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Genotype by Environment Interaction and Yield Stability of Maize Hybrids Evaluated in Cameroon

Agriculture

KEYWORDS : Stable, hybrids, mega-environment, high-yielding.

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ABSTRACT

The objectives of this study were to determine the genotype by environment effect on yield of 121 maize hybrids evaluated in nine environments, isolate the mega-environments and identify the most high-yielding and stable maize hybrids across the nine environments. The results indicate that the genotypes contributed 4.03% to the variance partition from the total sum of square while the combination of the IPCA 1 and IPCA 2 explained 69.76% of the G x E interactions. The study environments were grouped into three mega-environments. Eight most stable hybrids out-yielded the best hybrid check by 20% and could be potential hybrids to be released after on farm trials.

INTRODUCTION

Maize (*Zea mays* L.) is produced in all the five agro-ecological zones of Cameroon and is an important source of income to the rural households. The average yield of maize is very low (1.8 t/ha) [1], [2]. Nowadays, the average yield ranged from 0.8 to 1 t/ha [3]. Low yields have been attributed to the use of low-yielding varieties, saved seeds, poor soil fertility, pests and diseases, limited use of fertilizers, low plant population, and inappropriate weed control. Significant potential improvements in yields could be achieved through the use of high-yielding hybrid maize varieties [4].

Crop breeders need to develop genotypes with superior grain yield, quality and other desirable characteristics over a wide range of environmental conditions. Prior to release of the new varieties, they are evaluated in yield trials at several locations for two or more seasons in multi-environmental trials which provides important information that enables selection and recommendation of crop cultivars [5], [6]. Genotype by environment interaction (GxE) makes it difficult to select the best performing and most stable genotypes because of the differential ranking of genotype across locations or years [4]. Badu-Apraku [7] reported that G x E influences the ranking of the genotypes in different environments with some locations being better for genotype evaluations than others

The statistical methods for analyzing GxE effect include analysis of variance, stability analyses and multivariate methods which are more often used to identify GxE interactions in multi-environmental experiments. However, the analysis of variance has limitations due to the assumption of homogeneity of variance [4]. The GGE biplot has been recognized as an innovative methodology in biplot graph analysis in plant breeding. Fan *et al.* [8] showed that the GGE biplot was a useful tool to identify locations that optimized hybrid performance and make better use of limited resources available for maize testing programs. The GGE biplot graphically displays genotype main effect plus G×E of multi-environment trials in a way that facilitates visual evaluation of cultivars and mega-environment identification [9]. Currently, the stability for grain yield of the developed hybrids is unknown, yet this is crucial in cultivar recommendation in specific or general environments. The objectives of this study were to:

- Determine the genotype by environment effect on yield;
- Identify the most high-yielding and stable maize hybrids across nine environments and identify the mega-environments.

I. II. MATERIALS AND METHODS

II.1 Plant materials

One hundred and twenty-one maize genotypes made up of 106 single cross hybrids, 12 top cross hybrids and three released open-pollinated varieties as checks, were used in this study (Table 1).

Table 1: The codes and names of maize hybrids in this study

Hybrids	Code	Hybrids	Code	Hybrids	Code	Hybrids	Code
Cla 183 x 9450	1	Cml 439 x 4001	21	Cam Inb gp1 17 (F) x 4001	41	ATP S8 26Y-3 x 9450	61
Cml 434 x Cam Inb gp1 17	2	Cml 439 x Cam Inb gp1 17	22	Cml 332 x 88069	42	ATP S9 36Y-BB x 88069	62
CMS 8704 x 9450	3	ATP S6 20Y-1 x 88069	23	Cml 437 x 9450	43	Cml 439 x 9450	63
Cml 437 x Cam Inb gp1 17	4	ATP S5 31Y-2 x 4001	24	ATP S9 30Y-1 x Cam Inb gp1 17	44	Cml 357 x 9450	64
ATP S6 31Y-BB x 9450	5	ATP S8 26Y-3 x Cam Inb gp1 17	25	CMS 8704 x 4001	45	Cml 479 x Cam Inb gp1 17	65
Cla 183 x 88069	6	Cam Inb gp1 17 (F) x 9450	26	D300-17 x 9450	46	Cml 357 x 88069	66
D300-17 x Cam Inb gp1 17	7	ATP S9 36Y-BB x Cam Inb gp1 17	27	Cml 304 x Cam Inb gp1 17	47	ATP S6 21Y-2 x Cam Inb pg1 17	67
C4RR SA4 x Cam Inb gp1 17	8	ATP S8 30Y-3 x 9450	28	Cml 435 x 4001	48	Cml 435 x 9450	68

ATP S8 30Y-3 x Cam Inb gp1 17	9	ATP S8 30Y-3 x 4001	29	Cml 435 x Cam Inb gp1 17	49	Cml 439 x 88069	69
ATP S5 31Y-2 x 9450	10	Cla 135 x Cam Inb gp1 17	30	ATP SR Y x 88069	50	Cml 434 x 4001	70
ATP S9 36Y-BB x 4001	11	Cml 434 x 9450	31	ATP S9 30Y-1 x 88069	51	ATP S9 30Y-1 x 4001	71
CMS 8704 x 88069	12	Cla 183 x Cam Inb gp1 17	32	Cam Inb gp1 17 (F) x 88069	52	ATP S6 20Y-1 x 4001	72
ATP SR Y x 4001	13	ATP S6 21Y-2 x 88069	33	ATP S6 21Y-2 x 9450	53		
Cml 535 x Cam Inb gp1 17	14	Cml 479 x 4001	34	Cml 437 x 88069	54		
Cml 304 x 9450	15	Cml 357 x Cam Inb gp1 17	35	Cam Inb gp1 17 x 88069 (**check**)	55		
ATP S9 30Y-1 x 9450	16	ATP S6 20Y-1 x 9450	36	ATP S8 26Y-3 x 88069	56		
Cla 135 x 9450	17	Cml 534 x 4001	37	Cam Inb gp1 17 x 9450 (**check**)	57		
Cla 135 x 88069	18	Cml 332 x Cam Inb gp1 17	38	9450 x 4001 **(check)**	58		
Cml 357 x 4001	19	Cml 434 x 88069	39	9450 x 88069 **(check)**	59		
ATP SR Y x Cam Inb gp1 17	20	C4RR SA4 x 88069	40	ATP-50 x 9450	60		

Table 1 cont'd: The names and codes of maize hybrids used for the study

Hybrids	Code	Hybrids	Code	Hybrids	Code
ATP-32 x Cam Inb gp1 17	73	Cml 533 x 9450	90	Cml 304 x 4001	107
C4RR SA4 x 4001	74	Cml 533 x 88069	91	Cam Inb gp1 17 x 4001 (**Hybrid check**)	108
Cml 435 x 88069	75	ATP S9 36Y-BB x 9450	92	ATP S8 30Y-3 x 88069	109
Cml 437 x 4001	76	ATP-50 x 88069	93	ATP S6 21Y-2 x 4001	110
Cam Inb gp1 17 (F) x Cam Inb gp1 17	77	Cla 183 x 4001	94	C4RR SA4 **(Check, introduced OPV)**	111
Cml 535 x 9450	78	Cml 479 x 9450	95	D300-17 x 4001	112
Cml 535 x 88069	79	Cml 535 x 4001	96	ATP SR Y **(Check, commercial OPV)**	113
Cml 332 x 9450	80	CLA 135 x 4001	97	ATP S5 31Y-2 x 88069	114
CMS 8704 x Cam Inb gp1 17	81	Cml 332 x 4001	98	ATP-32 x 88069	115
CMS 8704 **(Check, commercial OPV)**	82	ATP-50 x Cam Inb gp1 17	99	ATP S6 31Y-BB x 4001	116
Cml 534 x Cam Inb gp1 17	83	ATP-32 x 4001	100	ATP S8 26Y-3 x 4001	117
Cml 533 x 4001	84	C4RR SA4 x 9450	101	ATP S5 31Y-2 x Cam Inb gp1 17	118
ATP S6 20Y-1 x Cam Inb gp1 17	85	Cml 534 x 88069	102	ATP-32 x 9450	119
Cml 479 x 88069	86	Cml 304 x 88069	103	ATP S6 31Y-BB x Cam Inb gp1 17	120
D300-17 x 88069	87	Cml 533 x Cam Inb gp1 17	104	ATP S6 31Y-BB x 88069	121
Cml 534 x 9450	88	ATP-50 x 4001	105		
88069 x 4001 (**Hybrid check**)	89	ATP SR Y x 9450	106		

II.2 Description of the environments

The study was conducted at two sites located in the humid forest zone of Cameroon in two different soil treatments (acid soil and acid soil corrected by the application of 4 t/ha of dolomite as 'control') over a three-year period (2012, 2013 and 2014). A total of nine environments were obtained (Table 2).

Table 2: Description of the environments

Environment	Correspondence
NKA1_2012	site1*treatment1 (acid)*year1 (2012)
NKA1_2013	site1*treatment1 (acid)*year2 (2013)
NKA1_2014	site1*treatment1 (acid)*year3 (2014)
EBA2_2013	site2*treatment1 (acid)*year2 (2013)
EBA2_2014	site2*treatment1 (acid)*year3 (2014)
EBC1_2012	site1*treatment2 (control)*year1 (2012)
EBC1_2014	site1*tretment2(control)*year 3 (2014)
EBC2_2013	site2*treatment2 (control)*year2 (2013)
EBC2_2014	site2*treatment2 (control)*year3 (2014)

The trials were conducted in the same location at Nkoemvone in Ebolowa. Two planting dates that differed by three weeks were utilized each year for the two experimental trials to differentiate the environment as reported by Singh and Chaudhary [10].

II.3 Description of the experimental sites

Trials were carried out at two experimental sites at the research fields of IRAD, Nkoemvone in Ebolowa, the Southern Region of Cameroon, from 2012 to 2014. Nkoemvone is on altitude of 615 m above the sea level and on 12° 24 E, 2° 40 N [11]. The average temperature is 24° C with the annual rainfall is 1800 mm with bimodal distribution [12]. The soil is a highly weathered Kandiudox with high Al toxicity [13], [14].

II.4 Land preparation planting and field management

Each experimental site was cleared from grasses manually and plowed. Each experimental site had two treatments of the soil with 2 m alley in between. One treatment was a native acid soil considered as the stress environment and the other was used as a control where the acidity was corrected with the incorporation of 4t/ha of dolomite lime. The dolomite was incorporated into the soil by plowing.

Each genotype was planted in a 4m long row, with two replications. The distance between the rows was 0.75 m and within

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row was 0.5 m. Three seeds per hill were hand-sowing and later thinned to two plants per hole, which corresponded to an expected plant density of approximately 53,333 plants/ha. Weeds were controlled manually and sometime by the application of herbicides (Plantomaïs, Roundup). The field trials received the recommended rate of fertilizer in split application, which was a basal dose of 37 N, 24 P_2O_5 and 14 K_2O kg/ha applied 10 days after sowing and top dressed with 46 kg N per hectare, applied 30 days after planting [14].

II.5 Experimental Design

The hybrids were arranged in 11 x 11 simple lattice design with two replications and the evaluations were done over three years in nine environments. The genotypes were assigned at random to the plots within each block.

II.6 Data collection

The grain yield was measured on a whole plot basis following standard CIMMYT procedure [15] and was adjusted to 15% moisture using the formula below

GY (t/ha) = [Grain Weight (kg/plot) x 10 x (100-MC) / (100-15) / (Plot Area)]

Where MC = Grain Moisture Content.

II.7 Data analysis

The general linear model (GLM) of all the traits evaluated on the 121 genotypes was generated through SAS version 9.2 considering environment as random to estimate the means of the genotypes. The GGE biplot analysis was also done with Genstat software version 15. The mean yields of hybrids were arranged as recommended and analyzed using Breeding Management System (BMS) software [16].

The MIXED MODEL procedure of Statistical Analysis System (SAS) version 9.2 was used for the combined analysis, with blocks nested within replication by environments and replications within environments were treated as random factors and the genotype as fixed. The statistical model used for the combined analysis is as follows:

$$Yijkg = \mu + Ei + Rj(i) + Bk(ij) + Gg + EGig + \varepsilon ijkg$$

Where Yijkg is the observed measurement for the gth genotype grown in the environment i, in the block k in replicate j; μ is the; grand mean; Ei is the main effect of environment; Rj(i) is the effect of replicate nested within environment effect; Bk(ij) is the effect of block nested within replicate j by environment i; Gg is the effect of the genotype; EGig is the interaction effect between genotype and environment, and εijkg is the error term [17].

III. Results

III.1 Combined analysis of variance for yield

The combined Analyses of Variance (ANOVA) for yields of the 121 maize genotypes evaluated across nine environments are presented in Table 3. Highly significant difference ($P < 0.001$) for environments was observed. Genotypes were significantly different ($P < 0.05$). Genotype x environment interaction was also highly significant ($P < 0.001$). Two different IPCA (interaction principal component axis) were estimated and they were highly significant ($P < 0.001$). The IPCA 1 expressed 39.16% of the total variation while the IPCA2 expressed 15.30% giving a total variation due to G x E of 54.46%. The proportions of total sum of squares accounted for genotype, environment and their interaction were 3.77, 77.06 and 5.53% respectively. IPCA1 and IPCA2 accounted for 8.5 and 3.37% of the total variation of grain yield (Table 3).

Table 3: Combined analysis of variance for grain yield of 121 genotypes across seven environments

Source	DF	% SS GxE	SS	%SS	MS
Genotype	120		452	3.77	3.77*
Environment	8		2692	77.06	336.55***
Genotype x environment	960		5306	5.53	5.50***
IPCA 1	127	39.16	1079	8.50	8.50***
IPCA 2	125	15.30	421	3.37	3.37***
Residual	708		1255	1.77	1.77 NS

DF = degrees of freedom; SS = Sum of square; MS = Mean square *, ** and *** denote significant differences at $P < 0.05$, $P < 0.01$, and $P < 0.001$ respectively. IPCA= Interaction principal component axis, NS = non-significant.

III.2 GGE biplot analysis for yield

The GGE biplot was computed based on principal components 1 and 2 which expressed 35.87% and 14.72% of total variation (Figure 1). Three mega-environments (A, B and C) were identified from the biplot. The mega-environment A enclosed all the environments except EBC1_2014. These mega-environments overlapped at the origin of the biplot. The mega-environment B covered NKA2_2014, NKA2_2013, NKA1_2013, EBC2_2013 and EBC1_2014. The smallest mega-environment C had three environments which were EBC2_2013, NKA2_2013 and NKA1_2013.

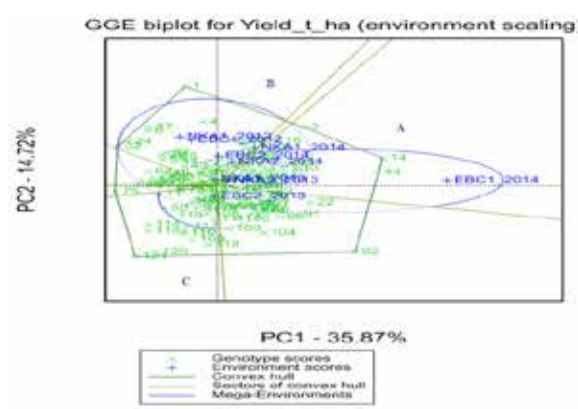
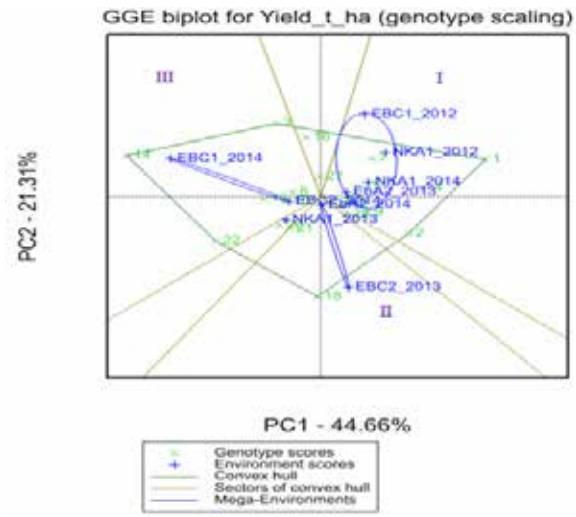


Figure 1: GGE biplot for yield of 121 maize hybrids under 9 environments

III.3 Genotype and genotype by environment interaction biplot analysis (GGE) for 20 best performing hybrids across all environments

The GGE biplot of the 20 most stable and high-yielding maize hybrids selected was constructed and the PCA1 and PCA 2 were shown to contribute to 65.97% of variation in grain yield across the environments (Figure 2). Similar biplot was constructed for the distribution of the hybrids in the target environments for yield (Figure 3). Under the nine environments, the 20 hybrids were distributed into six sectors of the biplot with 3 mega-environments (I, II and III). Mega-environment I was made up of 4 environments (EBC1_2012, NKA1_2012, NKA1_2014 and EbA2_2013). It covered 2 sectors of the biplot containing nine hybrids. The hybrids Cla 183 x 9450, Cml 434 x Cam Inb gp1 17,

Cml 437 x Cam Inb gp1 17 and D300-17 x Cam Inb gp1 17 were the best in this mega-environment. Mega-environment II had 2 environments (EBC2_2013 and EbA2_2014) covered by two sectors and containing two hybrids. Cla 135 x 88069 was the best hybrid or the most adapted hybrid. Mega-environment III had two environments (EBC1_2014 and EBC2_2014), covered by 2 sectors and containing six hybrids. The most adapted hybrids in this mega-environment were CMS 8704 x 9450, Cml 535 x Cam Inb gp1 17 and Cml 439 x Cam Inb gp1 17.



Note: EbA2_2013 and EbA2_2014 = EBA2_2013 and EBA2_2014 respectively.

Figure 2: GGE biplot of the top 20 hybrids across environments

GGE biplot based on genotype-focused caling was also constructed in order to detect the best locations of hybrids (Figure 3). CMS 8704 x 9450 was the ideal genotype based on the orientation of the environment coordinates AEC (close to the center of concentric circles) and genotypes closer to the ideal genotypes are more desirable than the others. The hybrids ATP S9 30Y-1 x 9450, D300-17 x Cam Inb gp1 17, ATP S9 36Y-BB x Cam Inb gp1 17, Cml 304 x 9450, Cml 437 x Cam Inb gp1 17 and Cla 183 x 9450 were the most stable. However, hybrids ATP S9 30Y-1 x 9450, D300-17 x Cam Inb gp1 17 and ATP S9 36Y-BB x Cam Inb gp1 17 were undesirable because of their low yield performance (Figure 5 and Table 7). Cml 535 x Cam Inb gp1 17 was very unstable but was high-yielding and was specifically adapted to EBC1_2014 environment.

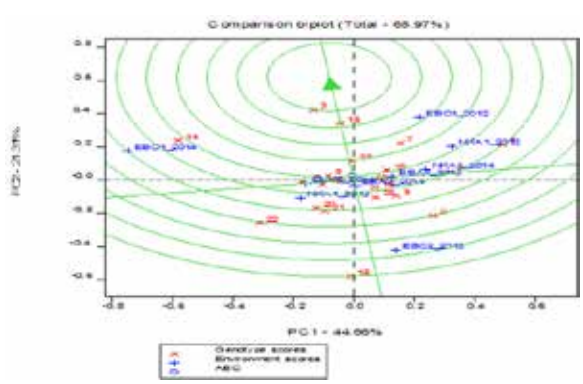


Figure 3: Genotype and genotype by environment interaction biplot based on genotype-focused scaling for the top 20 yielding maize genotypes.

IV. Discussion

The yields recorded among hybrids were significantly different meaning that they responded differently to each other. The significant effect of environments showed the differences were between environments used for the study. The result also suggests that the ranking of genotypes was different between environments and this may complicate selection because of the different responses of the genotypes in the environment and therefore there was a need to identify high-yielding and stable genotypes across the test environments [18], [19], [20].

Genotypes contributed 4.03% to the variance partition from the total sum of square while the combination of the IPCA 1 and 2 explained 69.76% of the G x E interactions. This result implies that the variation observed among mean yields of hybrids was mainly due to the environment as well as G x E interaction. According to Gauch and Zobel [21] in the normal multi-location yield experiments, location accounted for about 80% of the total variation whilst genotype and G x E interaction each accounted for about 10%. The percentage and the contribution of the G x E interaction accounted for 5.53% of total variation in maize yield. This suggests that the mean yield of genotype varied from one environment to another. These results were different from those of Ndhlela [19] who partitioned the total sum of square into 40.7% for the environment, 3.6% for genotype and 6.7% for the G x E interaction. The difference in the G x E interaction percentage of variation observed between these two studies could be due to the different environments used. The phenotype of an individual is a combination of its genotype (G) and the environment (E) where the genotype is grown and the genotype × environment interaction (G × E). The G × E usually complicates the process of selecting superior genotypes. According to Crossa [22] (1990), a number of genotypes respond to certain environments in a systematic, significant, and interpretable manner whereas noise suggests that the responses are unpredictable and uninterruptable. In the current study, the incomplete block design was used to reduce the GXE effect with the genotypes assigned at randomly to the plots within each block as reported by Bos and Caligari [23].

The different environments were ranked based on their variance associated with the mean of genotypes obtained within. The environment EBC1_2014 was the best with the overall mean of 6.66 t/ha and was followed by EBC1_2012. This shows that the most adapted high-yielding hybrids identified in these environments (EBC1_2014 and EBC1_2012) could also do well in other environments where the conditions are the same. Badu-Apraku *et al.* [7] in another study involving the locations Ejura, Sotouboua, Bagou, and Katibougou made the same observations.

Similarly, environments that were more alike tend to group together. As a result, twenty most stable hybrids were selected. CMS 8704 x 9450 was the first most stable hybrid, followed by Cml 304 x 9450, Cml 437 x Cam Inb gp1 17 and Cla 183 x 9450. Cml 535 x Cam Inb gp1 17 had low stability but was high-yielding and was specifically adapted to EBC1_2014 environment. The mean yield of the selected hybrids across environments was 5.14 t/ha. Eight of these hybrids out-yielded the best hybrid check (Cam Inb gp1 17 x 9450, 4.4 t/ha) by 20%. They were Cla 183 x 9450 with 5.84 t/ha, Cml 535 x Cam Inb gp1 17 with 5.58 t/ha, CMS 8704 x 9450 with 5.56 t/ha, ATP SR Y x 4001 with 5.35 t/ha, ATP S5 31Y-2 x 9450 with 5.33 t/ha, CMS 8704 x 88069 with 5.33 t/ha, Cml 437 x Cam Inb gp1 17 with 5.28 t/ha and Cml 439 x 4001 with 5.27 t/ha. Among them were three top crosses (CMS 8704 x 9450, ATP SR Y x 4001, CMS 8704 x 88069). All these hybrids had at least one introduced parent except CMS 8704 x 88069. These results suggest that the introduction of inbred lines is necessary for the development and the identification of the high-yielding and stable maize hybrids under acid soils of the humid forest zone of Cameroon. These varieties could be

released after on-farm trials. The importance of top crosses is based on the ability to produce more seed when needed since one parent is an open-pollinated variety. The best hybrids were able to tolerate Al toxicity in the acid soil stress environments. These hybrids might contain the Al tolerant genes which must have enabled them and survive and yielded well under the stress conditions.

In the GGE biplot analysis, Principal Components 1 and 2 (PC1 and PC2) together explained 50.59% of variation in grain yield. This shows that 50.59% of the variation in yield was due to genotype and genotype by environment effects. Result from the GGE biplot also called "which won where, grouped the nine test environments into three mega-environments. Mega-environment A had all the study environments except EBC1_2014. The mega-environment B had NKA2_2014, NKA2_2013, NKA1_2013, EBC2_2013 and EBC1_2014. The mega-environment C contained EBC2_2013, NKA2_2013 and NKA1_2013. This result indicated that some of the study environments were similar and were grouped together [7], [18], [19], [24].

The GGE biplot of the 20 high-yielding and most stable maize hybrids selected were constructed and the PCA1 and PCA 2 contributed to 65.97% of variation in grain yield across all environments. These hybrids were also grouped in three mega-environments (I, II and III). The mega-environment I had EBC1_2012, NKA1_2012, NKA1_2014and EbA2_2013. Three study environments were acidic soils. The most adapted and high-yielding hybrid identified in this mega-environment was Cla 183 x 9450. Therefore this hybrid (Cla 183 x 9450) was the highest-yielding and most stable under acid soil environments. The mega-environment III had only control environments (EBC1_2014 and EBC2_2014). The most adapted hybrid identified under these conditions was Cml 535 x Cam Inb gp1 17. This hybrid could perform well where acid soils are not a limiting factor to plant growth. When all environments fall into a single sector, this indicates that, a single cultivar had the highest yield in those environments. When the environments fall into different sectors, this indicates that different cultivars won in different sectors. The ideal genotype was a genotype to be on average environment coordinate (AEC) on positive direction and had vector length equal to the longest vectors of the genotypes on the positive side the AEC with the longest vector length of high-yielding genotypes [25], [5]. In this regard, Cla 183 x 9450 was an ideal genotype suitable to all the environments and EBC1_2012 was the most discriminating environment.

V. VI. Conclusions

This study has confirmed the year-to-year fluctuation and variability among sites and level of treatments (acid soil and control) as the important contributors for the G x E interactions. The study environments were grouped into three mega-environments. Eight most stable hybrids out-yielded the best hybrid check by 20%. They were Cla 183 x 9450, Cml 535 x Cam Inb gp1 17, CMS 8704 x 9450, ATP SR Y x 4001, ATP S5 31Y-2 x 9450, CMS 8704 x 88069, Cml 437 x Cam Inb gp1 17 and Cml 439 x 4001. Among them were three top cross hybrids (CMS 8704 x 9450, ATP SR Y x 4001, CMS 8704 x 88069). The most adapted hybrid under acid soil conditions was Cla 183 x 9450 while under control environments, Cml 535 x Cam Inb gp1 17 was the most adapted. All these hybrids had at least one introduced parent except CMS 8704 x 88069. The introduction of inbred lines was necessary and efficient for development and identification of high-yielding and stable maize hybrids under acid soils of the humid forest zone of Cameroon. These varieties are proposed for potential released after on farm trials involving farmers.

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