

**SELECTION OF LOCAL OKRA (*Abelmoschus esculentus* L.) GENOTYPES  
FOR STABILITY UNDER SALINE CONDITIONS**

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**ABSTRACT**

This investigation aimed to observe genotypic stability (with respect to pods yield) of thirteen local okra genotypes across three locations: Kaha Horticulture Research Station, Kaluobia Governorate, Experimental Farm of the Desert Research Center at Ras Sudr, South Sinai Governorate location 1,2 (both salinity condition). In addition to group, the genotypes having similar response pattern over all environments. Moreover, studying the effect of salinity conditions on plant growth performance. Multi-environmental trials (MET), generally, have significant main effects and significant multiplicative genotype x environment interaction effect. AMMI (Additive main effect and multiplicative interaction analysis) offers a more appropriate statistical analysis to deal with such situations, compared to traditional methods like ANOVA, PCA and Linear regression.

The results showed that (I) the obtained results satisfied one of the breeder's goals for selecting the best-suited genotype for cultivation in a wide salinity range of environments; (II) the analysis of variance of thirteen local okra genotypes in three locations (Kaha, Ras sudr 1 and Ras sudr 2) shows that genotype (G), environment (E) and their interaction were significant ( $P < 0.01$ ) for genotype; (III) the AMMI model was very effective for studying GEI interaction, the first bilinear AMMI (IPCA1) model terms accounted for 71.268%; (IV) no genotype has superiority performance in under all studied environments; although, the biplot shows that the genotypes BG9, BG6, BR27 and BR20 are best-suited for cultivation in a wide range of environments; (V) the salt stress has affected the Okra plant growth and development.

**Key words:** AMMI model, biplot, Okra, salinity, yield stability.

**1. INTRODUCTION**

Excess amount of salt in the soil adversely affects plant growth and development. Nearly 20% of the world's cultivated area and nearly half of the world's irrigated lands are affected by salinity (Ashraf 1994). For improving the salt stress tolerance of crop varieties by plant breeding, it is necessary to identify donor genotypes that have proven tolerance to salt stress during all the growth stages. Genotype x environment (G x E) interaction plays a major role in evaluation of genotypes under different environments (salinity stress) to identify genotypes suitable to different stresses (Munns and James 2003). Genotype – environment interaction (GEI) is the differential response of genotypes to changing environmental conditions.

An ideal variety should have a high mean yield combined with a low degree of fluctuation, when grown over diverse environments. Two main contrasting concepts of stability are

distinguished: "static" (Type 1) and "dynamic" (Type 2) (Lin *et al.*, 1986; Becker and Leon, 1988). For static stability, the best genotype tends to maintain a constant yield across environments. Dynamic stability implies for a stable genotype a yield response in each environment that is always parallel to the mean response of the tested genotypes, *i.e.* zero GEI (Annicchiarico, 2002). Analyzing of GEI for varieties can reduce errors in the breeding process as the selection in one condition cannot provide advantage in others (Lin *et al.*, 1986). The analysis of variance (ANOVA) provides no insight into the particular pattern of the underlying interaction (Gauch and Zobel 1988, Zobel *et al.*, 1988); while, the Linear regression model of Eberhart and Russell, 1966 is most frequently used for GXE interaction study and in this model a stable genotype should have low deviation from regression ( $S^2_d$ ). So, many genotypes having very high yield potential often get rejected due to high  $S^2_d$  over the range of

environments. Thus, a genotype showing high positive interaction at certain environments and negative interaction at others is likely to show high  $S^2_d$  and would be classified as unstable. The LR model does not provide for critical analysis of interaction of genotypes in specific environments and does not help in identifying promising genotypes to take advantage of their high positive interaction with the agro-ecological conditions of specific locations or specific agro-management conditions like early or late sowing, high or low fertility, rained or irrigated etc. (Misra *et al.*, 2009). On the other hand, the AMMI analysis model is additive and effectively describes the main (additive) effects, while the interaction (residual from the additive model) is non additive and requires other techniques, such as principal component analysis (PCA) to identify interaction patterns. Thus, ANOVA and PCA models combined to constitute the additive Main – effect and Multiplicative interaction (AMMI) model (Gauch and Zobel 1988, Zobel *et al.*, 1988). The AMMI model is, therefore, a hybrid statistical model incorporating both ANOVA (for additive component) and PCA (for multiplicative component) for analyzing two-way (genotype – by –environment) data structure. The model has, in recent past, been recommended for statistical analysis of yield trials, and was preferred over other customary statistical analyses, such as ordinary ANOVA, principal component analysis and linear regression analysis (Gauch 1988, Zobel *et al.*, 1988). The results of AMMI analysis are useful in supporting breeding program decisions such as specific adaptation and selection of environment (Gauch and Zobel, 1997). Usually, the results of AMMI analysis shown in common graphs are called biplot (Gabriel, 1971). The biplot shows both the genotypes and the environment value and relationships using singular vector technique (Eckart and Young 1936 C.A. Tarakanovas and Ruzgas, 2006).

The present study was initiated to achieve the following objectives:

- \* To observe genotypic stability (with respect to pods yield) of 13 local Okra genotypes across 3 locations (Two of them with the properties of salinity) in Egypt.
- \* To group the genotypes having similar response pattern over all environments.

## 2. MATERIALS AND METHODS

Thirteen accessions /genotypes of local okra, "Balady" green (BG) characterized by semi-long stemmed (106 cm); green, moderate spiny pods,

and "Balady" red (BR) characterized by short – stemmed (85 cm); red-cornered, smooth pods. These thirteen genotypes were obtained from previous selection program (Hamed *et al.*, 2003). The multi locational evaluation trials were carried out during cropping seasons 2009 – 2010 conducted at different three locations in Egypt, with respect to average salinity (whether soil and irrigation water) (Table 1) and Table (2), respectively.

The genotypes namely; BG4, BG14, BG6, BG21, BG7, BG12, BG9, BR21, BR16, BR20, BR15, BR27 and BR4.

Data were recorded on the following characters:

- 1- Pod weight (g)      2- Yield per plant (g).
- 3- Plant height (cm).    4- No. of branches/plant.
- 5- Pod diameter (cm)    6- Pod length (cm).
- 7- No. of total pods/ plant.
- 8- Germination percentage    9- Root length (cm).
- 10- Shoot length (cm)
- 11-  $\text{Na}^+$  10n concentration (mM/L)
- 12-  $\text{K}^+$  ion concentration (mM/L).
- 13-  $\text{Na}^+ / \text{K}^+$  ratio concentration (%)

Measurements of root length, shoot length and chemical analyses were conducted on seedling stage (after about 21 days of planting in the field). Seeds of the used genotypes were sown in seedling trays on 15 March. After sowing, the seedlings (15 days old), of each genotype were transplanted in the field. The area of the plot was divided into 6 ridges. Each ridge was 70 cm wide and 3.5m long. Seedlings were transplanted on only one side of the ridge at distances of 50cm. All experimental units received identical care regarding cultivation, manuring, fertilization, irrigation, pest control, and all other agricultural practices; that were performed as commonly followed in the experiment districts. The  $\text{Na}^+$  and  $\text{K}^+$  ion contents in the sap were measured with a flame photometer according to Chapman and Pratt (1961).

### Statistical analysis

Layout of all the experiments was Randomized Complete Block Design (RCBD) with three replications. To determine the effects of genotype x environment interaction on yields, the data were subjected to Additive Main effects and Multiplicative Interaction (AMMI) analysis using IRRISTAT package (IRRI, 2003) and the biplot drawn by placing both genotype and environment means on the x- axis or abscissa and the respective eigenvectors or scores (IPCAI) on the y-axis or model is:

The AMMI model is:

$$Y_{ger} = \mu + \alpha_g + \beta_e + \sum_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge} + C_{ger}$$

Wherein  $Y_{ger}$  = yield of genotype "g" in environment "e" for replicate r ;  $\mu$  = grand mean;  $\alpha_g$  = mean deviation of the genotype g [genotype mean minus grand mean] and  $\beta_e$  = mean deviation of environmental mean;  $\lambda_n$  = the singular value for IPCA axis n;  $\gamma_{gn}$  = the genotype g eigenvector value for IPCA axis n;  $\delta_{en}$  = the environment e eigenvector value for IPCA axis n;  $\rho_{ge}$  = the residual and  $C_{ger}$  = the error. The means were separated using Fisher's protected least significance difference test (LSD) at  $P = 0.01$ .

### 3. RESULTS AND DISCUSSION

#### 3.1. Stability and adaptation of local Okra genotypes.

AMMI analysis (Zobel *et al.*, 1988 and Purchase, 1997) gives estimate of total G x E interaction effect of each genotype and also further partitioned it into interaction effects due to individual environments. Low G x E interaction of a genotype indicates stability of the genotype over the range of environments. A genotype showing high positive interaction in an environment obviously has the ability to exploit the agro-ecological or agro-management conditions of the specific environment and is therefore best suited to that environment. AMMI analysis permits estimation of interaction effect of a genotype in each environment and it helps to identify genotypes best suited for specific environmental conditions. Though analysis of G x E interaction of multilocation yield data in AMMI model have been reported by Vijaykumar *et al.*, 2001; Mahalingam *et al.*, 2006; Naveed *et al.*, 2007; Das *et al.*, 2009; Mohamadi *et al.*, 2007; Shinde *et al.*, 2002 and Hariprasanna *et al.*, 2008. All those researchers stressed the usefulness of AMMI analysis for selection of promising genotypes for specific locations or environmental conditions.

The AMMI analysis of variance for pod yield (g/plant) (Table 3) indicated that genotypes, environments and G x E interaction were significantly different ( $P < 0.01$ ). The AMMI model supplied an adequate fit to the data as first Interaction Principle Component Axis (IPCA) was significant ( $P < 0.01$ ). The sum of squares for genotypes, environments and IPCAI provided 97.333% (14.872% + 75.952% + 6.539%) of total sum of squares indicating that AMMI model effectively partitioned total sum of squares (Siddiq, 1968). The main effects of G and E accounted for 14.872 and 75.952%, respectively and G x E interaction accounted for 9.175% of the total variation in G x E interaction was further partitioned into IPCA 1 and IPCA 2, of which

IPCA 1 component was significant and accounted for 71.268% of the total G x E interaction sum of squares and used 13 of the total 24 available in the interaction, they were significant at  $P < 0.01$ . The obtained data confirm adequacy to the AMMI model. This made it possible to construct the biplot and calculate genotypes and environments effects (Yan and Hunt, 2001). The interaction principle component Axes (IPCA) scores of a genotype in the AMMI analysis indicate the stability of a genotype across environments. The closer the IPCA scores are to Zero, the more stable the genotypes are across their testing environments. Basically, these biplots belong to two types: AMMI 1 and AMMI 2 (Carbonell *et al.*, 2004). IN AMMI 1, the genotype and environment means are plotted on the abscissa, and the IPCA scores for the same genotypes and environments, on the ordinate. For interpretation of the scores of the IPCA 1 are observed; scores close to zero are characteristic of genotypes and environments, which contribute little to the interaction, that is, they are stable.

Table (4) shows effects of genotypes and locations values from the additive genotype x environment model. The large differences of effect on both genotypes and on environments were observed. Environments Kaha (-5.871 g/plant) and Ras Sudr 3 (-0.877 g/plant) have the main significant negative pod yield effects. The genotypes BG6 (1.893 g/plant), BR27 (1.637 g/plant) BR15 (1.538 g/plant) and BR4 (0.653 g/plant) had a positive pod yield (g/plant) significant effect. The majority of the local Okra genotypes had a small not insignificant main negative or positive effect. Thus, many of these genotypes showed differential performance under different planting conditions. In Figure (1), the IPCAI scores for both the genotypes (number and environments (upper case) were plotted against the pod yield for the genotypes and the environments, respectively. We can clearly see the association between genotypes and the environments plotting on the same graph. The IPCA scores of a genotype in the AMMI analysis are an indication of the adaptability over environments.

The graph space of Fig. 1 is divided into 4 quadrants from lower yielding environments in Quadrants 1 and 4 to high yielding in quadrants 2 and 3. The biplot shows not only the average yield of a genotype but also how it is achieved. The genotypes BG 6 (no. 3), BR 27 (no. 12), BR 20 (no. 10) and BG 9 (no. 7) posed in quadrant 2 and 3 show that they have good adaptation to a wide

**Table (1): Soil chemical analysis of each experimental location.**

Location*	Class texture	pH M/cm	E.C ds/m	CaCO <sub>3</sub> %	Soluble cations (M/L)				Soluble anions (M/L)				Macro elements (ppm)			Micro elements (ppm)			
					Ca <sup>+2</sup>	Mg <sup>+2</sup>	Na <sup>+</sup>	K <sup>+</sup>	CO <sub>3</sub> <sup>-2</sup>	HCO <sub>3</sub> <sup>-3</sup>	Cl <sup>-2</sup>	SO <sub>4</sub> <sup>-2</sup>	N	P	K	Fe	Cu	Zn	Mn
KAHA	Loam	8.4	0.39	3.6	1.0	0.65	2.19	0.48	-	1.9	0.9	1.5	38	30	5.58	4.1	2.8	1.75	2.7
Ras Sudr1	Sandy loam	7.7	4.77	54.73	24.00	11.00	10.53	2.18	-	6.00	31.20	10.50	-	-	2.18	-	-	-	-
Ras Sudr2	Sandy loam	8.22	8.03	56.99	19.3	2.31	19.9	0.75	-	0.72	27.8	12.2	1.39	-	0.75	-	-	-	1.02

\*KAHA: Kaha Horticulture Research Station (Kaluobia Governorate, Egypt. (E1)

Ras Sudr1: Experimental Farm of the Desert Research Center at Ras Sudr, South Sinai, Egypt. (E2)

Ras Sudr2: Experimental Farm of the Desert Research Center at Ras Sudr, South Sinai, Egypt. (E3)

**Table (2): Water chemical analysis of each experimental location.**

Locations *	pH M/cm	E.C ds/m	CaCO <sub>3</sub> %	Soluble cations (M/L)				Soluble anions (M/L)				Macro elements (ppm)			Micro elements (ppm)			
				Ca <sup>+2</sup>	Mg <sup>+2</sup>	Na <sup>+</sup>	K <sup>+</sup>	CO <sub>3</sub> <sup>-2</sup>	HCO <sub>3</sub> <sup>-3</sup>	Cl <sup>-2</sup>	SO <sub>4</sub> <sup>-2</sup>	N	P	K	Fe	Cu	Zn	Mn
KAHA	7.90	0.37	-	1.55	0.76	1.44	1.18	-	1.82	1.86	0.98	-	-	1.18	-	-	-	-
Ras Sudr1	8.40	5.47	-	23.65	19.18	56.66	0.51	-	2.50	16.22	81.33	-	-	0.51	-	-	-	-
Ras Sudr2	7.89	7.20	-	21.80	12.41	37.1	0.48	-	2.83	47.61	19.68	-	-	0.48	-	-	-	-

\*KAHA: Kaha Horticulture Research Station (Kaluobia Governorate, Egypt. (E1)

Ras Sudr1: Experimental Farm of the Desert Research Center at Ras surd, South Sinai, Egypt. (E2)

Ras Sudr2: Experimental Farm of the Desert Research Center at Ras surd, South Sinai, Egypt. (E3)

**Table ( 3 ): Analysis of variance of interaction principal components in AMMI for pod yield (g/plant) of 13 local okra genotypes tested in the three environmental conditions during 2009-2010.**

SOURCE	D.F.	S.S.	% of G-E SS	M.S.	P.	% of GxE InteractionSS
GENOTYPES	12	14844.5	% 14.872	1237.04	**	
LOCATIONS	2	75810.5	% 85.952	37905.3	**	
G x L	24	9157.85	% 9.175	381.577	**	
IPCA 1 <sup>a</sup>	13	6526.59	% 6.539	502.045	**	% 71.268
IPCA 2	11	2631.26	% 2.636	239.205		% 28.732
RESIDUAL	-					-
TOTAL	38	99812.9				

\*\* significance at the 0.01 probability levels.  
IPCA 1 = AMMI component 1

a = interactive principle component axis 1.  
IPCA 2 = AMMI component 2

**Table (4): Interaction (additive) effects and multiplicative scores of local okra genotypes for pod yield (g/ plant) in three environmental conditions.**

Genotype\ location	Environmental conditions			Genotype effects
	E1	E2	E3	
BG4	-1.273	-0.834	2.106	-3.412
BG14	-4.366	-2.860	7.226	-1.439
BG6	2.575	1.687	-4.262	1.893***
BG21	-1.627	-1.065	2.692	-0.290
BG7	5.371	3.517	-8.888	1.713
BG12	4.877	3.194	-8.071	-2.819
BG9	13.15	8.615	-21.77	-2.569
BR21	-1.868	-1.223	3.091	-2.109
BR16	-4.471	-2.928	7.399	-0.749
BR20	5.774	3.782	-9.556	5.954
BR15	-14.380	-9.418	23.80	1.538***
BR27	5.361	3.511	-8.873	1.637***
BR4	-9.129	-5.978	15.11	0.653***
Environment effects	-5.871***	6.749	-0.877***	

E1= Kaha location. E2= Ras Sudr location 1.  
E3= Ras Sudr location 2. \*\*\* Significance at the 0.001 probability levels.

range of environments. Genotypes located near the plot origin were less responsive than the vertex genotypes. Considering only the IPCA 1 scores it became clear that the Genotype BG 9 (no. 7) was the most stable genotype, it was well adapted to high yielding environments that are more favorable with respect to the test sites, Kaha (E1) location was most discriminating as indicated by the longest distance between its marker and the origin, the length of a genotype vectors reflects the amount of interaction for that genotype. Thus, according to Fig. 1, most genetic environment

interaction (GEI) is due to the fact that the genotype BR 20 (no. 10) has pod yield moderate average and large IPCA scores value in the trail. As a result, this genotype is most suitable for poor environments.

Fig. (2) gives the AMMI II biplot for yield. The IPCAI component accounted for 71.26 % of GXE interaction, while IPCA 2 accounted for only 28.73% (Table 3). Distribution of genotype points in the AMMI II biplot revealed that the genotypes BG 21(no.4), BR 16 (no.9) and BG minimal interaction of these genotypes with environments.

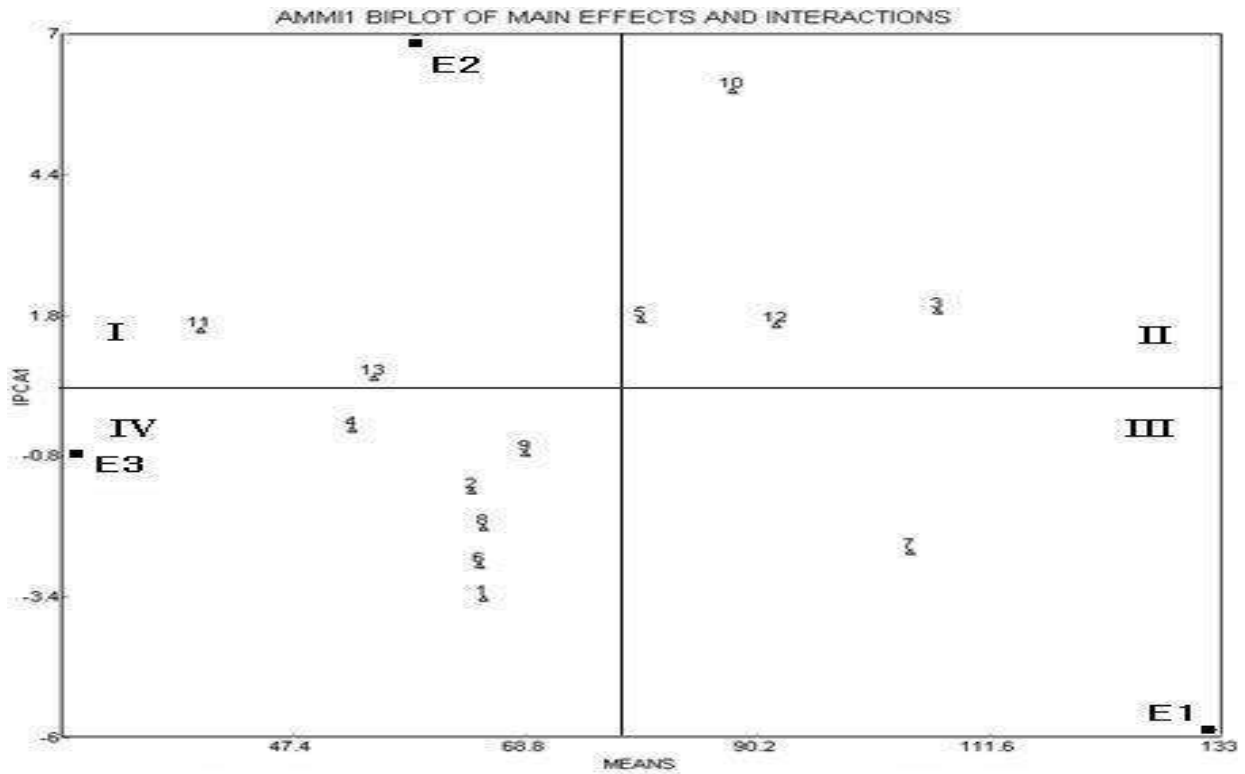


Fig. (1): AMMI I biplot of main effects and GxE interaction of 13 local Okra genotypes at three locations of Egypt. BG4(no.1), BG14(no.2), BG6(no.3), BG21(no.4), BG7(no.5), BG12(no.6), BG9(no.7), BR21(no.8), BR16(no.9), BR20(no.10), BR15(no.11), BR27(no.12) and BR4(no.13). E1=Kaha location 1, E2=Ras Sudr location 1, E3=Ras Sudr location 2.

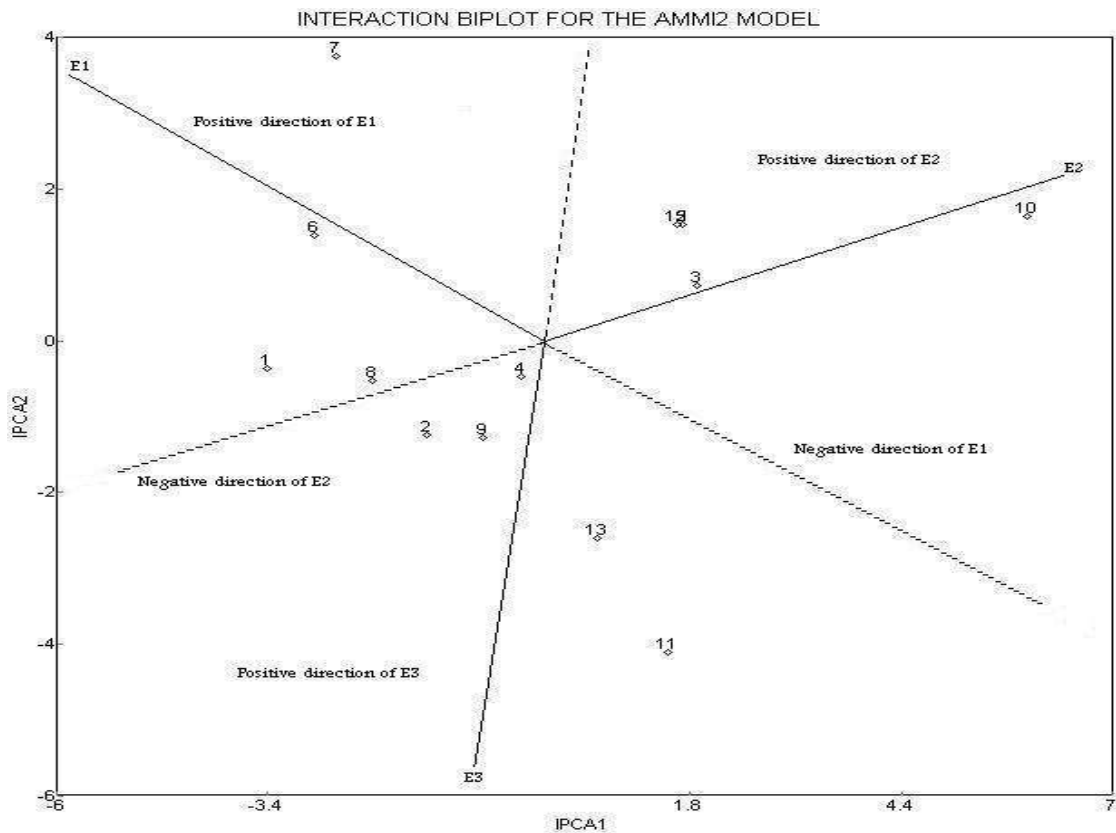


Fig. (2): AMMI II biplot of GxE interaction of 13 local Okra genotypes at three locations of Egypt. BG4(no.1), BG14(no.2), BG6(no.3), BG21(no.4), BG7(no.5), BG12(no.6), BG9(no.7), BR21(no.8), BR16(no.9), BR20(no.10), BR15(no.11), BR27(no.12) and BR4(no.13). E1=Kaha location 1, E2=Ras Sudr location 1, E3=Ras Sudr location 2.

**Selection of local okra (*Abelmoschus esculentus* L.).....**

Table (5): Means for various seedling and maturity traits of 13 genotypes at three locations during 2009 - 2010.																				
	Pod weight				yield per plant				Plant height				No. of branches/plant				Pod diameter			
	E1	E2	E3	GM	E1	E2	E3	GM	E1	E2	E3	GM	E1	E2	E3	GM	E1	E2	E3	GM
BG4	4.985 ±0.091	3.640 ±0.034	2.667 ±0.050	3.76 cd	143.2 ±17.2	27.31 ±6.86	24.26 ±3.52	64.93 de	92.67 ±4.67	69.00 ±1.00	41.00 ±0.57	67.55 bcd	3.667 ±0.66	3.667 ±0.33	3.667 ±0.33	3.66 ab	1.539 ±0.06	1.539 ±0.11	1.196 ±0.04	1.424 bc
BG14	5.093 ±0.184	4.091 ±0.110	2.793 ±0.135	3.99 bcd	127.6 ±10.6	37.59 ±7.11	26.63 ±5.33	63.92 de	92.0 ±3.51	55.667 ±0.88	38.228 ±0.33	62.00 de	3.257 ±0.33	4.000 ±0.01	3.333 ±0.32	3.55 ab	1.675 ±0.03	1.405 ±0.03	1.301 ±0.02	1.460 b
BG6	5.694 ±0.322	4.358 ±0.181	3.127 ±0.202	4.39 ab	158.00 ±32.0	107.67 ±6.14	55.27 ±3.10	106.97 a	107.00 ±4.51	59.00 ±0.557	41.67 ±1.67	69.22 bc	3.325 ±0.33	3.313 ±0.33	3.000 ±0.01	3.22 bcd	1.787 ±0.08	1.572 ±0.03	1.389 ±0.06	1.583 a
BG21	4.708 ±0.43	3.633 ±0.30	2.646 ±0.22	3.66 d	112.4 ±16.2	35.99 ±3.09	9.94 ±0.36	52.78 ef	79.67 ±3.53	61.333 ±0.66	45.33 ±1.45	62.11 de	4.000 ±0.01	3.667 ±0.33	3.647 ±0.33	3.77 a	1.669 ±0.07	1.435 ±0.02	1.297 ±0.05	1.467 b
BG7	4.848 ±0.342	3.700 ±0.336	2.724 ±0.164	3.75 cd	134.4 ±22.3	80.8 ±21.3	23.36 ±2.81	79.53 bcd	108.00 ±12.1	62.67 ±1.45	41.667 ±0.66	70.77 b	3.667 ±0.66	3.667 ±0.33	3.621 ±0.31	3.66 ab	1.618 ±0.02	1.165 ±0.05	1.257 ±0.01	1.347 c
BG12	4.942 ±0.285	3.673 ±0.226	2.743 ±0.158	3.78 cd	145.6 ±14.1	35.1 ±11.1	13.28 ±1.57	64.66 de	109.00 ±4.93	66.00 ±0.57	44.317 ±0.66	73.11 ab	3.661 ±0.33	3.526 ±0.23	3.24 ±0.30	3.66 ab	1.537 ±0.09	1.413 ±0.03	1.194 ±0.07	1.381 bc
BG9	5.893 ±0.307	4.446 ±0.120	3.271 ±0.171	4.53 a	192.1 ±25.4	81.8 ±20.6	38.98 ±0.56	104.28 a	118.17 ±7.45	71.67 ±1.67	46.324 ±0.88	78.77 a	3.660 ±0.33	3.521 ±0.21	3.224 ±0.26	3.66 ab	1.704 ±0.07	1.324 ±0.05	1.313 ±0.12	1.447 bc
BR21	5.448 ±0.668	3.867 ±0.212	3.057 ±0.348	4.12 abcd	135.1 ±29.4	35.80 ±1.53	24.18 ±4.38	65.02 de	87.00 ±8.33	63.42 ±4.06	40.00 ±0.57	63.44 cd	3.000 ±0.01	3.333 ±0.33	3.667 ±0.33	3.33 abc	1.739 ±0.05	1.202 ±0.04	1.351 ±0.04	1.431 bc
BR16	5.736 ±0.371	4.457 ±0.288	3.517 ±0.167	4.57 a	128.29 ±4.67	47.06 ±6.65	31.09 ±5.70	68.81 cde	69.33 ±1.20	52.57 ±1.20	45.667 ±0.88	55.77 f	2.326 ±0.23	3.667 ±0.35	3.00 ±0.33	3.00 cd	1.693 ±0.03	1.315 ±0.02	1.207 ±0.07	1.405 bc
BR20	5.342 ±0.572	4.084 ±0.448	3.298 ±0.147	4.24 abc	118.30 ±8.26	108.13 ±2.12	27.37 ±3.06	87.92 abc	64.62 ±3.84	56.35 ±3.38	44.75 ±0.66	55.00 f	3.524 ±0.35	3.621 ±0.23	3.629 ±0.21	3.55 ab	1.651 ±0.06	1.283 ±0.05	1.110 ±0.01	1.348 c
BR15	5.817 ±0.388	4.221 ±0.069	3.562 ±0.243	4.53 a	75.09 ±3.98	26.15 ±3.31	15.62 ±0.98	38.95 f	45.00 ±3.06	55.67 ±1.20	42.00 ±0.57	47.55 q	2.34 ±0.33	3.654 ±0.33	3.667 ±0.33	3.22 bcd	1.719 ±0.06	1.335 ±0.05	1.184 ±0.04	1.413 bc
BR27	5.691 ±0.547	4.089 ±0.101	3.492 ±0.288	4.24 ab	147.3 ±13.9	92.7 ±17.8	35.86 ±4.03	91.95 ab	65.55 ±2.89	51.23 ±0.57	35.56 ±2.00	50.33 fg	2.667 ±0.33	3.00 ±0.01	2.645 ±0.33	2.77 d	1.645 ±0.57	1.278 ±0.44	1.203 ±0.14	1.375 bc
BR4	5.569 ±0.574	3.994 ±0.143	3.424 ±0.388	4.32 ab	101.50 ±10.6	39.60 ±10.4	23.69 ±0.24	54.94 ef	72.33 ±3.38	56.33 ±0.33	40.00 ±0.57	56.22 ef	2.667 ±0.33	3.662 ±0.33	3.541 ±0.33	3.33 abc	1.808 ±0.03	1.404 ±0.02	1.166 ±0.14	1.459 b
GM	5.36 a	4.01 b	3.10 c		132.2 a	58.90b	26.88c		85.35 a	60.02 b	41.97 c		3.58 a	3.46 a	3.20 b		1.67 a	1.35 b	1.24 c	
LSD g	0.488				19.903				6.164				0.529				0.107			
LSD E	0.234				9.561				2.961				0.254				0.0517			

GM = grand mean  
g = genotypes  
e = environments  
E1= Kaha location., E2= Ras Sudr location 1. and E3= Ras Sudr location 2.  
Any means within rows or columns followed by the same letter are not statistically different at 0.01 level (Duncan's multiple test)

Cont.I Table (5): Means for various seedling and maturity traits of 13 genotypes at three locations during 2009 - 2010.																				
	Pod length				No. of total pods/plant				Germination percentage				Root length				Shoot length			
	E1	E2	E3	GM	E1	E2	E3	GM	E1	E2	E3	GM	E1	E2	E3	GM	E1	E2	E3	GM
BG4	3.533 ±0.20	2.779 ±0.21	1.961 ±0.11	2.75 ef	28.67 ±3.18	8.73 ±1.11	7.01 ±1.65	14.80 c	92.66 ±0.66	46.00 ±2.08	31.35 ±1.33	56.66 bc	9.169 0.59	5.867 ±0.39	3.355 ±0.10	6.13 a	14.106 ±0.30	11.224 0.19±	4.405 0.20±	9.91 ab
BG14	3.366 ±0.08	2.649 ±0.04	1.868 ±0.04	2.62 fg	25.00 ±1.53	9.65 ±2.21	9.35 ±1.64	14.66 c	97.67 ±1.45	58.66 ±0.88	29.67 ±1.20	62.0 a	5.959 ±0.91	5.022 ±0.39	3.327 ±0.09	4.76 bc	14.794 ±0.22	10.336 ±0.42	4.720 ±0.37	9.96 ab
BG6	3.733 ±0.18	2.867 ±0.21	2.072 ±0.10	2.89 de	27.45 ±3.93	24.40 ±1.26	17.56 ±1.13	23.09 a	92.00 ±1.15	46.57 ±1.45	27.34 ±2.85	55.22 c	6.881 ±0.31	3.676 ±0.29	2.139 ±0.29	4.23 def	15.280 ±0.15	10.523 ±0.55	4.136 ±0.05	9.97 ab
BG21	2.966 ±0.03	2.371 ±0.06	1.646 ±0.02	2.32 h	23.67 ±1.20	9.855 ±0.29	3.844 ±0.21	12.45 c	92.53 ±0.57	45.95 ±0.57	26.74 ±0.57	54.33 c	5.933 ±0.37	5.066 ±0.31	2.501 ±0.09	4.50 cde	14.254 ±0.57	10.654 ±0.35	4.949 ±0.06	9.95 ab
BG7	3.200 ±0.20	2.486 ±0.15	1.776 ±0.11	2.48 gh	27.67 ±4.26	20.88 ±4.12	8.626 ±0.54	19.05 b	97.67 ±1.45	52.42 ±1.45	23.47 ±1.20	57.77 b	8.107 ±0.39	5.274 ±0.04	2.425 ±0.06	5.23 b	16.482 ±0.59	10.055 ±0.27	4.409 ±0.12	10.31 a
BG12	3.066 ±0.06	2.416 ±0.04	1.702 ±0.03	2.39 h	29.84 ±1.20	8.93 ±2.38	4.870 ±0.60	14.37 c	88.67 ±1.33	60.65 ±0.66	20.00 ±1.15	56.44 bc	5.992 ±0.38	4.634 ±0.11	1.590 ±0.20	4.07 ef	15.682 ±0.30	9.326 ±0.33	3.022 ±0.37	9.34 bcd
BG9	3.800 ±0.15	3.053 ±0.19	2.109 ±0.08	2.98 cd	32.26 ±2.91	17.53 ±3.87	11.997 ±0.76	20.62 ab	97.00 ±2.52	54.51 ±0.66	16.00 ±2.08	55.77 bc	6.795 ±0.39	4.474 ±0.11	1.219 ±0.20	4.16 ef	15.252 ±0.68	9.637 ±0.22	3.082 ±0.30	9.32 bcd
BR21	3.733 ±0.13	3.001 ±0.20	2.072 ±0.07	2.95 cde	25.67 ±6.49	8.631 ±0.76	8.45 ±2.36	14.24 c	88.33 ±2.73	49.45 ±0.66	17.32 ±1.20	51.66 d	6.462 ±0.40	3.808 ±0.21	2.486 ±0.08	4.25 def	14.861 ±0.23	9.396 ±0.48	3.190 ±0.41	9.149 cd
BR16	4.033 ±0.16	3.201 ±0.17	2.238 ±0.09	3.15 bc	22.67 ±2.33	10.61 ±1.48	9.61 ±1.22	14.29 c	91.00 ±1.00	44.36 ±0.88	20.00 ±0.57	51.77 d	6.582 ±0.33	5.300 ±0.19	2.189 ±0.27	4.69 cd	15.305 ±0.47	10.122 ±0.61	4.391 ±0.29	9.939 ab
BR20	3.933 ±0.34	3.156 ±0.29	2.183 ±0.19	3.09 bcd	22.85 ±0.88	29.06 ±2.79	9.39 ±1.16	20.25 ab	92.00 ±0.57	63.25 ±2.40	31.62 ±1.86	62.22 a	7.022 ±0.39	3.592 ±0.02	2.002 ±0.20	4.20 def	15.256 ±0.50	8.298 ±0.21	3.056 ±0.26	8.870 d
BR15	4.200 ±0.05	3.363 ±0.06	2.331 ±0.03	3.29 ab	13.00 ±1.00	5.781 ±0.65	4.881 ±0.43	7.88 d	91.33 ±1.67	60.00 ±0.57	32.00 ±1.15	61.11 a	5.692 ±0.55	4.572 ±0.01	2.644 ±0.01	4.30 cde	15.029 ±0.53	10.130 ±0.34	4.236 ±0.16	9.79 abc
BR27	4.300 ±0.20	3.474 ±0.02	2.387 ±0.11	3.38 a	26.33 ±3.53	21.38 ±4.96	11.328 ±0.33	19.67 ab	92.67 ±1.20	64.25 ±1.33	32.67 ±4.06	63.22 a	6.053 ±0.26	3.670 0.30	2.445 ±0.48	4.05 ef	14.520 ±0.92	9.217 ±0.71	3.277 ±0.31	9.00 d
BR4	4.400 ±0.20	3.518 ±0.05	2.442 ±0.11	3.45 a	18.33 ±1.45	9.41 ±2.76	7.806 ±0.68	11.85 c	92.67 ±1.33	63.41 ±1.86	29.42 ±2.33	61.77 a	6.168 ±0.29	3.549 ±0.01	1.643 ±0.22	3.78 f	15.131 ±0.22	8.697 ±0.64	3.172 ±0.08	9.00 d
GM	3.71 a	2.94 b	2.06 c		24.79 a	14.21 b	8.82 c		92.74 a	54.46 b	25.87 c		4.66 a	4.44 ab	4.36 b		15.07 a	9.81 b	3.84 c	
LSD g	0.228				3.95				2.540				0.512				0.658			
LSD E	0.109				1.898				1.220				0.246				0.316			

GM = grand mean  
g = genotypes  
e = environments  
E1= Kaha location., E2= Ras Sudr location 1. and E3= Ras Sudr location 2.  
Any means within rows or columns followed by the same letter are not statistically different at 0.01 level (Duncan's multiple test)



**Cont. II Table (5): Means for various seedling and maturity traits of the 13 genotypes at three locations during 2009 - 2010.**

	Na <sup>+</sup> ion concentration				K <sup>+</sup> ion concentration				Na <sup>+</sup> /K <sup>+</sup> ion ratio			
	E1	E2	E3	GM	E1	E2	E3	GM	E1	E2	E3	GM
<b>BG4</b>	10.204 ±0.27	12.512 ±0.09	15.744 ±0.29	12.82 a	42.172 ±0.46	30.122 ±0.44	20.064 ±0.19	30.78 g	0.242 ±0.007	0.415 ±0.007	0.784 ±0.013	0.48 c
<b>BG14</b>	10.255 ±0.05	13.259 ±0.17	15.399 ±0.11	12.97 a	44.730 ±0.29	32.557 ±0.05	20.974 ±0.42	32.75 cd	0.229 ±0.01	0.407 ±0.01	0.734 ±0.01	0.45 d
<b>BG6</b>	11.498 ±0.06	12.534 ±0.02	14.336 ±0.09	12.78 a	42.473 ±0.05	35.086 ±0.30	18.326 ±0.07	31.96 ef	0.270 ±0.01	0.357 ±0.02	0.782 ±0.01	0.47 cd
<b>BG21</b>	7.811 ±0.12	10.472 ±0.11	14.481 ±0.23	10.92 d	48.835 ±0.77	36.289 ±0.29	10.233 ±0.45	31.78 f	0.159 ±0.01	0.288 ±0.01	1.420 ±0.06	0.62 a
<b>BG7</b>	8.491 ±0.06	10.380 ±0.09	15.513 ±0.13	11.46 c	44.529 ±0.21	32.051 ±0.26	15.457 ±0.12	30.67 g	0.190 ±0.01	0.323 ±0.01	1.003 ±0.01	0.50 b
<b>BG12</b>	10.563 ±0.01	12.496 ±0.08	13.601 ±0.18	12.21 b	44.970 ±0.32	34.432 ±0.43	20.234 ±0.28	33.21 c	0.234 ±0.01	0.363 ±0.01	0.672 ±0.01	0.42 e
<b>BG9</b>	7.711 ±0.07	9.689 ±0.09	12.623 ±0.02	10.00 e	39.842 ±0.20	35.622 ±0.20	20.104 ±0.22	31.85 f	0.193 ±0.01	0.272 ±0.01	0.628 ±0.01	0.36 f
<b>BR21</b>	9.448 ±0.16	10.488 ±0.07	13.671 ±0.14	11.20 cd	44.488 ±0.31	32.535 ±0.21	18.405 ±0.10	31.80 f	0.212 ±0.02	0.322 ±0.01	0.742 ±0.01	0.42 e
<b>BR16</b>	10.026 ±0.28	11.722 ±0.28	14.642 ±0.03	12.12 b	42.906 ±0.40	33.531 ±0.05	17.937 ±0.35	31.45 f	0.233 ±0.01	0.349 ±0.01	0.816 ±0.01	0.46 cd
<b>BR20</b>	7.51 ±1.02	9.528 ±0.22	12.562 ±0.04	9.86 e	44.371 ±0.25	34.663 ±0.10	20.683 ±0.15	33.22 c	0.169 ±0.02	0.274 ±0.01	0.608 ±0.01	0.35 f
<b>BR15</b>	7.613 ±0.95	10.447 ±0.09	15.488 ±0.28	11.18 cd	45.436 ±0.12	32.650 ±0.04	19.287 ±0.35	32.45 de	0.167 ±0.02	0.319 ±0.01	0.804 ±0.02	0.43 e
<b>BR27</b>	9.564 ±0.18	11.284 ±0.03	15.741 ±0.06	12.19 b	48.52 ±1.16	35.711 ±0.08	29.030 ±0.98	37.69 a	0.198 ±0.01	0.315 ±0.01	0.543 ±0.02	0.35 f
<b>BR4</b>	10.604 ±0.03	12.536 ±0.16	14.918 ±0.02	12.68 a	45.871 ±0.28	32.338 ±0.38	23.305 ±0.26	33.83 b	0.231 ±0.01	0.387 ±0.01	0.640 ±0.01	0.41 e
<b>GM</b>	9.33 a	11.33 b	14.51 a		44.53 a	33.66 b	19.53 c		0.21 c	0.33 b	0.78 a	
<b>LSD g</b>	0.428				0.580				0.023			
<b>LSD E</b>	0.205				0.278				0.011			

GM = grand mean  
g = genotypes e = environments E1= Kaha location., E2= Ras Sudr location 1. and E3= Ras Sudr location 2.  
Any means within rows or columns followed by the same letter are not statistically different at 0.01 level (Duncan's multiple test)

The remaining 10 genotypes scattered away from the origin in the biplot indicating that the genotypes were more sensitive to environmental interactive forces. Interaction of genotypes with specific environmental conditions was judged by projection of genotype points on to environment spokes. On this basis, the genotypes BG 12 (no. 6), BG 4 (no. 1) and GR 21 (no. 8) had moderate positive interaction and BR 4 (no. 13) and BR 20 (no. 10) had moderate negative interaction under Kaha condition (E<sub>1</sub>). Genotypes BR 20 (no. 10), GR 27 (no. 12), BG 7 (no. 5) and BG 6 (no. 3) had positive interaction and BG 21 (no.4) BR 16 (no. 9) had high negative interaction under Ras Sudr 1 (E<sub>2</sub>) condition. Genotypes BR 15 (no. 11) and BR 4 (no. 13) had high positive interaction and BG 6 (no. 3) had high negative interaction under Ras Sudr 2 (E<sub>3</sub>) condition. It can be concluded that:

1. The analysis of variance of 13 local okra genotypes in three environments shows that

genotype (G), environment (E) and their interaction were significant (P<0.01) for genotypes. The AMMI model was very effective for studying GEI interaction. The first bilinear AMMI model terms accounted for 71.268%.

2. No genotype has superior performance in all environments. The biplot shows that the genotypes BG 9 (no. 7), BG6 (no. 3), BR 27 (no. 12) and BR 20 (no. 10) are best-suited for cultivation in a wide range of environments; while, the genotype BR 20 (no. 10) is well – suited for cultivation in poor environments.

**3.2. Variation for salinity tolerance in Okra.**

The results for combined analysis of local okra genotypes characteristics across locations is given in Table (5). The salinity conditions (Ras Sudr 1 and Ras Sudr 2 locations) influenced the characteristics of all the genotypes grown under salinity conditions (Ras surd 1 and Ras surd 2) represent the significantly decrease as compared

to the Kaha condition (The lowest salinity). Genotypes BG 9 and BG 6 in general performed better than the other genotypes across all the three locations / environments. Mean pod weight, yield per plant, plant height, no. of branches/ plant and no. of total pods / plant over locations (4.53g, 104.28g, 78.77 cm, 3.66 and 20.62 g, respectively) identified BG 9 as the best yielding genotype and the same genotype (BG 9) recorded the lowest values in Na<sup>+</sup> ion concentration, K<sup>+</sup> ion concentration and Na<sup>+</sup>/K<sup>+</sup> ion ratio. (10.00 mM/L, 31.85 g/plant) as poorest yielding genotype. The highest grand mean of pod weight, yield per plant, plant height, no. of branches / plant, pod diameter, pod length, no. of total pods/plant, germination percentage, root length and shoot length were recorded at Kaha conditions (5.36 g, 132.2 g/plant, 85.35 cm, 3.58, 1.67 cm, 3.71 cm, 24.79, 92.74, 4.66 cm and 15.07 cm, respectively). So, this site was conductive / favorable for higher yield. Lowest values for the same characteristics were obtained at Ras Sudr 2 conditions (3.10g, 26.88 g/plant, 41.97 cm, 3.20, 1.24 cm, 2.06 cm, 8.82, 25.87, 4.36 cm and 3.84 cm, respectively) depicting that this site was less conductive /unfavorable for higher yield. Similar results were obtained by Allakhverdiev *et al.* (2000) who reported that a biotic stresses like heat, cold, drought and salinity effect the plant growth and productivity but the salt stress exerts more drastic effects in terms of low productivity (Munns, 2002). The plant exhibited the lowest germination percentage under salinity condition (Kafi and Goldani, 2001; Jamil and Rho, 2004). The depressed growth of plants may be due to the toxic effect of Na<sup>+</sup> and Cl<sup>-</sup> ions present in NaCl and low water potential in the rooting medium (Silveira *et al.*, 2009). It is reported that salt stress effects the plant growth and development by influencing fresh and dry weights of roots, shoot along with shoot length (Ashraf *et al.*, 2003). Growth attributes like plant height, shoot elongation, shoot and root length were severely decreased with salinity. It was noted that plants growing under saline condition remained stunted. The lower water potential in saline soil in turn lower cell turgor causing reduction in cell elongation and cell division (Greenway and Munns, 1980). Although plant height is genetically controlled, environmental factors also have strong influence in the expression of genes (Shahid *et al.*, 2011). The selective uptake of K<sup>+</sup> in contrast to Na<sup>+</sup> was considered one of the important physiological mechanisms contributing to salt tolerance in many plant species (Poustini

and Siosemardeh, 2004). Okra grown under salinity accumulated maximum amounts of Na<sup>+</sup> in their leaves and root, so, the growth of these plants was affected due to high concentration of Na<sup>+</sup> and low ratios of K<sup>+</sup> (Ahmadi *et al.*, 2009 and Dashti *et al.*, 2009). There was a decrease in K<sup>+</sup> concentration both in leaves and roots with increased NaCl salinity in the okra (Shahid *et al.*, 2011). Maintenance of higher K<sup>+</sup> / Na<sup>+</sup> ratio under low salt stress may be one of the reasons for superior growth (Ashraf and Ahmed, 2000). High levels of K<sup>+</sup> in young leaves are associated with salt tolerance in many plant species (Storey *et al.*, 1993 and Khatum and Flowers,1995).

It can be concluded that salt stress has affected the Okra plant growth and development Na<sup>+</sup> reduced the absorption of K<sup>+</sup>.

From the present investigation, it may be concluded that:

- 1- The results satisfied one of the breeder's goals for selecting the best –suited genotype for cultivation in a wide salinity range of environments (Kaha, Ras Sudr 1 and Ras Sudr 2).
- 2- The analysis of variance of 13 local okra genotypes in three environments showed that genotype (G), environment (E) and their interaction were significant (P<0.01) for genotype.
- 3- The AMMI model was very effective in studying GEI interaction, the first bilinear AMMI model terms accounted for 71.268%.
- 4- No genotype had superior performance in all environments.
- 5- The biplot showed that the genotypes BG 9 (no. 7), BG 6 (no. 3), BR 27 (no. 12) and BR 20 (no. 10) are best-suited for cultivation in a wide range of environments; while, the genotype BR 20 (no. 10) is well suited for cultivation in poor environments.
- 6- The salt stress affected the plant growth and development. In addition, Na<sup>+</sup> reduced the absorption of K<sup>+</sup>.

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## إنتخاب تراكيب وراثيه من الباميه المحليه للثبات تحت الظروف الملحيه

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### ملخص

تم زراعة ثلاثه عشر تركيبا وراثيا من أصناف الباميه المحليه ( الأحمر بنواره والأخضر البلدي) وهي: BG4,BG14,BG6,BG21,BG7,BG12,BG9,BR21,BR16,BR20,BR15,BR27,BR4 في ثلاثه مواقع مختلفه هي المزرعه البحثيه بقها – محافظه القليوبيه وتروى بماء عذب بينما الموقعين الأخرين تابعين للمزرعه التجريبيه برأس سدر: محافظه جنوب سيناء وبيرويان بماء مالح يختلف من حيث درجه الملوحة في كلا الموقعين مع ملاحظه أن طريقه الري المستخدمه في الثلاث مواقع هي الري غمر. أجريت الدراسه خلال الموسم الصيفي لعامي 2009-2010 لتحديد الثبات الوراثي لصفه محصول القرون لهذه التراكيب الوراثيه المحليه للباميه تحت الظروف المختلفه من درجه الملوحة . أستخدم نموذج تحليل الثبات الوراثي Additive Main Effect and Multiplicative Interaction Analysis الذي يعتمد علي تقسيم التباين الناتج من تباين التفاعل الكلي الى عدة تباينات يطلق عليها: Interactive principle component axis 1,axis2,.....etc.(IPCA1,IPCA2,IPCA3,.....etc). وهو أكثر كفاءه من الطرق التقليديه الأخرى مثل مقياس الانحدار(بناء على أبحاث متعدده) والذي يعتمد على الإنحراف المعياري. كذلك تقييم سلوك هذه التراكيب من حيث ثلاثه عشر صفه تحت هذه الظروف وهي: إرتفاع النبات - وزن القرن - قطر القرن - طول القرن - عدد الأفرع/النبات - عدد القرون/النبات - المحصول الكلي (وزن القرون/نبات) - نسبه إنبات البذور - طول الجذر ( للشتله) - طول المجموع الخضري (للستله)- تركيز أيون الصوديوم - تركيز أيون البوتاسيوم - النسبه بين تركيز أيون الصوديوم إلى البوتاسيوم.

وكانت أهم النتائج المتحصل عليها كالآتي:-

- 1- أظهرت نتائج التحليل التجميحي أن التباين كان عالي المعنويه بين التراكيب الوراثيه لصفه المحصول كذلك بين المواقع ، كما أظهرت أن التفاعل بين التراكيب الوراثيه والمواقع كان تفاعلا معنويا.
- 2- دل تحليل الثبات على أن المكون الأول من مكونات التفاعل IPCA1 قد شكل نسبة 71.268% من التفاعل الكلي.
- 3- أظهرت النتائج أنه لا يوجد تركيب وراثي يمكن القول أنه مميزا تحت جميع البيئات محل الدراسه ولكن كان هناك تراكيب أكثر ملائمته لمدى واسع من الظروف الملحيه وهي: BG9,BG6 BR27 and BR20.
- 4- أظهرت النتائج أن الإجهاد الملحي يؤثر سلبيا بصفه عامه على الصفات محل الدراسه. عموما واعتماداً على متوسطات التراكيب الوراثيه ودرجه ثباتها تبين أن أفضل هذه التراكيب و التي يجب استخدامها كأبء في برامج التربية و تطوير صفة التحمل للملوحة هي: BG9,BG6 BR27 and BR20.

المجلة العلمية لكلية الزراعة – جامعة القاهرة – المجلد (63) العدد الثاني (أبريل 2012):188-200