

RESEARCH ARTICLE

Combining ability and heterosis in egusi-melon *Citrullus lanatus* (Thumb.) Matsum and Nakai

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Abstract: This study was carried out to evaluate the genetic potential of seven egusi-melon genotypes for seed weight and its components following the diallel mating scheme. Seven parents were selected from among 28 genotypes obtained from indigenous farmers in five ecological zones (forest, derived savanna, southern, northern and Sudan savanna) of Nigeria. The experiment was laid out in a completely randomized block design with four replications. Specific combining ability variance was of greater importance than general combining ability variance in the inheritance of all the traits under study. Okwe-2-IM x KTGO-GMB was the best combiner for number of pods and pod weight per plant while KOGI-NITN x MOKWA-NG was the best combiner seed weight per plant. Positive and highly significant ($P < 0.01$) heterosis was recorded among crosses for number of primary vines, number of pods and seed production efficiency per plant indicating their importance in hybrid development for improved yield.

Running Title: Combining ability and heterosis in egusi-melon.

Keywords: *Citrullus lanatus*; Egusi-melon; combining ability; Heterosis; genetic potential.

INTRODUCTION

Egusi-melon is a member of the Cucurbitaceae family (Schippers, 2000). It is a variety of melon seed which is popularly called “egusi” in West Africa (Akpambang *et al.*, 2008). Egusi-melon is a multipurpose crop that is mainly cultivated for its seeds. The seed of egusi-melon is nutritious, and contains up to 41.6% crude protein and 57.3% total lipid which are exploitable (Fakou *et al.*, 2004). The crop is an important income earner in the food economics of most farmers especially women (DSC, 2006). Egusi-melon seeds are obtained either in shelled or unshelled forms in West African markets and used greatly in West African cookery (Akpambang *et al.*, 2008). The crop is useful as live mulch for weed control and soil moisture conservation at high populations (Ikeorgu *et al.*, 1989). It provides excellent ground cover (Lal, 1995), reduces surface runoff and controls erosion (Willy and Chinaka, 1985). In Nigeria limited attempt has been made for the genetic improvement of the crop. This may be due to the scanty information on

the nature of gene action controlling the expression of yield and yield contributing traits in the crop. The heterozygous nature consequent to the outcrossing breeding system of egusi-melon may open the scope of development of open-pollinated as well as hybrid varieties with better seed yield and quality. In a breeding program, it is important to know the combining abilities of parents to be constituted into hybrids. Combining ability and heterosis are the most important genetic parameters for breeding improved varieties. The variance of general combining ability (GCA) and specific combining ability (SCA) are related to the type of gene action. Information on the relative importance of the additive (GCA) and non-additive (SCA) gene action within a breeding population is important because it is used to determine as to which breeding procedure will effectively improve the performance of the trait of interest (Dudley and Moll, 1969). It is also necessary to have detailed information about the desirable parental combinations in any breeding program that can involve a high degree of heterotic response. Phenotypic selection of parents for hybridization based on their performance per se alone may not always be a viable procedure, since phenotypically superior genotypes may yield inferior hybrids and or poor recombinants in the segregating generations. It is essential that parents are selected on the basis of their genetic worth. Therefore, selection of potential parents based on genetic information and knowledge of their combining ability is important. Combining ability predicts performance of parents in cross combinations and thus helps in identifying the desirable parents as well as the crosses for crop improvement program. It also helps in getting idea about the nature of gene action for a particular trait (Nazzin Uddin *et al.*, 2009). Hybrids due to their high yield potential are used for increasing the productivity of crops. Shankara *et al.*, (2005) reported that hybrid tomato usually produces higher yield. Hybrid plants are usually heavy producers, and combine the character of the parent plants. Heterosis can be expressed when the parents of a hybrid have different allele at a locus and there is some level of dominance or epistasis among the alleles (Falconer and Mackay, 1996). Heterotic studies can provide the basis for the exploitation of valuable hybrid combinations

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in future breeding programs. Heterosis has been utilized in some crops, including cucurbits, to exploit dominance variance through the production of hybrids (Cramer and Wehner, 1999). Heterosis in a trait varies from population to population of the same crop species. Ghanderi and Lower (1979c) reported high-parent heterosis for fruit yield in cucumber while Cramer and Wehner (1999) did not observe heterosis and inbreeding depression for fruit yield in inbreeds parents of the same crop.

The objectives of this study were to use diallel analysis according to Griffing's (1956) Method 1, Model 11 to determine general and specific combining abilities of seven egusi-melon genotypes as well as gene action for six yield components and the heterotic performance of the F_1 hybrid progeny.

MATERIALS AND METHODS

Seven genotypes of egusi-melon taken from breeding program at the Federal College of Agriculture, Ishiagu, Ebonyi State, Nigeria, namely, AKARA-AB., OKWE-2-IM., KOGI-NITN., MOKWA-NG., MADLS-NG., KTGO-GMB and ABTK-ADP. were used to make a full diallel cross to obtain forty-nine treatments (7 parents, 21 F_1 s and 21 reciprocals). The experimental design was Randomized Complete Block Design with four replications. Three seeds of each genotype were planted at a spacing of 1.0 x 1.0 m which was later thinned down to one seedling at two weeks after planting. Each plot contained twenty plants per genotype. Data were collected from all plants for number of primary vines, leading vine length, number of pods, seed production efficiency and seed weight. Seed production efficiency is the proportion of dry seed weight to fresh fruit weight expressed as percentage and has been found to range between 2.0 – 2.75 percent in Nigeria (Philips, 1964). Analysis of combining ability was carried out according to Griffing's (1956) Model 1 and Method 2 following Sing

and Chaudhary (1976). The magnitude of heterosis was estimated in relation to mid-parent (Mp) and better-parent (Bp) values using the method of Hayes *et al.*, (1956). Test of significance was done as described by Hayes *et al.*, (1956).

RESULTS AND DISCUSSION

Analysis of variance

The analysis of variance showed that mean square due to diallel progenies was highly significantly different ($P < 0.01$) for all the traits under study except for leading vine length per plant ($P < 0.05$) indicating the existence of genetic variability among the egusi-melon diallel progenies for most of the traits under study (Table 1). The decomposition of the mean square due to diallel progenies for the traits under study into its components (Table 1) showed that parents were highly significantly different ($P < 0.01$) for number of pod per plant, pod weight per plant and seed weight per plant. Significant differences ($P < 0.01$) were observed among F_1 s progenies for all the traits under study except for seed production efficiency per plant ($P > 0.05$). Reciprocal progenies (rF_1 s) were highly significantly different ($P < 0.01$) from each other for all the traits (Table 1). Furthermore, the difference between F_1 progenies and their reciprocals (F_1 vs rF_1) were highly significantly different ($P < 0.01$) for two traits, pod weight per plant and seed weight per plant which indicate considerable reciprocal differences and suggesting the presence of maternal effects in the control of the expression of these traits. The difference between parents and crosses (Parents vs crosses) was highly significant ($P < 0.01$) for number of primary vines per plant, number of pods per plants, pod weight per plant and seed production efficiency indicating heterosis in resultant hybrid progenies (Table 1).

Analysis of variance for combining ability

Table 1: Analysis of variance for six traits among egusi-melon genotypes in a 7x7 diallel crosses.

Source of variation	d.f	No of primary vines plant ⁻¹	Leading vine Length (m) plant ⁻¹	No. of pods plant ⁻¹	Pod weight (kg) plant ⁻¹	% seed production efficiency plant ⁻¹	Seed weight (g) plant ⁻¹
Replications	3	8.59**	1.19	7.41**	2.13	0.35	345.57
Diallel progenies	48	0.79**	0.70**	4.61**	3.48**	0.53**	2528.82**
Parents	6	0.27	0.33	8.29**	3.64**	0.46	2531.56**
Crosses	41	0.75**	0.77**	3.60**	3.46**	0.53**	2599.37**
Fis (f)	20	0.83**	0.79**	2.09**	2.36**	0.42	1733.22**
rFis (r)	20	0.68**	0.78**	5.28**	4.36**	0.70**	3376.74**
f vs r	1	0.25	0.01	0.20	7.21**	0.05	4374.78**
Parents vs Crosses	1	5.08**	0.001	23.77**	3.59**	1.76**	17.27
Error	144	0.39	0.46	1.19	1.21	0.29	656.91

*, **significant at 0.05 and 0.01 level of probability, respectively

Analysis of variance for combining ability for the traits under study is presented in Table 2. The mean squares for general combining ability (GCA) for all the traits under consideration were non-significant ($P>0.05$) indicating that variability was not present among the parents for GCA for the six traits under study. On the other hand, mean squares for SCA were highly significant ($P<0.01$) for number of pods plant⁻¹, pod weight plant⁻¹ and seed weight plant⁻¹. This suggests the importance of non-additive gene effects in the expression of these traits. Mean squares for reciprocal effects were significant ($P<0.01$) for number of primary vines plant⁻¹, pod weight plant⁻¹ and seed weight plant⁻¹ (Table 2) indicating the importance of reciprocal effects in the expression of these traits.

The variance components given in Table 2 were estimated to determine the importance of additive and dominance components in the control of characters under study. The variance (δ_s^2) due to SCA was higher in magnitude than variance (δ_g^2) due to GCA for all the traits under study. Further, the values of GCA variance (δ_g^2) to SCA variance (δ_s^2) ratio which is less than 1.0 for all the traits support the predominance of non-additive gene effects in governing the expression of these traits. These results are encouraging from the point of view of heterosis exploitation. Ghaderi and Lower (1979) obtained similar results for fruit weight and Dogra and Kanwar (2011) for number of fruits and fruit weight in cucumber.

General combining ability effect

The general combining ability effect represents the additive nature of gene action and it is used to designate the performance of the parents in general combination. In the present study, GCA mean squares was non-significant ($P>0.05$) for all the characters under study indicating lack of variability in the general combining ability effects of the parents. As a result it was not necessary to estimate the general combining ability effect of the parents in the diallel crosses.

Specific combining ability effect

Specific combining ability effect signifies the predominance of non-additive gene action in the expression of traits. It denotes the highly specific combining ability leading to good performance of some specific cross combinations. The usefulness of a particular cross in exploiting heterosis is judged by the SCA effect of component parents. Table 3 revealed that OKWE -2 -IM x KTGO-GMB was the best cross combination for two traits: number of pods plant⁻¹ and pod weight plant⁻¹ while KOGI-NITN x MOKWA-NG was the best cross combination for seed weight plant⁻¹. Similar results showed that, MOKWA-NG x MADLS-NG was the best cross combination to increase seed production efficiency per plant⁻¹ on account of being associated with positive and significant SCA effect.

Table 2: Analysis of combining ability for six traits among egusi-melon genotypes in a 7x7 diallel crosses.

Source of variation	Df	No. of primary Vines plant ⁻¹	Leading vine Length (m) plant ⁻¹	No. of pods Plant ⁻¹	Pod weight (kg) Plant ⁻¹	% Seed production efficiency plant ⁻¹	Seed weight (g) Plant ⁻¹
gca effects	6	0.27	0.20	1.65	1.00	0.28	768.05
sca effects	21	0.13	0.20*	1.62**	0.65**	0.13*	545.92**
reciprocal effects	21	0.25*	0.14	0.60	1.06**	0.09	679.67**
Error	144	0.10	0.11	0.48	0.30	0.07	164.19
Variance components							
δ_g^2		0.01	0.001	0.002	0.021	0.013	16.502
δ_s^2		0.02	0.050	0.680	0.103	0.032	217.504
δ_r^2		0.08	0.010	0.060	0.382	0.014	257.743
δ_c^2		0.10	0.110	0.480	0.303	0.071	164.192
δ_g^2/δ_s^2		0.50	0.020	0.294	0.204	0.406	0.076

*, **significant at 0.05 and 0.01 level of probability, respectively

Table 3: Specific combining ability and reciprocal effects of six characters among egusi-melon genotypes in a 7x7 diallel cross.

Cross Combinations	No. of primary Vines plant ⁻¹		Leading vine Lt. (m) plant ⁻¹		No. of pods plant ⁻¹		Pod wt. (kg) Plant ⁻¹		% Seed pdn. efficiency plant ⁻¹		Seed weight (g) Plant ⁻¹	
	S _{ij}	r _{ij}	S _{ij}	r _{ij}	S _{ij}	r _{ij}	S _{ij}	r _{ij}	S _{ij}	r _{ij}	S _{ij}	r _{ij}
OKWE-2-IM x AKARA	0.39	0.16	0.50*	0.19	-1.31*	0.58	-0.31	-0.43	0.22	0.07	3.54	-9.60
OKWE-2-IM x KOGI-NITN	-0.23	0.24	0.02	0.78**	0.09	1.15	-0.95**	1.08**	0.06	-0.17	-26.83**	19.92*
OKWE-2-IM x MOKWA-NG	-0.41	-0.50	-0.03	-0.18	0.50	-0.30	0.50	-0.64	-0.36	0.38	-13.77	-3.32
OKWE-2-IM x MADLS-NG	-0.15	0.09	-0.04	-0.04	-1.21**	0.15	-0.80*	0.27	0.12	0.30	-1.16	5.45
OKWE-2-IM x KTGO-GMB	0.07	-0.23	-0.12	0.10	1.13**	-1.25	0.73*	-0.88*	0.04	-0.17	23.09**	-22.00*
OKWE-2-IM x ABTK-ADP	0.07	0.44	-0.57	-0.21	2.55	0.27	0.19	-0.02	0.10	0.36	20.95**	5.43
AKARA-AB x KOGI-NITN	0.14	-0.47	0.08	0.29	3.75	0.19	0.08	0.21	0.37	-0.03	9.35	3.66
AKARA-AB x MOKWA-NG	0.23	0.14	-0.33	0.20	0.79	-0.38	1.05	-1.85**	0.09	0.01	16.97*	-38.93**
AKARA-AB x MADLS-NG	-0.24	-0.18	-0.12	0.06	-0.41	0.54	-0.16	0.56	0.11	-0.22	-14.36	3.24
AKARA-AB x KTGO-GMB	0.07	0.01	0.18	0.01	-0.08	0.19	-0.19	-0.29	-0.16	0.10	-14.18	-3.22
AKARA-AB x ABTK-ADP	0.09	0.34	0.40	-0.52*	0.22	0.05	-0.02	-1.07**	-0.21	0.09	-11.21	-15.33
KOGI-NITN x MOKWA-NG	0.31	-0.61**	0.32	0.14	0.01	0.26	0.39	0.68	-0.28	0.37	3.01	33.96**
KOGI-NITN x MADLS-NG	-0.25	-0.39	-0.38	-0.20	-0.05	-0.11	0.17	0.36	-0.16	-0.21	4.74	7.83
KOGI-NITN x KTGO-GMB	0.04	-0.05	0.16	-0.17	-0.17	0.22	0.11	-0.03	0.16	0.07	9.33	-3.29
KOGI-NITN x ABTK-ADP	0.24	0.54*	-0.56**	0.08	0.82	0.13	0.15	0.05	0.17	0.06	4.51	0.00
MOKWA-NG x MADLS-NG	0.73	0.09	0.03	0.15	-0.11	-1.20	-0.79*	-1.29**	0.44**	0.16	-5.89	-29.52**
MOKWA-NG x KTGO-GMB	0.13	-0.05	-0.04	-0.24	-0.05	-0.50	-0.59	-0.15	0.39	-0.28	1.38	-15.12
MOKWA-NG x ABTK-ADP	-0.15	0.07	-0.04	0.14	-0.78	-0.38	-0.44	-1.00**	-0.02	-0.39	-12.90	-42.78**
MADLS-NG x KTGO-GMB	-0.11	0.13	0.17	-0.17	-0.63	0.10	-0.18	-0.02	-0.43*	0.52**	-10.74	5.15
MADLS-NG x ABTK-ADP	0.25	-0.23	0.24	-0.38	-0.65	0.20	0.23	0.38	-0.42*	-0.10	-1.70	2.68
KTGO-GMB x ABTK-ADP	-0.08	-0.39	0.03	-0.16	-0.61	-0.61	-0.34	-0.35	0.11	-0.14	-6.81	-10.94

*, ** significant at 0.05 and 0.01 level of probability respectively

Reciprocal effects

Reciprocal effects are important because they could detect a desirable female seed parent in hybridization programme, particularly for producing commercial F_1 hybrids (Sharma, 1988). Table 3 indicated that OKWE-2-IM will produce progenies with better performance for pod weight plant⁻¹ and seed weight plant⁻¹ when deployed as a female parent than as a pollen source. Bahari et al., (2012) obtained similar results for fruit yield and fruit number in cucumber. Pavasias et al. (1999) recommended that crosses portraying reciprocal effects should not be mixed with direct crosses.

Heterosis

Significant difference between parents and crosses which is an indication of heterosis was observed only for number of primary vines plant⁻¹, number of pods plant⁻¹ and percentage seed production efficiency plant⁻¹. Mid-parent and better-parent heterosis estimates for all the characters under study are presented in Table 4 and Table 5 for direct f_1 and reciprocal cross combinations, respectively. Generally, mid-parent heterosis estimates were higher than their corresponding better parent heterosis estimates. Both positive and negative mid-parent and better-parent heterosis were also recorded for these characters. The cross MOKWA-NG x MADLS-NG obtained a relatively high and positive mid-parent (>30%) and better-parent (>30%) heterosis for number of primary vines plant⁻¹ and seed production efficiency. Similar results in reciprocal cross showed that MOKWA-NG x KOGI-NITN obtained a relatively high and positive mid-parent (>40%) and better-parent (>30%) heterosis for number of primary vines plant⁻¹ while KOGI-NITN x OKWE-2-IM cross combination was associated with a relatively high and positive mid-parent (>23%) and better-parent (>11%) heterosis for seed production efficiency. Even though the differences between parents and crosses were non-significant ($P>0.05$) for pod weight and seed weight plant⁻¹ respectively, the cross KOGI-NITN x MOKWA-NG was associated with a relatively high mid-parent (>20%) and better-parent (19%) heterosis for pod weight and an equally high mid-parent (>40%) and better-parent (>40%) heterosis for seed weight plant⁻¹.

The results indicated preponderance of non-additive genetic variance in the expression of the six characters under study which offers good scope for the exploitation of heterosis or hybrid vigor in enhancing the productivity of egusi-melon. Furthermore, consideration should be given to specific combining ability and reciprocal effects in selecting sources of inbreds with potential for improving seed production efficiency and seed yield in egusi-melon.

Table 4: Mid-parent (Mp) and Better-parent (Bb) heterosis of six characters for direct fl diallel cross combinations of egusi-melon genotypes in a 7 x 7 diallel cross.

Diallel Crosses	No. of primary vines plant ⁻¹		Leading vine lt. (m) Plant ⁻¹		No. of pods plant ⁻¹		Pod weight (kg) plant ⁻¹		% seed production efficiency plant ⁻¹		Seed weight (g) plant ⁻¹	
	Mp	Bp	Mp	Bp	Mp	Bp	Mp	Bp	Mp	Bp	Mp	Bp
OKWE-2-IM x AKARA-AB	26.30**	13.94**	27.41 ^{NS}	20.00 ^{NS}	-49.59**	-55.67**	-22.55 ^{NS}	32.62 ^{NS}	21.43**	12.18*	-2.01	-4.17
OKWE-2-IM x KOGI-NITN	3.63 ^{NS}	3.22 ^{NS}	13.37 ^{NS}	6.53 ^{NS}	-37.50**	-40.21**	-5.76 ^{NS}	-13.00 ^{NS}	1.27 ^{NS}	-34.9 ^{NS}	-10.56	-2.11
OKWE-2-IM x MOKWA-NG	-49.59**	-55.67*	-10.67 ^{NS}	-1.05 ^{NS}	-18.43*	-29.28*	-9.63 ^{NS}	-10.17 ^{NS}	12.34 ^{NS}	-3.04 ^{NS}	-18.45	-31.49
OKWE-2-IM x MADLS-NG	1.27 ^{NS}	-34.9 ^{NS}	-7.10 ^{NS}	-7.63 ^{NS}	-63.53**	-68.81**	-31.94 ^{NS}	-41.37 ^{NS}	21.32**	5.29*	-31.46	-48.85
OKWE-2-IM x KTGO-GMB	7.96 ^{NS}	0.00 ^{NS}	1.33 ^{NS}	-1.71 ^{NS}	-39.31**	-52.58**	-16.75 ^{NS}	-17.73 ^{NS}	12.50 ^{NS}	11.83 ^{NS}	2.67	-2.57
OKWE-2-IM x ABTK-ADP	20.06**	14.75**	-31.65 ^{NS}	-32.69 ^{NS}	-18.41*	-36.49*	-7.33 ^{NS}	-20.80 ^{NS}	29.93**	9.43**	36.87	31.24
AKARA-AB x KOGI-NITN	12.00 ^{NS}	-5.41 ^{NS}	15.79 ^{NS}	2.29 ^{NS}	1.85 ^{NS}	-6.77 ^{NS}	14.75 ^{NS}	7.54 ^{NS}	25.49**	21.33**	33.10	13.35
AKARA-AB x MOKWA-NG	36.00**	30.77**	5.78 ^{NS}	-1.42 ^{NS}	10.50 ^{NS}	8.69 ^{NS}	-13.89 ^{NS}	-24.64 ^{NS}	11.48 ^{NS}	3.48 ^{NS}	19.04	-3.22
AKARA-AB x MADLS-NG	1.25 ^{NS}	-4.44 ^{NS}	7.44 ^{NS}	0.00 ^{NS}	-29.97**	-46.12**	-3.12 ^{NS}	-25.64 ^{NS}	-21.23*	-26.43*	-23.87	-44.65
AKARA-AB x KTGO-GMB	19.74**	16.35**	23.34 ^{NS}	18.84 ^{NS}	-3.28 ^{NS}	-15.76 ^{NS}	-13.70 ^{NS}	-23.73 ^{NS}	10.93 ^{NS}	3.05 ^{NS}	-7.34	-15.38
AKARA-AB x ABTK-ADP	30.63**	22.94**	1.20 ^{NS}	-6.65 ^{NS}	-3.13 ^{NS}	-13.59 ^{NS}	-31.48 ^{NS}	-32.91 ^{NS}	1.59 ^{NS}	-11.07 ^{NS}	-16.66	-23.13
KOGI-NITN x MOKWA-NG	7.34 ^{NS}	8.11 ^{NS}	6.26 ^{NS}	2.51 ^{NS}	5.13 ^{NS}	-5.19 ^{NS}	29.35 ^{NS}	19.14 ^{NS}	26.47*	12.17*	49.22	41.02
KOGI-NITN x MADLS-NG	-11.02*	-14.86*	-21.54 ^{NS}	-25.88 ^{NS}	-33.75**	-45.39**	-5.62 ^{NS}	-23.93 ^{NS}	-12.33*	-15.42 ^{NS}	-5.53	-22.32
KOGI-NITN x KTGO-GMB	9.01*	1.35 ^{NS}	-1.38 ^{NS}	-8.79 ^{NS}	-5.59**	-23.70 ^{NS}	-4.54 ^{NS}	-10.90 ^{NS}	32.11**	18.96**	14.92	6.36
KOGI-NITN x ABTK-ADP	31.80**	26.49**	-23.48 ^{NS}	-27.14 ^{NS}	17.81*	-5.19*	1.82 ^{NS}	-6.42 ^{NS}	20.11**	11.89**	10.26	1.04
MOKWA-NG x MADLS-NG	41.18**	38.48**	2.12 ^{NS}	1.98 ^{NS}	-50.34**	-62.23**	-55.53 ^{NS}	-61.88 ^{NS}	28.23**	27.39**	-44.71	-52.34
MOKWA-NG x KTGO-GMB	21.31**	20.00**	-3.81 ^{NS}	-7.08 ^{NS}	-11.61 ^{NS}	-21.91 ^{NS}	-21.78 ^{NS}	-22.25 ^{NS}	24.81**	8.26**	-5.72	-17.15
MOKWA-NG x ABTK-ADP	16.69**	14.12**	-5.04 ^{NS}	-6.09 ^{NS}	-32.91**	-41.01**	-41.50 ^{NS}	-49.76 ^{NS}	-8.86 ^{NS}	-11.48 ^{NS}	-59.68	-64.90
MADLS-NG x KTGO-GMB	9.76*	6.51 ^{NS}	3.66 ^{NS}	0.00 ^{NS}	-41.42**	-59.00**	-23.85 ^{NS}	-35.04 ^{NS}	6.12 ^{NS}	-26.24 ^{NS}	-22.04	-39.64
MADLS-NG x ABTK-ADP	13.98*	10.29*	-12.17 ^{NS}	-13.02 ^{NS}	-41.24**	-59.00**	-6.21 ^{NS}	-29.06 ^{NS}	-12.96*	-15.98*	16.31	-36.90
KTGO-GMB x ABTK-ADP	-1.82 ^{NS}	-5.00 ^{NS}	-5.22 ^{NS}	-9.42 ^{NS}	-25.23*	-25.64*	-29.03 ^{NS}	-38.74 ^{NS}	23.48**	4.51**	-9.98	-10.94

*, ** significant at 0.05 and 0.01 level of probability respectively

Table 5: Mid-parent (Mp) and Better-parent (Bp) heterosis of six characters for reciprocal cross combinations of egusi-melon Genotypes in a 7x7 diallel cross.

Diallel Crosses	No. of primary Vines plant ¹		Leading vine lt. (m) Plant ¹		No. of pods plant ¹		Pod weight (kg) plant ¹		% seed production Efficiency plant ¹		Seed weight (g) plant ¹	
	Mp	Bp	Mp	Bp	Mp	Bp	Mp	Bp	Mp	Bp	Mp	Bp
AKARA-A x OKWE-2-IM	16.79**	5.36**	17.13 ^{NS}	9.43 ^{NS}	-76.55**	-79.38**	0.54 ^{NS}	-12.53 ^{NS}	14.29**	5.58*	30.71	25.51
KOGI-NITN x OKWE-2-IM	-9.02*	-9.38*	-28.34 ^{NS}	-32.66 ^{NS}	-87.07**	-87.63**	-60.82 ^{NS}	-63.83 ^{NS}	24.87**	11.85**	-63.91	-68.14
MOKWA-NG x OKWE-2-IM	14.61**	7.24*	-4.27 ^{NS}	-8.50 ^{NS}	-4.16 ^{NS}	-73.21 ^{NS}	20.81 ^{NS}	20.09 ^{NS}	-25.94**	-36.09**	-10.15	-24.51
MADLS-NG x OKWE-2-IM	-3.52	-8.04	-5.11 ^{NS}	-5.65 ^{NS}	-68.66**	-73.21**	-42.86 ^{NS}	-50.77 ^{NS}	-8.63 ^{NS}	-20.70 ^{NS}	-42.63	-57.19
KTGO-GMB x OKWE-2-IM	20.98**	12.06**	-4.57 ^{NS}	-7.43 ^{NS}	26.65**	-1.03**	25.12 ^{NS}	23.64 ^{NS}	33.33**	32.54**	67.04	58.52
ABTK-ADP x OKWE-2-IM	-4.63	-8.85	-20.11 ^{NS}	-21.33 ^{NS}	-32.45**	-47.42**	4.56 ^{NS}	-10.64 ^{NS}	-5.11 ^{NS}	-20.08 ^{NS}	20.82	15.85
KOGI-NITN x AKARA-AB	32.24**	24.14**	-0.71 ^{NS}	-12.31 ^{NS}	-7.52 ^{NS}	-15.35 ^{NS}	2.24 ^{NS}	-4.19 ^{NS}	27.94**	23.70**	22.94	4.70
MOKWA-NG x AKARA-AB	27.36**	22.47*	-6.38 ^{NS}	-12.75 ^{NS}	31.22**	29.08**	87.41 ^{NS}	63.88 ^{NS}	11.01*	3.04 ^{NS}	19.74	78.65
MADLS-NG x AKARA-AB	27.36*	5.93	4.10 ^{NS}	-3.11 ^{NS}	50.52**	-61.93**	-28.06 ^{NS}	-44.79 ^{NS}	-1.89 ^{NS}	-8.37 ^{NS}	-30.61	-49.58
KTGO-GMB x AKARA-AB	19.09**	15.72**	22.71 ^{NS}	18.24 ^{NS}	-14.82 ^{NS}	-25.82 ^{NS}	-7.16 ^{NS}	-9.69 ^{NS}	0.55 ^{NS}	-6.60 ^{NS}	2.43	-6.46
ABTK-ADP x AKARA-AB	9.38*	2.94	32.43 ^{NS}	22.16 ^{NS}	-3.45 ^{NS}	-16.30 ^{NS}	38.01 ^{NS}	35.14 ^{NS}	-9.75 ^{NS}	-18.44 ^{NS}	30.49	20.36
MOKWA-NG x KOGI-NITN	42.45**	33.78**	-1.20 ^{NS}	-6.78 ^{NS}	-7.88 ^{NS}	-16.98 ^{NS}	-5.71 ^{NS}	-13.16 ^{NS}	-16.10*	-19.57*	-14.55	-30.40
MADLS-NG x KOGI-NITN	11.02*	6.22*	-11.17 ^{NS}	-16.08 ^{NS}	-29.84**	-42.17**	-20.89 ^{NS}	-36.24 ^{NS}	6.85 ^{NS}	3.08 ^{NS}	-20.02	-34.45
KTGO-GMB x KOGI-NITN	11.92*	4.05*	8.94 ^{NS}	-5.03 ^{NS}	-17.60*	-33.41*	-3.24 ^{NS}	-9.69 ^{NS}	25.26**	12.80*	23.30	14.12
ABTK-ADP x KOGI-NITN	1.41*	-2.70*	-27.80 ^{NS}	-31.16 ^{NS}	10.80 ^{NS}	-10.84 ^{NS}	-1.22 ^{NS}	-9.22 ^{NS}	15.16*	7.38*	10.26	1.04
MADLS-NG x MOKWA-NG	35.75**	33.14**	-6.36 ^{NS}	-6.50 ^{NS}	-4.14 ^{NS}	-27.09 ^{NS}	-4.29 ^{NS}	-17.95 ^{NS}	14.66 ^{NS}	13.91 ^{NS}	7.43	-7.40
KTGO-GMB x MOKWA-NG	24.42**	23.08**	9.97 ^{NS}	6.23 ^{NS}	20.19*	6.18 ^{NS}	-14.56 ^{NS}	-15.0 ^{NS}	52.38**	32.17**	30.48	14.66
ABTK-ADP x MOKWA-NG	12.78*	10.29*	-12.89 ^{NS}	-13.85 ^{NS}	-8.95 ^{NS}	-19.94 ^{NS}	14.21 ^{NS}	-1.91 ^{NS}	24.05**	20.49**	43.68	25.09
KTGO-GMB x MADLS-NG	2.13	-8.88	13.62 ^{NS}	9.60 ^{NS}	-45.61**	-61.93**	23.25 ^{NS}	-34.53 ^{NS}	-8.08 ^{NS}	-19.82 ^{NS}	-32.17	-47.48
ABTK-ADP x MADLS-NG	27.66**	23.53**	9.09 ^{NS}	8.03 ^{NS}	-49.63**	-64.86**	-23.16 ^{NS}	-41.88 ^{NS}	-4.46 ^{NS}	-7.79 ^{NS}	8.80	-40.97
ABTK-ADP x KTGO-GMB	21.53**	17.65**	3.77 ^{NS}	-8.31 ^{NS}	19.71 ^{NS}	19.05 ^{NS}	-9.40 ^{NS}	-21.79 ^{NS}	36.56**	15.57**	20.73	19.44

*, ** significant at 0.05 and 0.01 level of probability respectively

REFERENCES

- Akpambang, V.O.E., Amoo, I.A and Izuagie, A.A. (2008). Cooperative compositional analysis on two varieties of melon (*Colocynthis citrillus* and *Cucumeropsis edulis*) and a variety of almond (*Prunus amygdalus*). *Research Journal of Agricultural and Biological Sciences* 4(6): 639-642.
- Banerjee, P.P. and Kole, P.C. (2009). Combining ability analysis for seed yield and some of its component characters in Sesame (*Sesamum indicum* L.). *International Journal of Plant Breeding and Genetics* 3(1): 11-21.
- Bahari, M., Rafii, M.Y., Saleh, G.B. and Latif, M.A. (2012). Combining ability analysis in complete diallel cross of watermelon (*Citrullus lanatus* (Thunb.) Matsum & Nakai). *The Scientific World Journal* 2012. Article ID 543158, 6 pages doi:10.1100/2012/543158. Web document. Accessed 15/2/2012.
- Chanderi, A. and Lower, R.L. (1979a). Analysis of generation means for six crosses of cucumber. *Journal of the American Society for Horticultural Science* 104: 567-572.
- Chanderi, A. and Lower, R.L. (1979b). Gene effects of some vegetative characters of cucumber. *Journal of the American Society for Horticultural Science* 104: 141-144.
- Chanderi, A. and Lower, R.L. (1979c). Heterosis and inbreeding depression for yield in populations derived from six crosses of cucumber. *Journal of the American Society for Horticultural Science* 104: 564-567.
- Cramer, C.S and Wehner, T.C. (1998). Little heterosis for yield and yield components in hybrid of six cucumber inbreds. *Euphytica* 110: 99-108.
- Development, Security, and Cooperation (DSC) (2006). Lost Crops of Africa: Vol. 11: Vegetables: Washington, D.C., pp 154-171.
- Dogra, B.S. and Kanwar, A.B. (2011). Exploitation of combining ability in cucumber (*Cucumis sativus* L.) *Research Journal of Agricultural Science* 2(1): 55-59.
- Dudley and Moll, (1969). Interpretation and use of estimates of heritability and variances in plant breeding. *Crop science* 9(3): 257-262.
- Esmail, R.M. (2007). Genetic analysis of yield and its contributing traits in two intra-specific cotton crosses. *Journal of Applied Science* 3: 2075-2080.
- Fakou, E., Achu, M.B. and Techonarguep, M.F. (2004). Preliminary nutritional evaluation of five species of egusi seeds in Cameroon. *African Journal of Food, Agriculture, Nutrition and Development* 4(1): 1-3.
- Falconer, D.S and Mackay, T.F.C. (1996). Introduction to Quantitative Genetics. 4th Edition, Prentice Hall, Essex.
- Ghaderi, A. and Lower, R.I. (1979) Analysis of generation means for yield in six crosses of cucumber. *Journal of the American Society for Horticultural Science* 104: 567-572.
- Griffing, B. (1956). A generalized treatment of the use of diallel crosses in quantitative inheritance. *Heredity* 10: 32-50.
- Hayes, H.K., Immer, F.F. and Smit, D.C. (1956). Methods of Plant Breeding. McGraw Hill Book Publishing Company Inc., New Delhi. 328 pages.
- Ikeorgu, J.E.G., Ezumah, H.C. and Wahma, T. A.T. (1989). Productivity of species in cassava/ maize/ okra/ egusi – melon complex mixtures in Nigeria. *Field Crops Research* 21: 1-7.
- Lal, R. (1995). Sustainable management of soil resources in the humid tropics. *United Nations University Press, Tokyo Japan*. 394 pages.
- Nazim Uddin, M., Hussian, M.M., Rahman, S., Ahmad, A.K,M. and Quamruzzaman, R.O. (2009) Combining ability and gene action in Cucumber (*Cucumis sativus* L.) *SAARC Journal Agriculture* 7(1): 64-72.
- Pavasia, M.J., Shukla, P.T and Patel, U.G. (1999). Combining ability over environments for fibre character in upland cotton. *Indian Journal of Genetics and Plant Breeding* 59: 77-81.
- Schippers, R.R. (2000). African Indigenous vegetables. An Overview of the cultivated species. Chattam, Uk: Natural Resources Institute/ACP – EU Technical Centre for Agricultural and Rural Cooperation. 224 pages.
- Shankara, N., Joep, V.D.J., Marja, D.G., Martin, H. and Barbara, V.D. (2005). Cultivation of Tomato: Production Processing and Marketing, Agromisa Foundation, Wageningen, 63-64.
- Singh, R.K and Chandhary, B.D. (1976). Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publication 304 pages.
- Viana, J.M.S, Cruz, C.D. and Cardoso, A.A. (2001). Theory and analysis of partial diallel crosses. Parents and F₂ generation. *Acta Science* 23: 627-634.
- Willey, P.E. and Chinaka, C.C. (1985). Weed control in Pine and Gmelina plantation in Nigeria. In: Okonkwo, S.N.C., Akobundu, I.O., Ayeni, A.A (eds): Proceedings of 3rd Biannual conference of the West African weed Science Society Ibadan, Nigeria. pp 249-255.