uppermost ear including ear leaf after milk stage, root lodging two weeks before harvest, stalk lodging two weeks before harvest, sheath pubescence at flowering, tassel type at milk stage (primary, primary-secondary and primary-secondary-tertiary), days to ear leaf senescence, total number of leaves per plant after flowering, leaf orientation after flowering (erect; pendant), presence of leaf ligule after flowering, (Present =1 and Absent =0), tassel size after milk stage (Small, Medium, Large).

After harvest, ear data were recorded using all ears on at least 20 representative plants per accession on: kernel row arrangement (regular, irregular, straight, spiral), kernel type (floury, semi-floury, with an external layer of hard endosperm, dent, semi-dent, intermediate between dent and flint but closer to dent, semi-flint, flint with a soft cap, flint, pop, sweet, opaque 2/QPM, tunicate, waxy), kernel color (white, yellow, purple, variegated, brown, orange, mottled, white cap, red), shape of upper surface of kernel (shrunken, indented, level, rounded, pointed, strongly pointed).

### Data analysis

The analysis of variance (ANOVA) was performed using the PROC GLM in SAS version 9.2. The blocks were nested within replication by environments and replications within environments were treated as random factors and the genotype as fixed (Akinwale *et al.*, 2014). The statistical model used for the combined analysis is as follows:

$$Y_{ijk} = \mu + E_i + B_k(ij) + G_g + EG_{ig} + \epsilon_{ijk}$$

Where  $Y_{ijk}$  is the observed measurement for the  $g$ th genotype grown in the environment  $i$ , in the block  $k$  in replicate  $j$ ;  $\mu$  is the grand mean;  $E_i$  is the main effect of environment;  $B_k(ij)$  is the effect of block nested within replicate  $j$  by environment  $i$ ;  $G_g$  is the effect of the genotype;  $EG_{ig}$  is the interaction effect between genotype and environment, and  $\epsilon_{ijk}$  is the error term. A dendrogram was generated through Statistica 6 graphics software for field data.

## RESULTS

### Morphological characterization of the tassel, silk and leaf of lines from IRAD

The characters were observed on each line at the flowering stage (Table 2). The tassel was mainly of the primary – secondary type (found in 80% of the lines), except for line ATP S6 31Y-2 which had primary type and ATP S6 31Y BB which had the primary – secondary – tertiary type (Table 2) The sheath pubescence was mainly intermediate except for ATP 32, ATP S6 31Y-2, ATP S9 36Y BB and 4001 which had dense sheath pubescence.

Four inbred lines had dense compact type of the tassel, two lines had dense semi-compact structure, three lines had dense spread structure, one line (ATP 50) had semi spread structure and Cam Inb gp1 17 had spread structure of the tassel. Eight lines had pendant leaf orientation whilst three lines (ATP 50, ATP S8 30Y-2 and ATP S9 36Y BB) had erect leaf orientation. Most of the silk were reddish while four lines had whitish green silks. Three lines (88069, ATP S9 30Y-1 and ATP S6 31Y BB) had the leaf ligules (Table 3).

### Kernel character of lines from IRAD

All the lines had yellow, flint kernels and with an indented shape on the upper surface (Table 4). The kernel arrangement of rows on the cob was regular for most of the lines, irregular for ATP S9 36Y BB, ATP S8 26Y-2 and ATP S6 31Y-2. The arrangement of kernels on the cob was spiral for 4001 (Table 4).

### Agronomic performance of inbred lines

#### Mean square of quantitative traits

The analysis of variance for the yield and other related traits for all the 30 inbred lines (inbred lines from IRAD, CIMMYT and IITA) showed highly significant differences ( $P < 0.001$ ) for yield, plant aspect, ear aspect, ears harvested, plants harvested, ear height, plant height and day to anthesis. The ears per plant was significant at  $P < 0.05$  while the days to silk, the anthesis-silking interval and the plant stand showed significant differences among genotypes at  $P < 0.01$  (Table 5).

### Mean performance of quantitative traits of lines under acid soil

The overall mean yield recorded was 1.4 t/ha (Table 6). Seven genotypes yielded more than the overall mean under acid soil condition: Cml 535 gave 2.4 t/ha, Cam Inb gp1 17 (F) gave 3.1 t/ha, ATP 50 gave 2.5 t/ha, ATP S8 26Y-2 produced 1.5 t/ha, ATP S6 31Y-BB had 3.1 t/ha, ATP S5 31Y-2 yielded 1.6 t/ha and 88069 gave 1.7 t/ha. The mean of the plant aspect and ear aspect were 3.1 and 2.9 respectively. One ear per plant was recorded for all the lines.

Table 2. Morphological characteristics of maize genotypes

Genotype	Tassel type	Sheath pubescence	tassel color	Tassel size	silk color	Tassel criteria	Leaf orientation
ATP 32	Primary-secondary	Dense	reddish	Large	reddish	dense semi-compact	Pendant
ATP 50	Primary-secondary	Intermediate	reddish	Large	reddish	semi spread	Erect
ATP S6 31Y-2	Primary	Dense	whitish greenish	Small	reddish	dense spread	Pendant
ATP S6 31Y-BB	Primary-secondary	Intermediate	reddish	Medium	whitish	dense compact	Pendant
ATP S8 26Y-2	Primary-secondary-tertiary	Intermediate	greenish reddish	Large	whitish	dense spread	Pendant
ATP S8 30Y-2	Primary-secondary	Intermediate	reddish	Medium	reddish	dense compact	Erect
ATP S9 30Y-1	Primary-secondary	Intermediate	reddish	Large	reddish	semi-compact	Pendant
ATP S9 36Y-BB	Primary-secondary	Dense	whitish green	Large	whitish green	dense semi-compact	Erect
88069	Primary-secondary	Intermediate	reddish green	Large	whitish green	dense and spread	Pendant
Cam Inb gp1 17	Primary-secondary	Intermediate	whitish greenish	Large	whitish green	spread	Pendant
4001	Primary-secondary	Dense	greenish	Medium	reddish	dense compact	Pendant

Most of the tassels were reddish but some were greenish. Seven lines had large tassels while three lines (4001, ATP S8 30Y-2 and ATP S6 31Y BB) had medium tassel size and ATP 50 had small size of the tassel.

The mean ear height of the lines was 70.6 cm with a mean plant height of 159 cm. The silk emergence averaged 68 days to come out while the average pollen shedding was 67 days.

Table 3. Other morphological characteristics of lines

Genotype	Presence of leaf ligules (1 if present and 0 if not)	Number of ramification of tassel		
		Primary	Secondary	Tertiary
ATP 32	0	11	2	1
ATP 50	0	10	2	1
ATP S6 31Y-2	0	9	2	0
ATP S6 31Y-BB	1	11	3	0
ATP S8 26Y-2	0	11	1	0
ATP S8 30Y-2	0	9	1	0
ATP S9 30Y-1	1	12	1	0
ATP S9 36Y-BB	0	13	2	0
88069	1	9	0	1
Cam Inb gp1 17	0	10	2	1
4001	0	8	3	0
Mean		10	2	0.4

Table 4. Kernel characteristics of different inbred lines

Genotype	Kernel color	Kernel arrangement	Kernel type	Shape of upper surface of kernel
ATP 32	yellow	regular	flint	indented
ATP 50	yellow	regular	flint	indented
ATP S6 31Y-2	yellow	irregular	flint	indented
ATP S6 31Y-BB	yellow	regular	flint	indented
ATP S8 26Y-2	yellow	irregular	flint	indented
ATP S8 30Y-2	yellow	regular	flint	indented
ATP S9 30Y-1	yellow	irregular	flint	indented
ATP S9 36Y-BB	yellow	regular	flint	indented
88069	yellow	regular	flint	indented
Cam Inb gp1 17	yellow	regular	flint	indented
4001	yellow	spiral	flint	indented

Table 5. Analysis of variance for various quantitative traits in maize inbred lines

Source	df	Yield (t/ha)	pltas	earasp	epp	earhar	pltha	Earhgt (cm)	Pltght (cm)	Asi (day)	Silk (day)	Anthe (day)	plstd
Environment	3	6.4**	33***	23***	0.01NS	212***	311***	5381***	1420NS	113***	5811***	6299***	589***
Block (rep*envir)	9	2.6**	0.3 NS	1.1***	0.03 NS	19.5*	14.6 NS	231.5 NS	1085 NS	2.8 NS	23 NS	12 NS	21 NS
Genotype	29	4.1***	0.9***	1***	0.07*	31***	26***	517***	2291***	5**	32**	27***	26.8**
Geno x Envir	87	2.5***	0.4 NS	0.4NS	0.06*	23***	17**	224NS	836NS	2NS	13NS	11NS	17*
Error	108	1.2	0.36	0.3	0.04	10.8	9.7	190	620	2.7	16.5	8.7	11.8

Envir = environment, Geno = genotype (Inbred lines), df= degree of freedom, pltas = plant aspect, earasp = ear aspect, epp = ear per plant, earhar = ear harvested, pltha = plant harvested, earhgt = ear height, pltght = plant height, asi = anthesis-silking interval, plstd = plant stand, NS = non-significant, \* = significant at P<0.05, \*\* = significant at P<0.01, \*\*\* = significant at P<0.001.

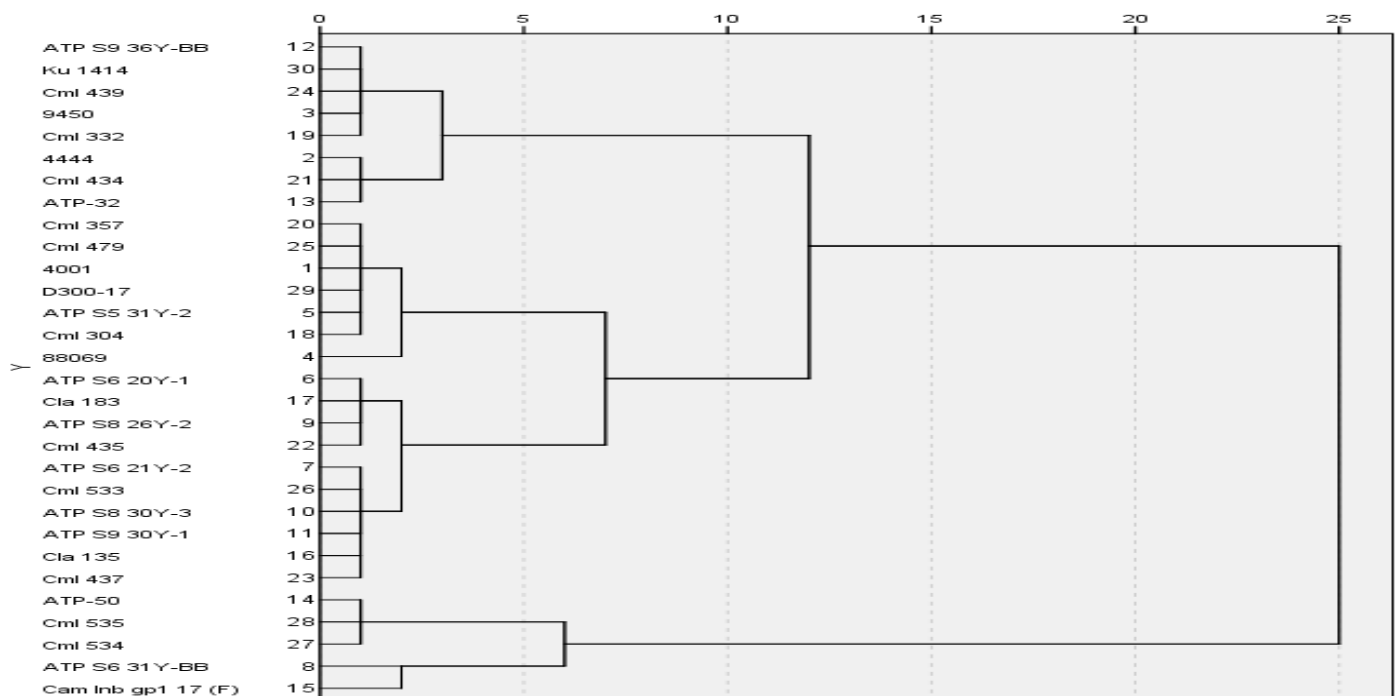


Figure 1. Dendrogram of 30 inbred lines based on the mean of the quantitative traits

**Table 6. Mean values for quantitative traits recorded on maize lines grown on acid soils**

Line	pltstd	Anthe	silk	Asi	plthght	earhgt	plthar	earhar	epp	earasp	pltasp	Yield t/ha)
4001	7.8	67.6	68	1	141.9	72.5	7.9	8.3	1	3.4	3.6	1.4
4444	7.8	70.5	72	2	108.1	45.6	6.4	5.8	1	4.1	4.3	0.4
88069	9.3	70	72	2	116.3	62.5	7.5	6.8	1	3.6	3.5	1.7
9450	5.6	70.3	73	3	111.9	60	5.1	5.3	1	3.8	3.8	0.7
ATP S5 31Y-2	12.1	65.6	69	3	133.6	59.8	10.3	10.3	1	3.6	3.3	1.6
ATP S6 20Y-1	8.4	69.1	72	3	111.1	54.8	7.5	6.1	0.8	3.9	3.6	1.1
ATP S6 21Y-2	10	68.1	70	2	123.1	60	9	8.8	1	3.6	3.3	1
ATP S6 31Y-BB	11.8	63.8	66	2	151.9	80.6	11.1	9.3	0.8	3.1	2.9	3.1
ATP S8 26Y-2	8.9	67.1	70	3	140.5	66.3	8.3	7.3	0.8	3.5	3.3	1.5
ATP S8 30Y-3	7.8	67.1	70	3	114.6	66.3	7.1	6	0.9	3.9	3.5	1.1
ATP S9 30Y-1	7.8	64.9	66	1	154.4	69.4	6.9	6	0.9	3.1	3.5	1.2
ATP S9 36Y-BB	9.4	67.8	71	3	113.1	58.1	7	5.4	0.7	3.9	3.4	1
ATP-32	7.6	71.8	74	3	116.3	53.1	6.5	4.9	0.8	4.3	4.4	0.5
ATP-50	9.3	68.3	70	2	133.8	64.4	8.9	8.3	0.8	3.5	3.3	2.5
Cam Inb gp1 17 (F)	12.5	66.5	69	2	140.3	70	11.8	12	1	3.1	3.7	3.1
Cl 135	7.3	66.5	68	2	140.8	60	8.5	8.2	1	3.9	3.4	1.3
Cl 183	9.6	68.6	71	2	121.1	61.1	8.8	7.8	1	3.8	4	1.1
Cml 304	7.1	69.1	72	2	120.6	58.7	7.9	7.3	0.9	3.7	3.5	1.4
Cml 332	7.1	70.6	73	2	102.5	59.4	6.6	5.6	0.9	4.3	4	1
Cml 357	8	67.8	70	3	128.5	60.7	8.9	8.1	1	3.6	3.4	1.6
Cml 434	5.5	66.3	69	3	120.5	55	3.9	3.9	1	3.8	3.4	0.5
Cml 435	7.4	66.8	68	2	115.3	61.6	6.6	6.5	1.2	4.1	3.6	1.1
Cml 437	6.6	70.3	72	1	112.6	62.3	6	5.8	1	4	3.5	0.9
Cml 439	6.6	66.6	70	4	107.8	46.3	5.6	4.6	0.9	4.1	3.5	0.8
Cml 479	8.6	67.9	68	0	148.1	66.9	7.8	7.3	1	3.6	2.9	2.1
Cml 533	7.4	69	72	3	134	72.9	6.3	6.1	1	3.7	3.7	0.9
Cml 534	12	66.8	68	2	159.1	70.6	11.1	11.8	1.1	2.9	3.1	2.4
Cml 535	10.4	66.2	69	2	152	66.3	9.4	9.3	1	3.4	3.2	2.4
D300-17	8	69.7	72	3	94.3	45.6	7	6.5	0.9	3.8	3.5	1.2
Ku 1414	7.9	68.3	70	2	127.4	59.8	7.6	6.4	1	4	3.6	0.9
Mean	8.5	67.9	70	2	126.5	61.7	7.8	7.2	1	3.7	3.5	1.4
lsd	3.4	2.9	4	1.6	24.6	13.6	3	3.2	0.2	0.6	0.6	1.1

df= degree of freedom, pltasp =plant aspect, earasp = ear aspect, epp = ear per plant, earhar = ear harvested, pltha = plant harvested, earhgt = ear height, pltght = plant height, asi = anthesis-silking interval, pltstd = plant stand, lsd = least significant difference.

**Table 7. Correlation among agronomic traits**

	pltstd	anthe	silk	asi	plthght	earhgt	plthar	earhar	epp	earasp	pltasp	Yield
pltstd												
anthe	-0.38**											
silk	-0.43**	0.98**										
asi	-0.27**	-0.10	0.07									
plthght	0.4**	-0.3**	-0.4**	-0.3**								
earhgt	0.30**	-0.5**	-0.5**	0.06	0.73**							
plthar	0.9**	-0.3**	-0.36**	-0.2**	0.43**	0.34**						
earhar	0.81**	-0.2**	-0.2**	-0.2**	0.44**	0.38**	0.9**					
epp	-0.03	0.026	0.01	-0.093	0.14	0.166*	0.003	0.36**				
earasp	-0.68**	0.57**	0.6**	0.27**	-0.58**	-0.47**	-0.6**	-0.6**	-0.13			
pltasp	-0.6**	0.741**	0.774**	0.17*	-0.4**	-0.4**	-0.6**	-0.5**	-0.1	0.8**		
Yield	0.616**	-0.03	-0.06	-0.17*	0.45**	0.37**	0.71**	0.83**	0.26**	-0.5**	-0.4**	

pltasp =plant aspect, earasp = ear aspect, epp = ear per plant, earhar = ear harvested, pltha = plant harvested, earhgt = ear height, pltght = plant height, asi = anthesis-silking interval, pltstd = plant stand, \* = significant at P<0.05, \*\* = significant at P<0.01.

### Correlation among agronomic traits

Yield was highly significant and positively correlated ( $P < 0.01$ ) with plant stand, plant height, ear height, plants harvested, ears harvested and ears per plant. Moreover, it gave negative and highly significant correlation with ear aspect and plant aspect. It expressed negative and significant ( $P < 0.05$ ) correlation with anthesis-silking interval. Yield had negative correlation with days to anthesis and days to silk but the correlation was not significant for any of the lines (Table 7).

### Principal Component analysis

The first principal component explained 43.3% of the total variation among the genotypes while the second one accounted for 18.5%. The highest eigen value was 7.4 from the principal component 2 whilst PC1 gave 5.2 (Table 8). Plant stand (pltstd), plants harvested (plthar), ears harvested (earhar), ear aspect (earasp), plant aspect (pltasp) and yield were the major discriminatory traits associated with PC I.

**Table 8. Principal components (PCs) for multi-genic traits of maize genotypes**

Traits	PC I	PC II
Eigen value	5.2	2.2
Cum. Eigen value	5.2	7.4
Total variance (%)	43.3	18.5
Cumulative variance	43.3	61.8
	Factor loadings	
	Factor 1	Factor 2
Pltstd	0.82	-0.36
Anthe	-0.65	-0.64
Silk	-0.66	-0.62
asi	-0.32	0.12
Plthght	0.52	0.32
earhgt	0.54	0.32
plthar	0.82	-0.43
earhar	0.78	-0.57
epp	0.03	-0.27
earasp	-0.81	-0.37
pltasp	-0.80	-0.07
Yield	0.65	-0.59

### Grouping of inbred lines based on field data

The mean value of 12 quantitative characters of 30 inbred lines was subjected to dissimilarity analysis. The matrix dendrogram was constructed to provide general view on the grouping of genotypes (Figure 1). The minimum genetic distance was recorded between Ku 1414 and ATP S9 36Y BB with a value of 0.00003 and the maximum was found between Cam Inb gp1 17 (F) and 4444 with a value of 3.55. Cluster analysis gave two major clusters (Table 9). The first major cluster was composed of three sub-clusters. The first sub-cluster contained 3 lines from IRAD and 4 introduced lines. The second sub-cluster had 3 lines from IRAD and 4 introduced lines. The third sub-cluster had 5 lines from IRAD and 5 introduced lines. The second major cluster contained 2 introduced inbred lines and 3 local lines. The introduced lines were distributed over the groups.

The plants were grown in acid soil prone environments which could influence their phenotypic aspect. Similar research study was done by Law *et al.* (2011) who characterized 152 maize inbred lines based on morphological traits. The knowledge of the existing genetic variation and associations between various agro-morphological traits is vital for any breeding program. These criteria were not enough to clearly discriminate them. Introduced inbred lines were incorporated into the evaluation and data on quantitative traits recorded. The mean yield of inbred lines in the environment under study was 1.4 t/ha. Eight inbred lines out-yielded the mean yield. Among those, two were introduced (Cml535 and Cml 534 (2.4 t/ha)). Also, yield was positively and highly correlated with plant height, ear height, and ears per plant and was negatively correlated with the anthesis-silking interval. The high-yielding inbred lines produced one ears per plant, with an average of 2 days for anthesis-silking interval, a plant height of 161 cm with ear height of 78 cm. The weaknesses on traits characteristics observed among the lines were also due to several self pollination techniques they went through.

The principal component analysis shows that the first principal component resulted in 43.3% of the total variation among all the inbred lines under investigation while the second principal component explained 18.5% of the variation for all the traits recorded. Therefore, 61.8% of the variance was explained by the principal component analysis. The grouping of genotypes based on field data was done. The lines with similar traits were grouped together. Two major clusters were identified. The first major cluster was divided into three sub-clusters (groups). Group I was made of 7 seven inbred lines of which four were introduced. The mean yield of genotypes in this group was 1.6 t/ha. The second group was also made of 7 inbred lines with four being introduced lines. The mean yield in this group was 0.8 t/ha. The third group had 10 inbred lines out of which five were being introduced. The mean yield of lines in this group was 1.1 t/ha.

**Table 9. Clusters based on quantitative traits of maize lines**

Cluster	Lines
Cluster 1: Sub-cluster I	4001, 88069, ATP S5 31Y-2, Cml 304, Cml 357, Cml 479, D300-17
Cluster 1: Sub-cluster II	Ku 14 14, Cml 439, Cml 434, Cml 332, ATP 32, ATP S9 36Y BB, 4444, 9450
Cluster 1: Sub-cluster III	ATP S6 20Y-1, ATP S6 21Y-2, ATP S8 26Y-2, ATP S8 30Y-3, ATP S9 30Y-1, Cla 135, Cla 183, Cml 435, Cml 437, Cml 533
Cluster 2	Cml 535, Cml 534, Cam Inb gp1 17 (F), ATP 50, ATP S6 31Y BB

## DISCUSSION

The description of maize inbred lines based on quantitative traits is the first way for identify them. Results from this study indicated that all the local inbred lines (IRAD) had flint and indented, yellow kernels. Most of them had primary – secondary tassels with reddish color. The similarities found among inbred lines could be attributed to the fact that almost all of them were developed from the same acid tolerant population under similar stress conditions of soil acidity. The difference observed in some cases could be explained by the genetic factors of the lines and also by the environmental interaction based on where they were grown.

The last group (second major cluster) was made up of five inbred lines out of which two introduced included were Cml 535, Cml 534, and three local (Cam Inb gp1 17 (F), ATP 50 and ATP S6 31Y-BB0). The introduced were spreaded all over the different groups. This result suggested that there were similarities among the local and the introduced inbred lines. Similar results were reported in India by Yadav and Singh (2010) where 30 maize inbred lines were divided into three groups using their morphological characters. In the present study, based on the average yield of each group compared to the mean yield, genotypes were classified as followed: The lines of group II (0.8 t/ha) and group III (1.1 t/ha) were considered as susceptible to acid soils; the lines of group I

(1.6 t/ha) were considered as moderately tolerant and the lines of group IV (2.7 t/ha) considered as tolerant. The minimum genetic distance of 0.00003 was observed between Ku 1414 and ATP S9 36Y BB indicating that the two lines were genetically closely related. Ku 1414 was introduced from IITA and ATP S9 36 BB is a local inbred line from IRAD. Yadav and Singh (2010) found that the minimum distance for closely related inbred lines was 0.35 while a distance of 1.92 was observed between inbred lines that differed from each other. For a crop like maize, the strategy of developing good hybrids depends on genetic diversity present in the available inbred lines. Analysis of genetic diversity and of relationship among the elite breeding materials could significantly aid in crop improvement. Moreover, the lines find themselves close to clusters due to a decrease in variation between them.

## Conclusion

Local inbred lines had flint and indented kernel, with a yellow color. Most of them had primary–secondary tassel type with reddish color. Based on the average yield of each group compared to the mean yield, genotypes were classified in four groups: The lines of group II and group III were considered as susceptible to acid soils; the lines of group I were considered as moderately tolerant and the lines of group IV were considered as highly tolerant. In general, the variability among morphology of the local ATP lines was not much. In the molecular grouping, two ATP lines were distinct from all the rest. The four inbred lines used as heterotic testers in the next chapter were found to be in different sub-clusters of the main cluster I. Tester 9450 was genetically similar to several CIMMYT Cml lines and was closely related to Cam Inb gp1-17. Testers 88069 and 4001 were in adjacent sub-clusters suggesting that they were genetically closed. In general, the genetic distance between the study lines was low. The prediction of the heterosis effect of the crosses between them would have been in the negative way. The variability among these inbred lines was not very high.

## Acknowledgment

The fund of this research work was provided by AGRA through the program of West Africa Centre for Crop Improvement (WACCI).

## REFERENCES

- Akinwale, R. O., Badu-Apraku, B., Fakorede, M. A. B. and Vroh-Bi, I. 2014. Heterotic grouping of tropical early-maturing maize inbred lines based on combining ability in striga-infested and striga-free environments and the use of SSR markers for genotyping, *Field Crops Research* 156, pp. 48-62.
- CIMMYT 1985. Managing trials and reporting data for CIMMYT international maize testing program. Mexico, D.F. CIMMYT.
- IBPGR 1991. Descriptors for maize, International Maize and Wheat Improvement Center, Mexico City/International Board for Plant Genetic Resources, Rome, p. 100.
- Prasanna, B. M. 2012. Diversity in global maize germplasm: Characterization and utilization, *Bioscience*, 37, pp. 843-855.
- The, C., Calba, H., Horst, W. J. and Zonkeng, C. 2001. Maize grain yield correlated responses to change in acid soil characteristics after 3 years of soil amendements. Seventh Eastern and Southern Africa Maize Conference, 222-227, pp. 222 - 227.
- The, C., Mafouasson H., Calba H., Mbouemboue P. and Zonkeng C. *et al.* 2006. Identification de groupes hétérotiques pour la tolérance du maïs (*Zea mays* L.) aux sols acides des tropiques *Cahiers Agricultures*, 15(4), pp. 337 - 346.
- The, C., Tandzi, N. L., Zonkeng, C., Ngonkeu, E. L. M. and Meka, S. *et al.* 2005. Contribution of introduced inbred lines to maize varietal improvement for acid soil tolerance. IN Badu-Apraku, B., Fakorede, M. A. B., Lum, A. F., Menkir, A. & Ouedraogo, M. (Eds.) *Demand-Driven Technologies for Sustainable Maize Production in West and Central Africa*. IITA-Cotonou, Bénin, International Institute of Tropical Agriculture (IITA)
- Udaykumar, K., Deepa, M., Laxman, M. and Prakash, G. 2013. Genetic diversity studies in newly derived inbred lines of maize (*zea mays* l.), *Molecular Plant Breeding* 4(9), pp. 77-83.
- Yadav, V. K. and Singh, I. S. 2010. Comparative evaluation of maize inbred lines (*zea mays* l.) according to dus testing using morphological, physiological and molecular markers, *Agricultural Sciences*, 1(3), pp. 131-142.
- Yemefack, M., Rossiter, D. G. and Njomgang, R. 2005. Multi-scale characterization of soil variability within an agricultural landscape mosaic system in southern Cameroon, *Geoderma*, 125, pp. 117-143.
- Yuan, L., Zhang, S., Warburton, M., Li, X. and Fu, J. *et al.* 2002. Assessment of genetic similarities among maize inbred lines using SSR markers. , In: *Proceedings of the Eighth Asian Regional Maize Workshop*, Bangkok, pp. 50-58.

\*\*\*\*\*