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Diallel analysis of selected yield-contributing traits in Okra [*Abelmoschus esculentus* (L.) Moench]

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Abstract: Information on gene action controlling quantitative traits is important for effective selection. A five-parent diallel cross, which generated 10 F_1 hybrids of okra (*Abelmoscus esculentus*) were evaluated during the early and late planting seasons of 2019 in Ibadan, Nigeria. Data obtained were subjected to diallel analysis and genotype by yield-trait (GYT) biplot analysis to estimate combining ability effects and identify stable hybrids for measured traits respectively. Genotype mean squares were significant (p≤0.01) for all most measured traits. Furthermore, General Combining Ability (GCA) and Specific Combining Ability (SCA) mean squares were significant (p≤0.05/0.01) for most measured traits, indicating the influence of additive and non-additive gene actions in expression of these traits. Preponderance of non-additive gene effects shows the high influence of the environment on most of the considered traits in this study. Iwo Nla had the most desirable GCA estimates of -0.98 and 1.14, for days to 50% flowering (DTF), number of fruits per plant (NoF) respectively while IK11 had the most desirable GCA values for mature-fruit width (0.21) and 1000-seed weight (5.71). SCA estimates were most desirable for NH47-4 × LD88, NH47-4 × Iwo Nla, with values of -4.21 and 4.32 for DTF and NoF respectively. Hybrids NH47-4 × Iwo Nla and IK11 × Clemson associated with higher NoF x trait might be useful for improvement of number of fruits per plant in this population.

1. Introduction

Okra (*Abelmoschus esculentus* L. Moench) is an important food crop in Africa and belongs to the Malvaceae family (Kochhar, 1986). It is a widely-cultivated vegetable across West Africa and is well adapted to tropical environments. The vegetable is grown in almost all the agro-ecological regions across Nigeria because of its importance to the economic development of rural dwellers, and can be found in most markets across the country (Siemonsma and Kouame, 2004; Christo and Onuh, 2005; Mohammed and Miko, 2009).

Fresh okra pods serve as soup thickeners because of its unique mucilage properties and are known to be good sources of vitamins and minerals (Schippers, 2000). The edible fruits contain 86% water, 2.2% protein, 10% carbohydrate, 0.2% fat and vitamins A, B, and C (Berry *et al*., 1988). Despite the important role played by okra in meeting the daily nutritional and economic needs of the society in the region, minimum efforts and resources have been directed towards its genetic improvement to meet the desired preferences of farmers and consumers, such as earliness and increased number of fruits with smooth pod per plant. Okra research in developing countries has for long been concentrated on germplasm characterization and development of pure line varieties, with little or no efforts directed towards development of hybrid varieties despite its huge potential and market. Okra hybrids are gradually becoming the favorites of many farmers regardless of associated high cost of seeds since hybrid varieties are usually characterized by higher yield and uniformity, coupled with tolerance to diseases and pests. Heterosis which is widely referred to as the superiority of F_1 hybrid over the mean performance of its better inbred parents, has been reported to enhance yield and component traits in okra by about 86% (Elmaksoud *et al.*, 1986, Ahmed and Adam, 2014). Hybrid variety development is a quick path to combining economic and desirable horticultural traits in vegetable crops such as okra. The floral pattern of okra which enables easy emasculation and pollination coupled with the ability to produce a large number of seeds from a single pollination, has made commercial exploitation of heterosis a profitable venture in okra hybrid seed production (Reddy, 2010).

Heterosis breeding is a means to improve yield and its component traits in okra (Jindal *et al*., 2009). In many developing countries of West Africa, minimal work has been reported on the use of two or more okra genotypes in heterotic studies for estimating hybrid vigor relative to fruit yield and its component traits. Positive heterosis favors genetic improvement of yield and yield contributing traits whereas negative heterosis is encouraged when breeding for traits such as earliness (Biswas *et al.,* 2005). The objective of this study was to (i) determine gene action and identify superior parent combination(s) for measured traits and (ii) identify stable hybrids for desired traits of okra with a view to providing information for future breeding programs.

2. Materials and Methods

Study area

Two experiments were conducted at the National Horticultural Research Institute (NIHORT), Ibadan, Oyo state, Nigeria during the early planting season (April to July) and late planting season (from August to December) of 2019. NIHORT is located in the humid forest savanna transition zone (210 masl, 7°30'N, 3°54'E), with a bimodal annual rainfall pattern spanning across 120-128 rainy days, amounting to 1200-1400mm. Pan Evaporation is between 1550-1600mm. Wet season extends from March through October and dry season from November to February, with annual maximum temperature ranging between 27-34°C and annual minimum temperature ranging between 20-23°C (Ogungbenro and Morakinyo, 2014).

Plant material and field establishment

Genetic materials evaluated in this study comprised of 10 newly-developed F_1 hybrids obtained from diallel mating and their 5 parents namely: NH47-4, IK11, Iwo Nla, LD 88, and Clemson. The parents and their hybrids were grown in Randomized Complete Block Design with two replicates during the early and late planting seasons of 2019. Three seeds per hill were sown directly in 3-cm holes and later thinned to one plant per hill after seedling establishment. Plants were spaced at 60 cm x 50 cm between and within rows respectively on a 2-m bed constituting 10 stands per plot. Regular plant protection and other agronomic activities were carried out as when due to ensure full expression of desired traits and safeguard crops from pests. Manual weeding was done at three weeks after planting while a compound fertilizer, NPK 15:15:15, was applied at three-week interval after sowing to enhance vegetative growth at the recommended rate of 60 kg/ha (Adigun *et al*., 2018). Insect pest control was done by spraying Cyperfits (synthetic pyrethrum) at the rate of 80 g ai/ha.

Data collection

Data on agronomic attributes were recorded on five randomly selected competitive plants in each plot according to okra descriptors by Charrier (1984) and IPGRI (1991) for days to 50% flowering (DTF), plant height at maturity (PH) (cm), matured fruit width and length (cm), average number of fruits (fruits per plant) obtained by the ratio between the

total number of fruits and the number of plants in the plot, internode length (cm), number of ridges per pod and 1000-seed weight (g).

Data analysis

Each season was considered an environment. Pooled data for the two environments were subjected to analysis of variance (ANOVA). The MIXED MODEL procedure of Statistical Analysis System (SAS) (SAS Institute, 2002) was used, with replication within environment treated as random factor and genotype (crosses) as fixed factor. The statistical model used for the combined analysis is:

$$Yijg = \mu + Ei + Rj(i) + Gg + EGig + \varepsilon ijg$$

where Yijg is the measurement for the gth Genotype grown in Replicate j within Environment i; μ is the grand Mean; Ei is the main effect of Environment i; Rj(i) is the effect of Replicate nested within Environment effect; Gg is the effect of the Genotype; EGig is the interaction effect between Genotype and Environment, and εijg is the error term.

Mid- and better-parent heterosis were calculated according to the procedure of Singh (1973) described by Amiteye *et al*. (2019).

General (GCA) and specific combining ability (SCA) estimates were generated for each of the traits according to the procedure of Griffing (1956), employed by Medagam *et al*. (2012), for diallel analysis model B (Mixed), method 2 using AGD-R software version 3.0 (Rodríguez *et al*., 2015).

The statistical model for the diallel analysis is as follows:

$$Yijk = \mu + Ee + gi + gj + sij + gEeg + sEes + \varepsilon ijk$$

where Yijk is the observed measurement for the ij^{th} cross grown in the k^{th} environment; μ is the grand mean; Ee is the main effect of Environment; gi and gj are the GCA effects; sij is the SCA effect; gEeg is the interaction effect between GCA and Environment; sEes is the interaction effect between SCA and Environment, and εijk is the error term.

The GCA and SCA effects were tested for significance using t-test at 5 and 1% levels of probability as suggested by Mather and Jinks (1982), Kearsey and Pooni (1996). Standard error (SE) estimates of GCA and SCA were obtained from PB Tools software version 1.4.0 (PB Tools, 2014). The formulae for the SEs were described by Ahmed and Adam (2014) as follows:

SE (gi) = $[(n-1)\sigma^2e/n(n+2)]^{½}$ and SE (gi-gj) = $[(2\sigma^2e/n+2)]^{½}$ for GCA effects and SE (sij) = $[n(n-1)\sigma^2e/(n+1)(n+2)]^{½}$ and SE (sii-sjj) = $[2(n-2)\sigma^2e/n+2)]^{½}$ for SCA effects where S.E. (gi) = S.E. for GCA effects of parents, S.E. (gi-gj) = S.E. of difference between GCA effects of the ith and jth parents, S.E. (sij) = S.E. for SCA effects of the diallel hybrids, S.E. (sii-sjj) = S.E. of the difference between the SCA effects of the ith and jth hybrids, σ^2e is the error mean square value in the diallel analysis, and n is the number of parents.

The proportions of the additive and non-additive genetic variances were computed as the percentages of GCA and SCA sums of squares (SS) respectively of the cross SS across environments (Fasahat *et al*. 2016). Means of observed data were used to obtain pair-wise correlation (Pearson's) coefficients, to determine the level of association among measured traits. The modified genotype × trait (GYT) biplot approach of Yan and Fregeau-Reid (2018) was used to profile the 10 diallel F_1 hybrids for measured traits. The GYT incorporates yield into other traits, rather than as a standalone trait. Here, GYT is the interaction of genotype and the combination of other traits with NoF. In this study, the procedure for obtaining the NoF-trait combination estimates was based on the direction of association of other traits with NoF. Thus, the estimates were obtained by multiplication for all measured traits except DTF, FWT, and INL which were negatively correlated with NoF, and were obtained by division. Biplotswere obtained using the GGEBiplotGUI package in R.

3. Results

Analysis of variance for pooled data over the two environments (seasons) revealed significant ($P \leq 0.01$) genotype (G) mean squares for all measured traits while environment (E) mean square was significant ($P \leq 0.01$) for DTF and NOF. The mean square of the G×E interaction was found to be significant ($P \leq 0.05$) for NOR. Number of days to flowering (DTF) ranged from 46.5 days for NH47-4 × Clemson to 57.75 days for LD88 while NOS ranged from 30.50 for NH47-4 × LD88 to 117.15 for LD88 × Iwo Nla. Iwo Nla × Clemson produced the longest peduncles with a mean length of 3.50 cm while LD88 had the shortest peduncle lengths averaging 1.50 cm (Table 1).

Diallel analysis of hybrids revealed significant ($P \leq 0.05$ or 0.01) cross mean squares for all measured traits necessitating the partitioning of the mean squares into GCA and SCA components. Mean squares of GCA and SCA were significant ($P < 0.05$ or

Table 1 - Analysis of variance of 15 genotypes of okra evaluated for selected traits across research environments

Genotype		DTF (days)	PH (cm)	NoF	LNT (cm)	FWT (cm)	PL (cm)	INL (cm)	NoS	THS (g)	NoR
Clemson		48.25 ef	62.25 de	5.00 cde	12.92 a	2.39 d	3.00 b	6.50 de	68.75 de	50.00 d	7.38 efg
IK11		49.25 def	104.00 abc	6.00 b-e	7.75 cd	3.4 abc	1.63 ef	8.63 cd	79.50 bcd	70.00 a	6.75 g
IwoNla		47.75 f	74.00 b-e	5.75 b-e	10.22 bc	2.91 dc	2.00 ed	6.75 de	64.75 e	60.00 c	5.25 h
LD88		57.75 a	122.75 a	4.50 de	6.70 d	3.34 abc	1.50 f	12.50 ab	82.25 bc	45.00 e	9.00 ab
NH47-4		52.50 bc	63.75 de	5.00 cde	7.95 cd	3.51 abc	2.50 c	6.75 de	65.50 e	70.00 a	8.00 def
NH47-4 × IK11		48.25 ef	73.50 b-e	8.75 b	8.77 cd	3.43 abc	2.38 cd	5.50 e	68.25 de	60.00 c	5.25 h
NH47-4 × LD88		52.13 bcd	106.25 ab	7.75 bc	12.16 ab	2.84 cd	3.00 b	10.50 bc	66.00 e	70.00 a	8.13 cde
NH47-4 × Clemson		51.25 b-e	73.00 b-e	8.25 b	9.71 bc	3.25 bc	3.00 b	6.00 e	72.50 cde	65.00 b	8.00 def
NH47-4 × Iwo Nla		49.38 def	42.25 e	4.25 e	8.44 cd	4.08 a	1.78 ef	7.13 de	36.00 f	60.00 c	5.75 h
IK11 × LD88		53.75 b	76.50 b-e	7.50 bc	13.93 a	3.16 dbc	3.50 a	5.75 e	61.00 e	60.00 c	8.88 abc
IK11 × Clemson		50.50 c-f	107.25 ab	7.75 bc	9.12 cd	3.82 ab	2.50 c	6.75 de	117.25 a	60.00 c	8.25 bcd
IK11 × Iwo Nla		47.50 f	70.25 cde	7.25 bcd	11.92 ab	2.91 dc	2.50 c	6.50 de	84.75 b	70.00 a	9.25 a
LD88 × Clemson		50.88 b-e	96.50 a-d	7.25 bcd	8.90 cd	3.93 ab	1.75 ef	13.25 a	72.25 cde	70.00 a	7.25 fg
LD88 × Iwo Nla		51.00 b-e	74.75 b-e	12.25 a	13.61 a	2.72 dc	2.25 cd	9.50 c	68.50 de	60.00 c	5.00 h
Clemson × Iwo Nla		48.25 ef	75.50 b-e	4.00 e	6.74 d	2.93 dc	2.00 de	13.00 a	30.50 f	42.50 e	7.75 def
Source	DF	DTF	PH	NOF	LNT	FWT	PL	INL	NOS	THS	NOR
Rep (Environment)	2	**	NS	**	NS	NS	NS	NS	NS	NS	NS
Environment (E)	1	**	NS	**	NS	NS	NS	NS	NS	NS	NS
Genotype (G)	14	**	**	**	**	**	**	**	**	**	**
G×E	14	NS	NS	NS	NS	NS	NS	NS	NS	NS	*
Error	28	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS
R-Squared		0.86	0.71	0.82	0.84	0.72	0.92	0.88	0.94	0.95	0.95

*,** significant at p≤0.05 and p≤0.01 respectively; NS= not significant; Rep= Replicate; DTF= days to 50% flowering; PH= plant height at maturity; NOF= number of fruits per plot; LNT= fruit length; FWT= fruit circumference; PL= Pedicel length; INL= internodal length; NOS= number of seeds per pod; THS= 1000-seed weight; NOR= number of ridges per pod.

0·01) for all traits measured except GCA for FRTWDT while cross × environment and SCA × environment interaction mean squares were significant only for NOR. With the exception of 1000-seed weight, SCA effect consistently accounted for higher proportion of total the variation among measured traits compared to GCA effects. The SCA accounted for 93.35% and 41.56% of the total variation for number of seeds per pod and 1000-seed weight respectively (Table 2).

Clemson and Iwo Nla had significant (P<0.05 or 0.01) and negative General Combining Ability (GCA) effects for DTF while LD88 showed significant (P<0.01) positive GCA effect for PH. Iwo Nla had significant (P<0.01) positive GCA effect for NoF. Significant negative and positive GCA effects for FRTLNT and FRTWDT was recorded for IK11 and LD88 respectively while NH47-4, IK11 and LD88 showed significant (P<0.05 or 0.01) positive GCA effects for 1000-seed weight (Table 3). Days to flowering had significant negative Specific Combining Ability (SCA) for NH47-4 × LD88, NH47-4 × Clemson and IK11 × LD88 while NH47-4 × IK11, IK11 × KD88, and LD88 × Clemson had high significant positive SCA effects for PH. Similarly, NH47-4 × Iwo Nla and LD88 × Clemson had significant (P<0.05 or 0.01) and positive SCA for NOF and FRTLNT while significant positive SCA effects were observed for FRTWDT for NH47-4 × IK11, IK11 × LD88, LD88 × Iwo Nla and Clemson × Iwo Nla. Furthermore, NH47-4 × IK11, NH47-4 × Clemson, IK11× Clemson, LD88× Clemson and LD88 × Iwo Nla exhibited high significant positive SCA for NoS and 1000-seed weight (Table 3). The proportion of additive genetic variance ranged from 0.07 for NoS to 0.58 for 1000-seed weight while the non-additive genetic variance estimates ranged from 0.42 to 0.93 for THS and NoS respectively (Table 4). Generally, the non-additive variance was higher than the additive

Table 2 - Mean squares from diallel analysis of variance of okra genotypes evaluated in two environments

Source of variation	DF	DTF (days)	PH (cm)	NoF	LNT (cm)	FWT (cm)	PL (cm)	INL (cm)	NoS	THS (g)	NoR
Rep (Env)	2	22.92 **	1023.90 NS	40.08 **	4.13 NS	0.04 NS	0.08 NS	6.93 NS	41.22 NS	0.83 NS	0.19 NS
Environment (E)	1	39.20 NS	32.27 NS	40.02 NS	1.80 NS	0.02 NS	0.00 NS	0.00 NS	0.15 NS	0.00 NS	0.04 NS
Crosses	14	30.07 **	1817.21 **	18.89 **	23.45 **	0.90*	1.39 **	30.09 **	1588.48 **	327.38 **	8.10 **
GCA	4	38.99 NS	1187.64 **	18.52 *	38.17 *	1.32 NS	2.09 **	37.33 **	369.98 *	669.64 **	11.27 **
SCA	10	26.50**	2069.04 **	19.04 **	17.56 **	0.73 *	1.11 **	27.19 **	2075.88 **	190.48 **	6.83 **
Crosses × E	14	6.11 NS	58.48 NS	1.87 NS	2.70 NS	0.27 NS	0.01 NS	0.78 NS	47.69 NS	0.00 NS	0.69 *
GCA×E	4	8.56 NS	30.10 NS	1.87 NS	4.42 NS	0.48 NS	0.01 NS	2.10 NS	40.85 NS	0.00 NS	0.52 NS
SCA×E	10	5.12 NS	69.83 NS	1.88 NS	2.01 NS	0.19 NS	0.01 NS	0.25 NS	50.42 NS	0.00 NS	0.76 *
Residuals	28	3.3	416.11	3.23	2.55	0.23	0.06	2.1	49.43	7.98	0.25
GCA Proportion (%)		37.05	18.67	28.01	46.51	41.97	42.96	35.45	6.65	58.44	39.76
SCA Proportion (%)		62.95	81.33	71.99	53.49	58.03	57.04	64.55	93.35	41.56	60.24

*,** significant at p≤0.05 and p≤0.01, respectively; NS= not significant; Rep= Replicate; DTF= days to 50% flowering; PH= plant height at maturity; NOF= number of fruits per plot; LNT= fruit length; FWT= fruit circumference; PL= Pedicel length; INL= internodal length; NOS= number of seeds per pod; THS= 1000-seed weight; NOR= number of ridges per pod.

Table 3 - Estimates of general (GCA) and specific combining ability (SCA) effects of okra parents and hybrids respectively for measured traits

Parent/Hybrid	DTF (days)	PH (cm)	NoF	LNT (cm)	FWT (cm)	PL (cm)	INL (cm)	NoS	THS (g)	NoR
NH47-4	-0.1	-6.36	0.04	-0.35	0.01	-0.09 *	0.82	-4.01 *	2.50 *	0.19
IK11	-0.18	5.29	-0.14	-0.69 *	0.21	-0.19 *	0.59	-1.34	5.71 **	-0.19
LD88	2.00 **	8.29	-1.14 **	-1.13 **	0.17	-0.19 *	1.09 *	-0.84	-7.50 **	0.67 **
Clemson	-0.75 *	-5.43	0.11	1.87 **	-0.33 *	0.47 **	-1.25 *	0.34	-0.71	0.33 *
Iwo Nla	-0.98	-1.79	1.14 *	0.3	-0.06	0	-1.25 *	5.84 *	NE	-0.99 **
S.E. (gi)	0.31	3.45	0.3	0.27	0.08	0.04	0.25	1.18	0.48	0.08
S.E. (gi - gj)	0.49	5.45	0.48	0.43	0.13	0.07	0.39	1.88	0.75	0.13
NH47-4 × IK11	0.6	16.07 *	0.61	0.02	0.47 *	-0.32 **	3.51 **	8.42 **	0.95	-0.07
NH47-4 × LD88	-4.21 **	-7.93	-1.64 *	-1.70 **	-0.49*	-0.07	2.76 **	-33.83 **	-13.33 **	-0.43 *
NH47-4 × Clemson	-2.21 **	0.54	0.36	0.48	-0.01	-0.23 *	-1.40 **	19.24 **	7.38 **	1.41 **
NH47-4 × Iwo Nla	1.52 *	1.39	4.32 **	3.74 **	-0.47 *	-0.02	1.60 **	-2.51	-3.33 **	-1.52 **
IK11 × LD88	-3.01 *	-52.82 **	-1.21	0.33	0.45 *	-0.20 *	-2.89 **	-31.01 **	0.95	-2.05 **
IK11 × Clemson	2.49 **	24.89 **	1.04	1.06	-0.27	0.37 **	2.83 **	-2.19	4.17 **	0.66 **
IK11 × Iwo Nla	1.85 *	-12	0.5	0.17	-0.14	0.84 **	-1.67 **	-1.19	-1.55	1.86 **
LD88 × Clemson	1.93 **	-7.86	1.79 *	3.27 **	0.08	0.87 **	-2.42 **	-7.69 **	7.38 **	0.55 **
LD88 × Iwo Nla	-1.08	19.25 *	1	0.03	0.47 *	0.34 **	-1.42 **	43.06 **	6.67 **	1.25 **
Clemson × Iwo Nla	-0.58	-0.79	0.75	-3.32 **	0.58 **	-0.45 **	-0.33	-7.12 *	-0.12	-1.41 **
S.E. (Sij)	0.63	7.04	0.62	0.55	0.17	0.09	0.50 **	2.43	0.97	0.17
S.E. (Sii-Sij)	0.84	9.44	0.83	0.74	0.22	0.12	0.67	3.25	1.31	0.23

*,** significant at p≤0.05 and p≤0.01 respectively; S.E.= standard error; gi= GCA effects of parents; gi-gj= difference between GCA effects of the ith and jth parents; Sij= SCA effects of the diallel hybrids; Sii-Sjj= difference between the SCA effects of the ith and jth hybrids; NE= not estimated; DTF= days to 50% flowering; PH= plant height at maturity; NOF= number of fruits per plot; LNT= fruit length; FWT= fruit circumference; PL= Pedicel length; INL= internodal length; NOS= number of seeds per pod; THS= 1000-seed weight; NOR= number of ridges per pod.

Table 4 - Proportion of additive and non-additive genetic variances for measured traits across the two environments

Trait	Additive variance	Non-additive variance
DTF (days)	37	63
PH (cm)	19	81
NoF	28	72
LNT (cm)	47	53
FWT (cm)	42	58
PL (cm)	43	57
InteL (cm)	35	65
NoS	7	93
ThSW (g)	58	42
NoR	40	60

DTF= days to 50% flowering; PH= plant height at maturity; NOF= number of fruits per plot; LNT= fruit length; FWT= fruit circumference; PL= Pedicel length; INL= internodal length; NOS= number of seeds per pod; THS= 1000-seed weight; NOR= number of ridges per pod.

variance for all measured traits except THS.

Estimates of mid-parent heterosis (MPH) and better-parent heterosis (BPH) of diallel crosses of okra are presented in Table 5. Significant positive and negative heterosis was observed for all traits. Desirable significant BPH and MPH for earliness was observed for NH47-4 × LD88 (-16.45% and -6.24%), NH47-4 × Clemson (-9.52% and -2.85%), IK11 × LD88 (-14.50 and -3.86%), and LD88× Iwo Nla (-12.55% and -2.13%). LD88 × Clemson also showed desirable high significant BPH of -6.93% for DTF. For NoF, all the hybrids showed desirable significant (P<0·05 or 0.01) BPH and MPH with the exception of NH47-4 × IK11, NH47-4 × LD88, and IK11 × LD88 for BPH, and NH47-4 × LD88 and IK11 × LD88 for MPH. Intermodal length (Intel) recorded high negative significant BPH and MPH for IK11 × LD88, LD88 × Clemson, and LD88 × Iwo Nla while LD88 × Iwo Nla only had significant (P<0.05 or 0.01) negative BPH for the same trait.

Table 5 - Estimates (%) of heterobeltiosis of ten diallel crosses of okra for measured traits

Hybrid	DTF (days)		PH (cm)		NoF		FRTLNT (cm)		FRTWDT (cm)	
	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH
NH47-4 × IK11	-3.1	0	-7.21	7.53	20.83	15.91*	11.87*	6.66*	12.02*	6.91**
NH47-4 × LD88	-16.45**	-6.24**	-38.49**	-9.52*	-20	-7.89	-15.23*	-4	-16.45**	-7.19**
NH47-4 × Clemson	-9.52**	-2.85**	10.2	5.75	45.00**	22.50**	-7.68	7.14*	-17.18**	-0.72
NH47-4 × Iwo Nla	-2.86	0.87	1.01	4.26	113.04**	63.95**	33.24**	24.92**	-22.57**	-7.66**
IK11 × LD88	-14.50*	-3.86**	-65.58**	-31.37**	-29.17*	-9.52	8.85	8.37*	19.95**	10.50**
IK11 × Clemson	5.84*	3.46**	2.16	13.91**	29.17*	20.45**	-5.86	8.84*	-16.32**	-0.85
IK11 × Iwo Nla	4.06	2.84**	-29.81**	-8.99*	37.50**	20.21**	-4.99	4.02	-4.2	1.63
LD88 × Clemson	-6.93**	0.71	-37.68**	-8.65*	50.00**	28.95**	7.84	20.99**	-5.44	5.14*
LD88 × Iwo Nla	-12.55**	-2.13*	-12.63	4.51	34.78*	25.61**	-10.68	3.93	14.47*	11.19**
Clemson × Iwo Nla	0	0.26	-0.68	3.94	52.17**	31.40**	-32.13**	-12.10**	17.91**	14.75**
Standard error	2.31	0.91	7.22	3.92	11.86	6.19	5.35	3.2	4.93	2.3

Hybrid	PL (cm)		INL (cm)		NoS		ThSW (g)		NoR	
	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH
NH47-4 × IK11	-30.00**	-7.58	53.62**	36.18**	-9.12	-0.17	0	0	-9.38	-0.85
NH47-4 × LD88	-20.00*	0	4	17.53*	-62.92**	-29.36**	-39.29**	-13.04**	-13.89*	-4.41
NH47-4 × Clemson	-16.67*	-4.55	-3.7	-0.94	23.27*	13.13*	0	8.33**	15.63*	10.16**
NH47-4 × Iwo Nla	-10	0	40.74**	20.37**	4.58	2.59	-14.29**	-3.85	-37.50**	-12.26**
IK11 × LD88	9.23	6.8	-43.00**	-16.27*	-56.23**	-27.74**	-14.29**	2.17	-36.11**	-13.49**
IK11 × Clemson	0	14.86**	21.74	19.42**	-16.98	-5.48	0	8.33**	10.17	7.52*
IK11 × Iwo Nla	50.00**	32.76**	-30.43*	-10.98	-8.81	0.26	-7.14	0	18.52**	16.67**
LD88 × Clemson	16.67*	27.78**	-54.00**	-19.74**	-25.84*	-9.6	20.00**	13.16**	-1.39	4.2
LD88 × Iwo Nla	25.00**	21.43**	-46.00**	-14.94*	42.55**	29.76**	0	7.14**	-8.33	7.89*
Clemson × Iwo Nla	-20.83*	-2.5	-18.52	-8.49	-0.73	1.12	0	4.55*	-28.81**	-8.42*
Standard error	7.48	4.32	11.23	5.86	9.69	5.25	4.58	2.24	6.13	3.06

*,** significant at p≤0.05 and p≤0.01 respectively; BPH and MPH= Better- and Mid-parent heterosis, respectively; DTF= days to 50% flowering; PH= plant height at maturity; NOF= number of fruits per plot; LNT= fruit length; FWT= fruit circumference; PL= Pedicel length; INL= internodal length; NOS= number of seeds per pod; THS= 1000-seed weight; NOR= number of ridges per pod.

Significant positive percentage for BPH and MPH were also obtained for NH47-4 × Clemson (23.27 and 13.13%) and LD88 × Iwo Nla (42.55 and 29.76%) while NH47-4 × Clemson, IK11 × Clemson, LD88 × Clemson, LD88 × Iwo Nla and Clemson × Iwo Nla displayed significant positive (desirable) BHP and MPH for 1000-seed weight.

The tester vector view of the genotype × NoF-trait (GYT) biplot showing associations among the NoF-trait combinations is presented in figure 1. Since all NoF-trait combinations have NoF as a component, positive correlation was observed between all possible pairs. There was correspondence between the GYT biplot and Pearson correlation (Table 6) among the traits. Positive correlation was recorded between NoS and THS while INL associated negatively with

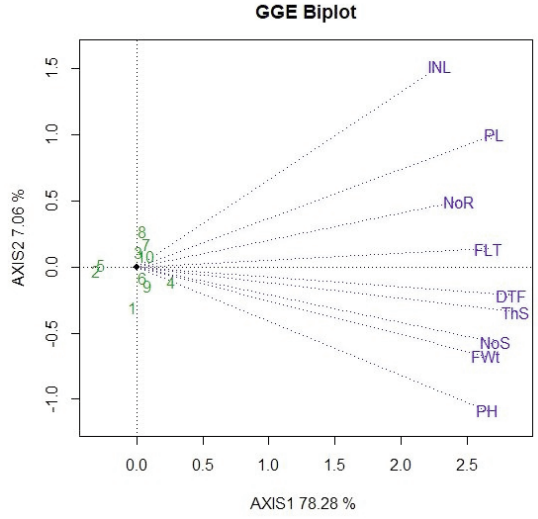

Fig. 1 - The tester vector view of the genotype by NoF x trait (GYT) biplot showing associations among the NoF x trait combinations.

Fig. 2 - The polygon view of the genotype by NoE x trait (GYT) biplot to identify genotypes with outstanding trait profiles.

NoS and THS (Table 6). The GYT biplot, shows the magnitude of angles among INL, NoS, and THS while figure 2 is the polygon view of the GYT biplot displayed in figure 1.

Hybrid was the vertex cultivar for the sector containing all the NoF-trait combinations except INL while LD88 × Clemson, NH47-4 × Clemson, IK11× Iwo Nla, and Clemson × Iwo Nla were associated with the polygon sector containing INL. The superiority ranks of the hybrids based on their NoF-trait combinations is shown in figure 3. Hybrid NH47-4 × Iwo Nla was the farthest above average from the origin, followed by LD88 × Iwo Nla and Clemson × Iwo Nla while NH47-4 × LD88 was the farthest below average performance across NoF-trait combination. The shortest vector lengths were observed for IK11 × LD88, NH47-4 ×

Table 6 - Pearson correlation coefficients among pairs of traits of okra hybrids

	PH	NOF	LNT	FWT	PL	INL	NOS	THS	NOR
DTF	0.52 *	-0.01	-0.09	0.18	0.02	0.32	0.18	-0.13	0.46
PH		0.09	-0.23	0.09	-0.23	0.52 *	0.58 *	-0.01	0.37
NOF			0.57*	-0.17	0.32	-0.17	0.35	0.37	-0.27
LNT				-0.58 *	0.71 **	-0.37	0.09	0.21	0
FWT					-0.42	0.05	0.11	0.27	-0.04
PL						-0.55*	0.08	0.16	0.34
INT							-0.2	-0.28	0.12
NOS								0.29	0.31
THS									-0.01

* and ** significant at p ≤ 0.05 and p ≤ 0.01 respectively; DTF, days to 50% flowering; PH, plant height at maturity; NOF, number of fruits per plot; LNT, fruit length; FWT, fruit circumference; PL, Pedicel length; INL, internodal length; NOS, number of seeds per pod; THS, 1000-seed weight; NOR, number of ridges per pod.

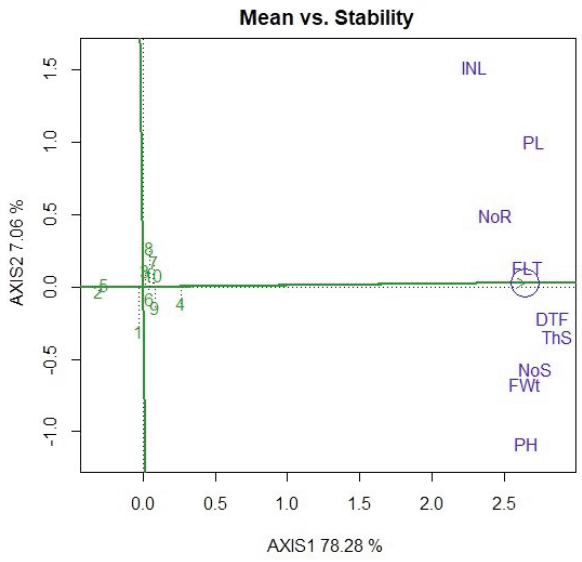

Fig. 3 - The average tester coordination view of the genotype by NoF x trait (GYT) biplot ranking the hybrids based on overall superiority and their strengths and weaknesses.

LD88 (below-average performers) and NH47-4 × Iwo Nla and IK11 × Clemson (above-average performers).

4. Discussion and Conclusions

The significant genotype mean squares observed for all traits is an indication of sufficient genetic variation among the genotypes for measured traits and this shows the feasibility of improving these traits through selection. Wammanda *et al*. (2010) observed similar level of genotypic variability for DTF, PH, NoF, INL, LNT and FWT in okra. The significant GCA and SCA mean squares for most measured traits indicates that both additive and non-additive gene actions were important in the inheritance of these traits. The proportion of total variation accounted for by SCA was larger than that of GCA for all the traits except 1000-seed weight thus indicating that 1000-seed weight is majorly controlled by additive gene action. Having most of the traits controlled by additive and non-additive gene effects implies that substantial breeding progress could be made using breeding methods such as backcrossing and heterosis breeding techniques which exploit the two modes of gene action. This supports the work of Reddy *et al*. (2012) on the preponderance of non-additive gene action for several traits of okra.

The significant negative GCA effects for DTF observed for Clemson and Iwo Nla implied that these genotypes could possess useful genes for improvement of earliness in okra while Iwo Nla with significant positive GCA effect for NoF might be a good donor for genes associated with increased number of fruits and seeds. In the same vein, Clemson and Iwo Nla, with significant negative GCA for INL could be useful in developing new okra breeding lines with short internode and enhanced branching thereby improving yield. This result agress Atanu and Sabesan (2009) who reported significant GCA effects for DTF, NoF, NoR, LNT and FWT through diallel crosses in okra.

The significant and desirable SCA effects (negative for DTF and INL) observed for most measured traits among the 10 hybrids suggests the presence of favourable gene combinations for most horticultural traits of interest in this study. Thus, NH47-4 × LD88, NH47-4 × Clemson, and IK11 × LD88 with significant and negative SCA effects for DTF contains favourable gene combinations for earliness while NH47-4 × IK11, NH47-4 × Clemson, and LD88 × Iwo Nla might be harbouring gene combination associated with seed-increasing effects. Majority of the hybrids except NH47-4 × LD88 and IK11 × Iwo Nla have gene combinations in favour of LNT, FWT and 1000-seed weight. The above mentioned sets of hybrids could be deployed for heterosis breeding in favour of associated horticultural traits such as earliness and increased number of seeds. Furthermore, they can be intercrossed and advanced to generate breeding populations with a large gene pool that might be useful in identification and selection of new promising segregants. Similar results have been reported for okra by Oyetunde and Ariyo (2015), Reddy *et al.* (2012) and Anyaoha *et al.* (2021).

Significant and negative MPH and BPH is desired for DTF and INL improvement of earliness and increased number of branches respectively. The significant and negative BPH and MPH observed for these traits in hybrids: NH47-4 × LD88, NH47-4 × Clemson, IK11 × LD88, IK11 × Iwo Nla, LD88 × Clemson and LD88 × Iwo Nla could be exploited through heterosis breeding. Khanorkar and Kathiria (2010) and Prakash *et al*. (2019) reported similar findings for number of days to flowering in okra.

Selecting okra genotypes with tall plant architecture and short INL might lead to increased number of pods per plant in this study. Although none of the hybrids possessed desirable heterosis for PH and INL, a cross between IK11 × Clemson with significant positive MPH for PH, and IK11 ×LD88, IK11×Iwo Nla, LD88

× Clemson, and LD88 × Iwo Nla with significant and negative MPH and BPH for INL might produce tall multiple hybrids with short INL. Hybrid combinations NH47-4 × Clemson, IK11 × Iwo Nla and LD88 × Iwo Nla and IK11 × Clemson, LD88 × Clemson and Clemson × Iwo Nla displayed significant and positive BPH and MPH respectively for seed-increasing traits NoS, 1000-seed weight and NoR. It looka apparent from the findings of this study that high heterotic effects for measured traits might be due to the dominance nature of genes controlling considered traits. Reddy *et al*. (2012) explained that heterobeltiosis of more than 20% could offset the cost of hybrid seed. Thus, hybrids NH47-4 × Clemson and LD88 × Iwo Nla with BPH of 23.27% and 42.55% respectively for NoS could be useful resources to exploit heterosis for okra hybrid seed production. However, with the exception of NH47-4 × IK11, NH47-4 × LD88, and IK11 × LD88, majority of the hybrids exhibited the potential for use to enhance NoF per plant in okra.

The GYT biplot (Yan and Frégeau-Reid, 2018) used in this study allows genotype evaluation by graphically ranking genotypes based on their level in combining major traits of interest (such as increased number of fruits per plant) with other target traits. The single-arrow line passing through the biplot origin and the average yield-trait combination is called the average tester axis (ATA). The arrow points towards the higher genotype mean values across all NoF-trait combinations and serves the purpose of ranking genotypes based on superiority. The double-arrow line perpendicular to the ATA separates genotypes better than average (on the same side as the ATA arrow) from those poorer than average (on the opposite side of the ATA) and also indicates how balanced the trait profile of a genotype is as well as its strengths and/or weaknesses in terms of adaptation to specific traits. Genotypes placed close to ATA (with short projections to the double-arrowed line) have balanced trait profiles whereas those placed away from the ATA in either direction have obvious strengths and/or weaknesses. The polygon view of the biplot allowed visualization of the trait profiles of the hybrids such that the genotypes placed on a vertex had the largest values for the NoF-trait combinations placed within the corresponding sector.

Hybrid NH47-4 × Iwo Nla had the highest values for NoF-trait combinations indicating that they are top performers in combining NoF with the respective traits. On the other hand, LD88 × Clemson, NH47-4 × Clemson, IK11 × Iwo Nla, and Clemson × Iwo Nla had the highest values for INL showing that these hybrids were the best in combining NoF with the respective traits INL.

The ranking of the hybrids based on the NoF-trait combinations was as followed: NH47-4 × Iwo Nla> LD88 × Iwo Nla> Clemson × Iwo Nla ≥ IK11 × Iwo Nla> LD88 × Clemson> IK11 × Clemson > NH47-4 × Clemson > NH47-4 × IK11> IK11 × LD88> NH47-4 × LD88. The short vector lengths of the hybrids IK11 × LD88, NH47-4 × LD88, NH47-4 × Iwo Nla and IK11 × Clemson implied that these hybrids were the most stable across the various trait combinations.

In conclusion, the pooled analysis of variances successfully identified the extent of genetic variability among parents and hybrids. High significant differences among parents, crosses and parents vs. crosses for most traits indicated sufficient level of variability among the genotypes. The parental genotypes, Clemson and Iwo Nla, are promising sources of genes for earliness while Iwo Nla was promising as a gene donor towards improvement of NoS. The new promising hybrid combinations NH47-4 × LD88, NH47-4 × Clemson and IK11 × LD88 identified from this study could be exploited towards creating early maturing hybrid okra varieties while NH47-4 × Clemson, IK11 × Clemson, IK11 × Iwo Nla, LD88 × Clemson were identified as hybrids with useful heterotic patterns for seed-increasing traits. Promising hybrids NH47-4 × Iwo Nla and IK11 × Clemson that were stable and above-average for NoF-trait combinations and ranked high by the GYT biplot might be useful for okra genetic improvement programmes targeting increased number of fruit per plant over seasons in the region.

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