GENOTYPE X ENVIRONMENT INTERACTION FOR FRUIT YIELD OF SOME CUCUMBER (*Cucumissativus*) GENOTYPES

A.G. IWO AND O.E. ODOR

ABSTRACT

The present study was performed to analyze the genotype x environment (G×E) interaction for fruit yield of 5 genotypes in four environments; Ikom, Calabar, Obubra and Obudu located at different agro-ecological zones of Cross River State. The cucumber genotypes were grown in randomized complete block design in three replicates in 2015 cropping season. The yield data was analyzed using additive main effect and multiplicative interaction (AMMI) and genotype plus genotype by environment (GGE). Additive main effect and multiplicative interaction (AMMI) analysis of variance showed statistically significant effect of genotypes, environments and the genotype x environment interaction (P < 0.01%). The environment explained 59.59%which showed high differences in variety response to different locations tested. Genotype (G) and genotype x environment interaction (G x E) accounted 15.83% and 11.89% respectively. The first interaction principal component axis (IPCA1) was significant (P < 0.01) except the (IPCA 2) and explained 11.50% and 0.36% of the G X E sum of squares respectively. The Additive main effect and multiplicative interaction stability value (ASV) showed that significant difference existed in the G x E component. Based on the stability parameters, it revealed that none of the genotypes were stable for fruit yield, however according to ASV, and GGE Bi-plot graphical representation, Ashley genotype in relative terms was stable. The genotypes Poinsett (48.43 t ha^{-1}),Ashley(47.49 t ha^{-1}) and Marketer (41.66 t ha^{-1}) were considered to have adaptability to favorable environments, while Market More (MM 13.97t ha^{-1}) and Super Marketer (SM 16.66 t ha^{-1}) adapted to unfavorable conditions for fruit yield. Based on AMMI and GGE bi-plot, ASL had the widest adaptation and was considered as the ideal genotype, whereas P.ST showed specific adaptation. The ideal environments were IKOM (66.85 t ha^{-1}) and OBURA (56.93 t ha^{-1}). Through the GGE bi-plot and AMMI analysis, the superior genotypes identified could serve as references for genotype evaluation and inclusion in further testing in other seasons and environments.

KEYWORD: Environment, Genotype, Interaction, Stability and Yield

INTRODUCTION

Cucumber (*Cucumissativus*L) is an economically important crop in the family,Cucurbitaceae.There are seventy genera and seven hundred and fifty species of cucumberswithin the family (Thoa, 1998 and Best, 2000). Cucumber origin is traced to Asia and Africa where it has been utilized for over 3,300 years, however great number of cultivars have emerged and are widely grown and are consumed globally (Hector *et al.,* 1989). There are three main types of cucumber which include; slicing, pickling and burp types within which several cultivars have been developed.Cucumber is the second largest of all cucurbits and the fourth most cultivated vegetable globally (Jack *et al.,* 2008). Agricultural land under cucumber production worldwide is nine million hectares with yields of 184 million tons. China is the highest producer of cucumber with global output of 76%, followed by Turkey, Iran, Russia and Ukraine (FAO, 2015).

The nutritional profile of cucumber has revealed that cucumber provides phytonutrients which are beneficiary to health. These include flavonoids (such as apigenin, luteolin, quercetin and kaempferol), lignans (such as pinoresinol, lariciresinol and seciosolariciresinol) and triterpenes (cucurbitacines A, B and C). Lee *et al.,*(2010), and Thoennissen et *al.,* (2009) maintained that the plant phytonutrients especially the lignans are potent in reducing cardiovascular diseases and also various cancer types. The nutritional composition of cucumber shows that a fruit of cucumber per 100% edible portion contains 3% carbohydrate, 1% protein, 0.5% fat and 1% fibre, cucumbers are also excellent sources of vitamins K, C and B_1, and minerals like Molybdenum, Potassium, Manganese, Phosphorous, Magnesium, Copper. Cucumber is a very rich source of hair and nails promoting, silica. Other nutrients include pantothenic acid and biotin (USDA, 2014).

ODOR, E.O: Department of Crop Science, University of Calabar , Calabar. PMB 1115, Calabar, Cross River State Nigeria.
IWO, G.A: Department of Crop Science, University of Calabar , Calabar. PMB 1115, Calabar, Cross River State Nigeria.

Multi-environment trials (MET) are conducted to evaluate yield stability performance of genetic materials under varying environmental conditions (Delacy et al., 1996; Yan et al., 2000; Yan and Rajcan, 2002). A genotype grown in different environments will frequently show significant fluctuations in yield performance. These changes are influenced by the different environmental conditions and are referred to as genotype-by-environment (GE) interaction (Allard and Bradshow, 1964). However, GE interaction reduces the genetic progress in plant breeding programs through minimizing the association between phenotypic and genotypic values (Comstock and Moll, 1963). Hence, GE interaction must be either exploited by selecting superior genotype for each specific target environment or avoided by selecting widely adapted and stable genotype across wide range of environments (Ceccarelli, 1989).

In Nigeria, cucumber production is commonly carried out in the middle belt agro-ecological zone where it is believed to be well adapted; although few places in the southern part of the countrygrow it. Multi-location trial provides sufficient method of assessing varietal adaptation, yield and its stability.With the rising knowledge of the health benefits of cucumber and the agribusiness opportunity that lies in its production, due to the agrarian nature of the state and in the humid tropics with bimodal weather condition holds great potentials for cucumber production. Notwithstanding, little or no details on cucumber response to different environments and yield stability in Cross River States is known. Therefore, to investigate genotype x environment interaction on yield and yield stability in Cross River State to reduce the genotype and environment selection complications necessitated this research in four locations namely, Calabar, Ikom, Obudu and Obubra across the state.

Therefore, the purpose of the study was to investigate the interaction between cucumber genotypes and environments in four locations in Cross River State; to determine the yield stability of cucumber genotypes across the different locations and to identify specific genotypes and their ideal environments.

MATERIALS AND METHODS

i. GGE Model: $Y_{ij} - u - \beta_j = \alpha_i + j_{ij...}$
ii. AMMI Model: $Y_{ij} - u - \beta_j - \alpha_i = j_{ij}$

Where $Y_{ij}$is the measure mean of the ith genotype in jth environment, μ is the grand mean, a_i is the main effect of ith genotype, $\beta_j$is the main effect of the jth environment, $j_{ij}$is the interaction between$i$th genotype and jth environment.

The study was carried out during the early cropping season at four locations in 2015: Obudu (6^0.40 N, 9^0.10 E with annual rainfall estimated between the range of 2000mm to 3000mm it has temperature range of between 18^0c to 40^0C with optimum temperature of 29^0C)Ikom (5^0. 57. 40 N, 8^0 42. 39 E average rainfall 2332mm and temperature of 26^0C) Obubra (6^0.05. 0 N, 8^0 20 E, average annual rainfall of 2250-2500mm and optimum temperature of 27^0C) and Calabar ($4^0$58"N, $8^0$21"E average annual rainfall of 2915-3500mm with optimum temperature of between 24-26^0C). These locations represent the different agro-ecological zones in Cross River State in south-south part of Nigeria. Five commercial cucumber genotypes: Ashley (ASL), Market more (MM), Marketer (MK), Poinsett (P.ST) and Supper marketer (SM) were obtained from the National Institute of Horticulture (NIHORT) MbatoOkigwe, Imo State Nigeria.

The experimental sites were cleared and plots of 5m by 1.5m dimension were made manually. The experiment was laid out in randomized complete block design in three replications. The entire plot size measured 17m x 15m ($255m^2$) and was separated by 1m alley way.Each plot was made up of three (3) rows of 5m in length. Two seeds were planted per hole at the planting depth of 2cm and a spacing of 1m x 0.5. This was later thinned to one plant per stand after emergence. Data were recorded from six sampled plants from the net plot to reduce border effect for the following attributes: vine length at 3, 5 and 8 weeks after planting, number of primary lateral vines at 5 and 8 weeks after planting. Yield parameters(fruit length, fruit diameter, and number of fruits per net plot, fruit weight and total fruit yield) were determined at harvest. The total yield was extrapolated to tonnes per hectare. Management practices like weed control, fertilizer application and staking were carried out in the four locations.

A combined analysis of variance (ANOVA) was carried out and the significant genotype by interaction was further substantiated by using different statistical analytical tools. The means of all parameters were recorded. The Duncan Multiple Range Test (DMRT) was used for the separation of significant means at 5% probability level. AMMI and GGE bi-plot models wereused to analysedgenotype by environment interaction.

Additive Main Effect and Multiplicative Interaction (AMMI) Stability analysis value

The AMMI and the GGE bi-plot were computed with the use of Plant Breeding Tool and R-Package software (IRRI 2007) and GGE bi-plot software version 4 (Yan 2000) model. The nature of genotype x environment interaction was investigated with the use of AMMI model which combines the standard analysis of variance with principal component analysis (Zobel$et al.,$ 1988). Genotype stability ranking in these studies was calculated using the formulaby Purchase (1997) as follows

$$ASV = \sqrt{[\frac{SSIPCA1}{SSIPCA2} (IPCA1Score)]^2 + [IPCA2Score]^2}$$

ASV= AMMI Stability Value
SSIPCA=Interactive Principal Component Analysis Sum of squares 1 and 2.
IPCA1Score= Interactive Principal Component Analysis 1and 2 Scores.

The GGE bi-plot methodology (Yan $et al.,$ 2000) was used to graphically analyze the genotype x environment interaction data.

RESULTS AND DISCUSSION

The results of the combined analysis of variance (ANOVA) for both growth and yield parameters of the five genotypes over four environments revealed differences in sources of variations of which environment (E) and genotype (G) for all the characters measured were highly significant at P< 0.01 except for genotype fruit diameter(Table 1).The G x E was not significant at both (P<0.01 and P< 0.05) for all growth characteristics examined except for lateral vine at eight (8) weeks after sowing (P<0.05). Among all the yield characters studied, genotype (G) and interaction (G x E) were not significant in fruit diameter (FD). However, they were significant in numbers of fruits per plot (NFP), fruit length (FL) fruit weight (FW) and total fruit yield (TFY) in tonnes per hectare (Table 1). The implication is that there is genotype discrimination among the locations, (agro ecological zones), (Nzuve*et al*., 2013). Similar significant G x E results was reported by Thanki*et al.,*(2010), Derera*et al*. (2008), Makumbi, (2005); on durum wheat. The relative sizes of the sources of variability differed as revealed by their variance components in(Table 1). The environment sum of squares revealed that the locations selected differ significantly causing the variations observed in the fruit yield.

Themeans yield and growth parameters for cucumber genotypes under combined analysis are shown in Table 2. The result showed significant differences (P <0.01) in the mean yield of genotypes revealing variability in the genetic constitution of the genotypes; conferring the possibility of these genotypes as source of breeding materials to create new varieties with better performance than the parent lines. The mean yield ranged between 48.43 t ha^{-1} for Poinsett, and 13.96 t ha^{-1} for Market More. The genotypes Poinsett (P.ST), Ashley (ASL) and Marketer (MK), were consistently high yielders across the environment with mean fruit yields of 48.43, 47.49 and 41.66 t ha^{-1} respectively that exceeded the grand mean (33.46 t ha^{-1}). The genotypes Market More and Super market (13.97 and 16.66 tha[-1]) had the lowest mean yields. There were differences in genotype response to different environments for fruit and other yield parameters.

The mean yield results for four environments used for genotype x environment findings, is presented are presented in (Table 3).

Concerning yield across environments, the highest mean fruit yield (tha[-1]) were recorded at Ikom and Obudu with overall mean fruit yields (66.85 and 56.93 tha[-1]) respectively. This indicated that the two environments are favourable or suitable for cucumber production. All the genotypes performed well and gave mean fruit yields higher than the grand mean. Ikom (IK) recorded (66.8 t ha^{-1})as the highest mean fruit yield and Calabar (CAL) recorded (0.53 tha[-1]) as the lowest mean fruit yield. There was significant difference in location at (P < 0.05%) for vine length, lateral vine (growth attributes) and number of fruits per net plot across the time intervals of measurement but was not significantly different from Obudu in yield and yield components like fruit length fruit diameter and fruit weight. Ikom was significantly different from other locations. Obudu andObubra showed no location difference but were different from CAL in all the attributes evaluated.

Table 1: Mean squares from combined ANOVA for yield and growth parameters of five cucumber genotypes over four environments

sov	Df	VL21DAP (cm)	VL5WAP (cm)	VL8WAP (cm)	LV5WAP	LV8WAP	NFP	FL (cm)	FD (cm)	FW (kg)	TFY t/ha
Rep	2	4.730	0.9644	1745.8	0.9644	6.448	462.5	13.043	56.17	37.20	57.21
E	3	132.779**	33.1696**	71671.2**	33.1696**	153.152**	14127.2**	748.930**	117.55*	1145.62*	17.62*
G	4	36.185**	5.3495**	5732.6**	5.3495**	12.610**	3418.8**	66.385**	23.26 ns	228.33**	35.11*
G x E	12	1.515 ns	0.4211 ns	1269.9 ns	0.4211 ns	6.205*	764.1*	33.128**	47.08 ns	57.15*	87.88*
Error	38	3.343	0.8922	978.6	0.8922	1.893	227.9	5.393	36.56	17.28	26571

* And * = significant level at P<0.01 and P<0.05 respectively; ns=not significant; and df=degree of
Freedom, E= environment; G= genotype; GEI = genotype environment interaction
Parameters:VL21DAP= Vine length at 21 days after planting, VL5WAP= Vine length at 5 weeks after planting,VL8WAP= Vine length at 8 weeks after planting, LV5WAP= Lateral vines at 5 weeks after planting,LV8WAP= Lateral vines at 8 weeks after planting, FL = Length of fruit, FD = Diameter of fruit,
FW = Weight of fruit, NFP = Fruit number per plot, TFY = Fruit yield total

Table2: Means for yield and growth parameters in cucumber genotypes under combined Analyses

Environment	VL21DAP (cm)	VL5WAP (cm)	VL8WAP (cm)	LV5WAP (cm)	LV8WAP (cm)	NFP	FL (cm)	FD (cm)	FW (kg	TFY t ha^{-1}
CAL	2.54$_c$	17.92^c	34.37^c	0.37^c	0.90^d	0.33^d	4.13^c	1.39^b	0.04^b	0.53^b
IK	9.61^a	114.79^a	185.97^a	3.96^a	8.37^a	66.67^a	18.97^a	8.23^a	17.95^a	66.85^a
OB	7.07^b	61.65^b	174.28^a	2.46^b	6.62^b	48.20$_b$	18.51^{ab}	5.23^{ab}	14.25^a	56.93^a
OBR	6.88^b	72.43^b	143.24^b	1.83^b	4.90^c	13.07^c	16.98^b	4.94^{ab}	2.57^b	10.26^b
Overall mean	6.51	66.70	134.46	2.15	5.20	32.07	14.65	4.95	8.70	33.65

Means with the same superscript letter(s) in the same column are not significantly different (P ≤ 0.05) following Separation by Duncan Multiple Range Test.
Genotypes:

ASL= Ashley,MK= Marketer, MM= Market more, P.ST= Poinsett, SM= Supper marketer
Parameters: VL21DAS= Vine length at 21 days after sowing, VL5WAS= Vine length at 5 weeks after sowing
VL8WAS= Vine length at 8 weeks after sowing, LV5WAS= Lateral vines at 5 weeks after sowing
LV8WAS= Lateral vines at 8 weeks after sowing, FL = Fruit length, FD = Fruit diameter,FW = Fruit weight

Table 3: Combined analysis yield and growth parameters in cucumber at four environments

Means with the same superscript letter(s) in the same column are not significantly different (P ≤ 0.05)

Environments:IK = Ikom, OB = Obudu , OBR = Obubra, CAL = Calabar
VL21DAS= Vine length at 21 days after sowing VL5WAS= Vine length at 5 weeks after sowing, VL8WAS= Vine length at 8 weeks after sowing , LV5WAS= Lateral vines at 5 weeks after sowing, LV8WAS= Lateral vines at 8 weeks after sowing, FL = Length of fruit, FD = Diameter of fruit, FW = Weight of fruitNFP = Fruits number per plot.

The production potential of an environment is the ability of the environment to support superior performance from a series of genotypes. This was evident at IK location where all the attributes evaluated performed consistently better than other locations.

AMMI Stability Value.

The AMMI analysis of variation for yield (t ha^{-1})of five genotypes of cucumber tested at four locations and its stability value is presented in (Tables 5 and 6). Based on this model, fruit yield showed significant variation for both main and interaction effect at (p<0.001) indicating a wide range of variation between the genotype, environments and their interaction. The significance showed by G x E implied that each of the genotype reacted differently in various environment evaluated. The additive component of the analysis, results revealed that the mean squares of the IPCA1(the first interaction principal component axis) was highly significant (P<0.01) for genotype, environment and the interaction. The treatment sum of squares due to GEI of the multiplicative variance of was divided into IPCA1 and IPCA2 (interaction principal component analysis) and residual variation. IPCA1 of the interaction sum of squares explained 96.7%, IPCA2 explained 3.1% and residual explained 0.21%.
IPCA1 was greater than IPCA2 sum of squares showing the presence of differences in fruit yield performance of

the cucumber genotypes as a result of the interactive effect. This indicated that, one basic factor influenced the GEI which could be genotypic or environmental in nature. This result is in conformity with the findings of Vasanthumar*et al.*(2015) on water melon and Felix *et al.* (1997) on cucumber. Both results of the combined analysis of variation (ANOVA) and AMMI analysis of variation showed that environment (E) constituted the highest variation source accounted for 59.60% of the total sum of squares (TSS), while genotype (G) 15.83% (GE) Interaction source of variation accounted for 11.89% error 6.64% and replication 6.02% of the total variation, respectively.
The genotype stability and adaptability over range of environments is indicated by the IPCA scores in AMMI analysis. The greater the IPCA score not minding the positive or the negative sign the more specific adapted genotypes to certain environments. The closer the IPCA with small scores close to zero have low interaction and stable, genotype ASL had the most stable yield across environment compared to P.ST, MK, MM and SM. By considering the IPCA1 alone genotype ASL scored the lowest and it is considered the most stable both in

favorable and unfavorable environments. Genotypes P.ST, MK and ASL, maintained high yields in all the environments implying that they are adaptive to the locations, so they could be deployed in the locations or used for subsequent improvement of stable genotypes. SM and MM were determined to be poorly adapted to all the environments with their resultant low yields in the entire environments.

The AMMI Stability Value (ASV) for the five genotypes was computed. Lower ASV genotypes are considered more stable than the higher ASV genotypes. According to the ranking, based on this model, irrespective of their signs, ASL had the lowest ASV, so it was considered the more stable followed by MK, whereas genotypes P.ST, MM, SM were unstable (Table 6). Quantitative stability measure is very important for quantifying genotypes

based on their yield stability rank yet AMMI model does not provide such measurements.

In AMMI 1 model bi-plot, the plot visualized the productivity average of the varieties, locations and their interactions, (Yan and Hunt, 1998).

There was overlapping of genotypes across the environments indicating that crossover interactions among the genotypes occurred (Fig. 1). There was an interaction at IK, among the high yielding genotypes in this order (P.ST > MK > ASL). Crossover interaction occurred at OB with ASL crossing over P.ST and MK in the following order (ASL>P.ST>MK). There was also a crossover between P.ST and MK, at OBR, (ASL >MK >P.ST). Crossover interaction between the low yielding genotypes, only took place at OBR with MM crossing over SM.

Table 5: ANOVA table for AMMI model

Source	DF	SS	MS	Total variation (%)	
Total	59	8868758	150318		
Treatments	19	7744644	407613**	87.32	
Genotypes	4	1404570	351142**	15.83	
Environments	3	5285425	1761808**	59.59	
Block	8	534552	66819 **	6.03	
Interaction	12	1054649	87887 **	11.89	
IPCA1	6	1019970		169995**	11.50
IPCA2	4	32512	8128	0.36	
Residuals	2	2166	1083	0.02	
Error	32	589562	18424	6.64	

** And * = significant level at *P*<0.01 and *P*<0.05 respectively; ns=not significant; and df=degree of freedom, E= environment; G= genotype; I = genotype environment interaction
AMMI = Additive main effect and multiplicative interaction

TABLE 6: AMMI Stability Values of Genotype Yield Performance

Genotype	NG	GM	IPCA1	IPCA2	ASV
ASL	1	461.0	6.25372	8.60837	33.94
MK	2	462.1	8.63429	2.55612	48.29
MM	3	141.5	-14.5865	-0.31799	-81.83
P.ST	4	474.8	11.17652	4.42486	62.75
SM	5	167.0	-11.4779	1.94537	-65.25

key
NG= Number of genotype, GM= Genotype mean, IPCA1=Interactive principal component analysis 1 IPCA2=Interactive principal component analysis 2, ASV= AMMI Stability Value, ASL= Ashley, MK= Marketer
MM= Market more, P.ST= Poinsett, SM= Supper marketer

The above result agrees with the report of Vijendra Das (2005) that when cultivars are compared in different environments, their performance relative to each other may not be the same. One genotype could perform in one environment and the second may supersede in others. It was very evident from (Fig.1) that Ashley had the highest at Obudu and Obubra. But Poinsett excels at Ikom. Between the poor yielders, Market more was

highest at Obubra, but Supper Marketer excels at Obudu and Ikom.

The genotypes x environment interactions are of immerse importance to breeders in many ways; the necessity for breeding ideotypes is actuated by the knowledge of the interaction of genotypes with predictable environmental factors. Special genotypes may be needed for different environment. The response of genotypes to unstable productivity levels among environments provides an understanding of the stability of performance. This further provides the understanding of the environmental stability of genotypes and the determination of their suitability for the irregularity in growing conditions that could be encountered.

The four environments were grouped based on their productivity potential as indicated by their scores on the

AMMI 1 Bi-plot presented in Fig 2. The bi-plot has four quadrants with environments and genotypes grouped in only two quadrants out of the four. The grouping of the environments in to two quadrants indicated the importance of AMMI model in establishing the distinction among environments in terms of conditions necessary for potential growth.
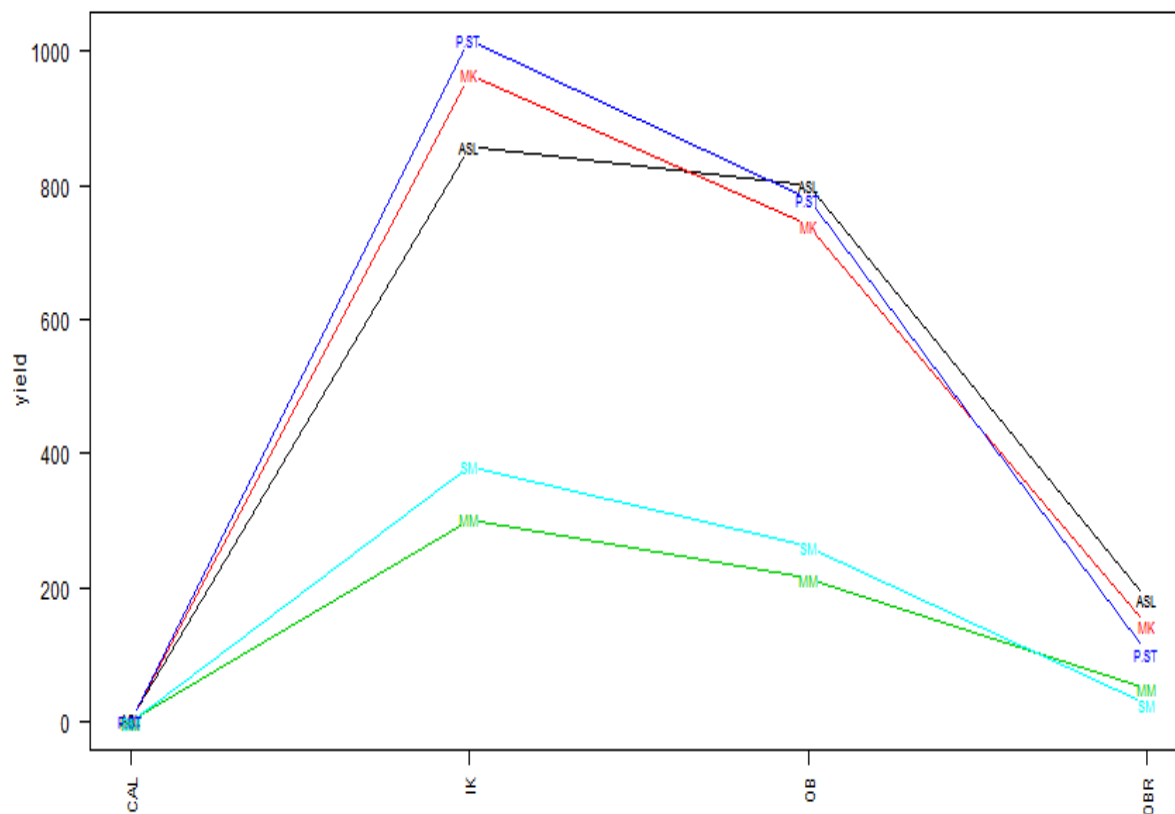
Environment
Figure 1: GGE bi-plot of yield response and cross over interaction of genotypes across environment.
Key: Env.=Environment; ASL= Ashley; MK= Marketer; MM= Market more; P.ST= Poinsett; SM= Supper marketer; IK = Ikom; OB = Obudu; OBR = Obubra; CAL = Calabar

This aspect is very crucial because environments are selected based on the similarity of response and suitability. This is very essential in decision making for selection of best environments and genotypes, thereby reducing the cost for commercial farmers. Based on the AMMI 1 bi-plot, environments IK and OB had the highest environmental mean yields; they were grouped together indicating their similarities in terms of yield performance. Genotypes ASL, MK and P.ST had the highest genotypic mean yields and were grouped together in the same quadrant with the highest environments. This showed that these genotypes (ASL, MK and P.ST) were very responsive to favourable environments. Environments CAL and OBR, according to the AMMI1 bi-plot were grouped together in the same quadrant with genotypes MM and SM having both low environmental and genotypic mean yields indicating that they were unfavourable environments for the production of cucumber.
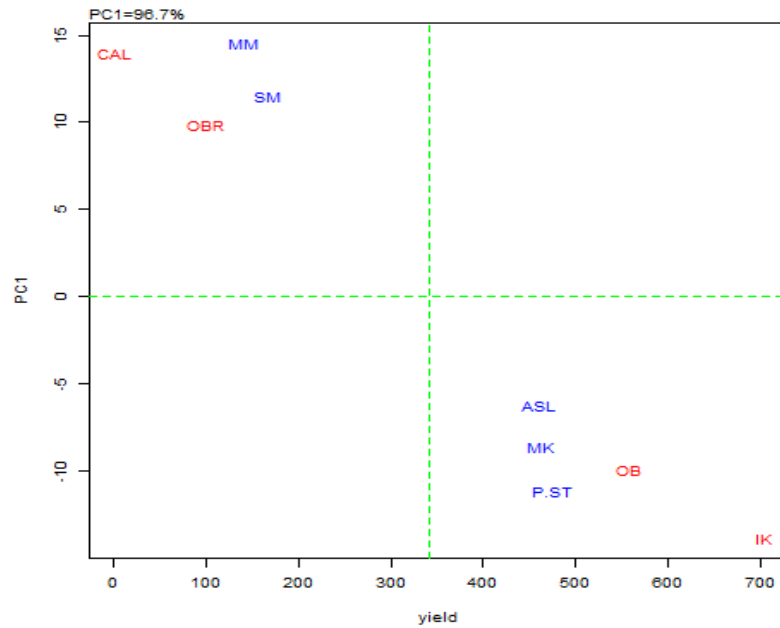
Figure 2: AMMI bi-plot: fruit yield (t ha^{-1}) x IPCA1.
Key :PC1(%) = Principal component ; ASL= Ashley; MK= Marketer; MM= Market more; P.ST= Poinsett; SM= Supper marketer; IK   =   Ikom; OB   = Obudu ; OBR = Obubra; CAL = Calabar

GGE Bi-plot Analyses

Fig.3. presents the polygon view of GEI for five the genotypes over four test environments tested. The polygon view of the bi-plot is the easiest means of visualizing the interactions effect of genotypes and environments (Yan and Kang, 2003), to show the cross over GE interaction is present or not, which helps to estimate of mega-environments possibly if they exist (Guach and Zobel, 1997, Yan and Rajcan, 2002). The pictorial viewof the "Which-won-where" pathway of locational trial data information is essential to explore mega environment in the production areas, (Guach and Zobel 1997).A polygon was formed to show "which-won where" by linking the genotypes at the vertexwith straight lines and one of the genotypes placed within the polygon. The vertex genotype in each sector is the best genotype at environments whose markers fall into the respective sector.Environments within the same sector share the same winning genotype, and environments in different sectors have different winning genotype. The partitioning of the GEI through the GGE bi-plot analyses revealed that Principal component 1 and Principal component 2 accounted for 98.2% and 1.7% of the genotype + genotype environment sum of squares respectively in (Fig 3). This explains the variation of 99.9%. These vertex genotypes in this study were (P.ST), (ASL), (MM) and (SM). They were either the highest yielders or the lowest yielders in some of the environments; therefore they were farthest from the origin of the bi-plot. On the account of the polygon view, the genotypes fell into three sections and the test environments fell into two sections. The first section hadIkom (IK) Environments within the same sector share the same winning genotype, and environments in different sectors have different winning genotype.
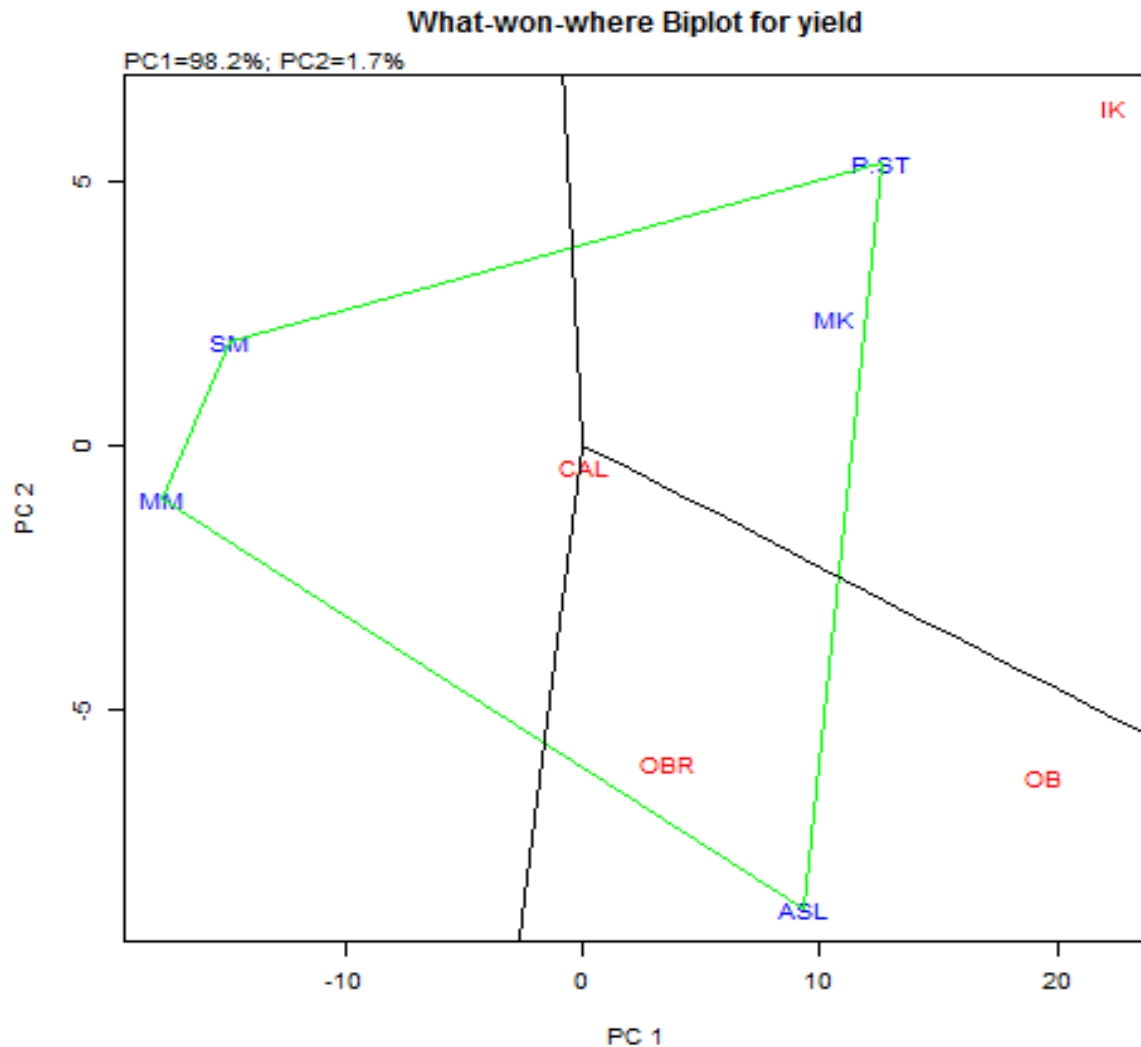
Fig.3. polygon view of genotype x environment interaction for five cucumber genotypesover four test environments; PC1=First Principal component; PC2=Second Principal component ;ASL= Ashley MK= Marketer; MM= Market more; P.ST=Poinsett;SM = Super Marketer; IK = Ikom; OB = Obudu   ;   OBR   =   Obubra; CAL = Calabar

This had the genotype Poinsett (P.ST) as the best yielder.Obudu (OB), Obubra (OBR) and Calabar (CAL) where Ashley (ASL) was the best variety. From the GGE bi-plot graphical representation, the vertex genotypes (MM) and (SM) were not top yielding in graphical representation, the vertex genotypes (MM) and (SM) were not top yielding in any of the environments. This study is in conformity with the reports of Ezatollah*et al.,* (2014) in wheat-barley disomic addition lines.

An ideal genotype evaluation
Genotypes relative to an ideal genotype are shown (Fig.4).The ideal genotype according to Yan and Kang (2003) is a genotype with high mean performance and absolute stability. The length of the vector determines the ideal genotype. An ideal genotype must have high yield across the locations with zero GEI. (Ezatollah *et*

is used as a yardstick for genotype evaluation. On this basis a concentric circles were drawn with the ideal genotype as the core. This enables the view of the genotypes distances from the ideal genotype. The genotypes were represented according to their code as shown in Fig 4. The genotype ASL (Ashley) was more ideal, hence, it was the closest to the ideal genotype, the order ofranking relative to the ideal genotype was as follows; ASL>MK>P.ST. The lower yielding genotypes SM>MM, were not favoured therefore, they are located far away from the position of the ideal genotype. In line with the graphical representation, thegenotype, Poinsett (P.ST) had the longest vector which indicated that it had the highest mean fruit yield and Market More (MM) had the lowest mean fruit yield (Fig.4).The genotype found ideal can be used as an advertence for genotype assessment.

CONCLUSION:

A genotype Ashley which has relative consistent yield performance in the three environments (Obudu, Obubra and Calabar) according to Baye and Wilke (2010) possesses a broad-based adaptation to environmental factors.(Soil type, temperatures, soil nutrient).Tesifaye*et* *al.* (2011) reported that the growth and the totality of plant are often impacted by its environments. They maintained that the presence of a particular variety in a given environment is mediated by the genetic component which enables the genotype to adapt to a particular environment.
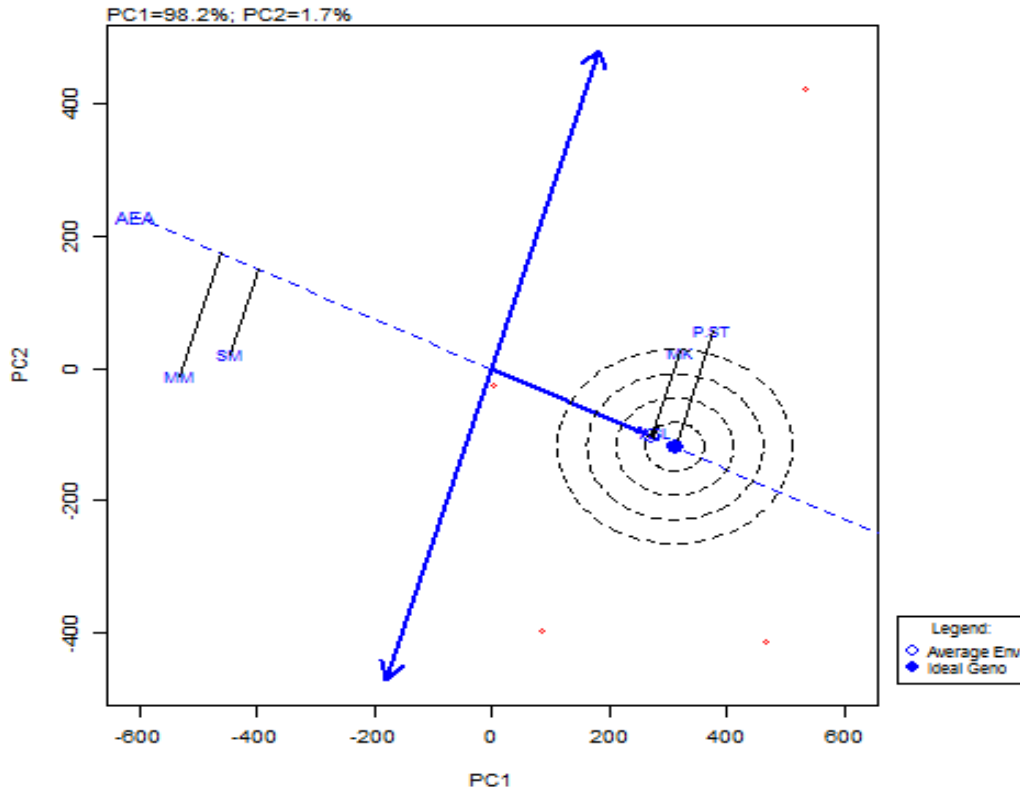

Fig. 4. GGE Bi-plot - Genotype View for yield based on ideal genotype.

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