

Combining ability studies and potential for oil quality improvement in sesame (*Sesamum indicum* L.)

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Abstract

Five distinct accessions of sesame were employed in a diallel mating to study combining abilities and assess potentials for seeds oil quality improvement. Specific combining ability (SCA) mean square values were greater than general combining ability (GCA) for most traits indicating the preponderance of non-additive gene action except for 1000-seed weight. PACH was the best general combiner for number of pods per plant, number of seeds per pod, number of seeds per plant, seed oil and protein contents (%). Cross S530xPACH exhibited good combination for 1000-seed weight, seed weight per plant, seed oil and protein contents (%). Cross 65-8B x PACH had the highest significant positive mid and better parent heterosis for seeds per plant, primary branches, plant height while cross S530 x PACH for 1000-seed weight and seed oil (%). Seeds of cross 65-8BxPACH showed exceptional high level of linoleic acid (52.08%) and unsaturated fatty acids (94.45%), suggesting the possibility of developing superior cultivars with improved oil quality through selection in segregating population.

Keywords: Sesame, diallel mating, heterosis, fatty acids, linoleic acid

1. Introduction

In Nigeria, sesame is widely used and very popular in parts of the central, North Western and North Eastern Zones where it is usually grown [1]. It is an important ancient oilseed crop whose oil is characterized for its stability and quality. Sesame contains about 50-60% seed oil [2,3] with superior quality comparable to olive oil. The stability of its oil has been attributed to the presence of antioxidant like sesamin, sesaminol, sesamol, sesamolinol and squalene [4].

Despite the nutritional value and oil quality of sesame seeds, research on this important crop plant has been scarce [5], especially in Nigeria where funding was generally poor. Nigeria is one of the largest exporters of sesame seeds in the world and it occupied the 6th position in 2000 as the major

producer [6]. This position was maintained in 2004 but in 2007, Nigeria dropped to the 7th position as the major producer after countries like India, Myanmar, China, Sudan, Uganda and Ethiopia [7].

General combining ability (GCA) is the result of the average behavior of lineages when crossed with each other while specific combining ability (SCA) represents the behavior of two individuals in a number of hybrid combinations [8]. The concept of a combining ability analysis gives precise estimates of the nature and magnitude of gene actions involved in the inheritance of quantitative characters. This facilitates identification of parents with good general combining ability effects and crosses with good specific combining ability effects [9,10]. The knowledge of combining ability and type of gene action controlling the expressions of different

characters would help in selecting the most suitable breeding procedure [10] for proper planning of a successful breeding programme [11].

The exploitation of hybrid vigour is one of the methods used in plant breeding to bring about cultivars development with high yielding potential. Although sesame is largely self-pollinated, high levels of heterosis have been reported for certain hybrid combinations from various countries. In some cases, the yields of F₁ hybrids being considerably higher than those of the better parents have been reported [12,13].

Like in many other crops, the magnitude of heterosis in sesame is related to the degree of genetic divergence of the parents. In previous studies, significant negative relative heterosis, heterobeltiosis and standard heterosis for days to 50% flowering (less days to flowering) in three crosses and significant positive heterosis for number of primary branches per plant have been reported [14]. Also, there have been reports on significant positive heterosis for plant height [15, 14]. However, reports on combining ability and heterosis in sesame are very scanty in Nigeria since there is very little breeding effort on the crop.

The objectives of the present investigation were to identify (1) parents with best general combining ability, (2) crosses with specific combining ability and heterosis for seed yield and oil quality with a view to incorporate them in breeding programme for further improvement.

2. Method of analysis

Five morphologically diverse sesame genotypes namely S530, PACH, 69B-882, 65-8B and C-K2 were crossed in diallel mating design to produce F₁ crosses. Detailed information on these parent plant germplasm identities and places of collection were already reported in our previous work [16]. Seeds of five successful F₁ along with their parents were grown in a randomized complete block design with three replications on the demonstration farm at the back of the Department of Pure and Applied Biology, Ladoke Akintola University of Technology Ogbomoso, Oyo State, Nigeria. It is located on latitude 80°N and longitude 4°E, characterized by both wet and dry seasons with monthly mean temperature of 28°C. Each of the

accessions and crosses was represented by a single row of two meters, plant to plant distance of 0.4m and row to row spacing of 0.5m.

Observations were made on five randomly selected plants of each cross and parents for twelve traits i.e. plant height at maturity (PHM), height to first pod (HFP), number of branches per plant (NPB), number of pods per plant (NPP), length of pod (LOP), 1000 – seed weight (TSW), length of fruiting nodes (LFN), number of seeds per pod (NSP), number of seeds per plant (SPP) and seed weight per plant (SWP), percentage oil content (POC) and protein content (PPC) of the seeds (%). Diallel analysis was carried out to estimate general combining ability (GCA) among parents and specific combining ability (SCA) among the five successful crosses by following and adapting Griffing's [17] Model 1, Method 2, using SAS program [18] since this study includes F₁s without reciprocals. Heterosis demonstrated by the crosses for various traits considered was estimated using the following formulae [19];

$$\begin{aligned} \text{Mid Parent Heterosis (MPH)} &= (F_1 - MP) * 100 / MP \\ \text{Better Parent Heterosis (BPH)} &= (F_1 - BP) * 100 / BP \end{aligned}$$

Where

F₁ = First filial generation value
MP = mid-parental value
BP = better parent value.

The heterosis estimates were tested for significance using student t-tests, taking five individual values as units of observation. The fatty acids composition of seed oil of the five parent accessions and their crosses were determined using GC-MS analytical method [16].

3. Results

Analysis of variance for combining ability (Table 1) revealed that mean squares due to general combining ability (GCA) and Specific combining ability (SCA) were significant for all the traits studied in the F₁ except mean squares due to NPP. It was also observed that the mean square for the GCA was generally lower than the mean square due to SCA for all the traits studied except for TSW and SWP. The ratio of GCA mean square to SCA mean square was more than unity for TSW and SWP while those obtained for other characters were below unity.

Estimates of GCA effects for the twelve characters evaluated in the five parents are presented in Table 2. Parent PACH had significant positive GCA effects for most characters evaluated except for NPB. Parent 69B – 882 had significant positive GCA effects for only eight of the traits evaluated, GCA effects was negative for POC while it was positive but not significant for NPB, LFN and NPP. Significant positive GCA was also recorded for eight of the traits in parent 65 – 8B, NPB had significant negative GCA, NPP had negative but not significant GCA while the GCA effects for SWP was positive but also not significant. Parent S530 recorded significant positive GCA effect for only NPB, positive and significant for LNF while GCA effects were significant negative for other traits evaluated. The GCA effect in parent C – K2 was only significant positive for NPB.

Estimates of SCA effects for the twelve characters evaluated in the five parents are as shown in Table 3. Cross 65-8B x 69B-882 had significant positive SCA effects for nine characters, crosses S530 x PACH, 65-8B x C-K2 and 65-8B x PACH had significant positive SCA effects for eight characters each while cross 69B-882 x PACH showed significant positive SCA effects for only six of the characters. Cross S530 x PACH showed good combination for POC, PPC, TSW and SWP, cross 65-8B x C-K2 for NSP, LOP and LFN, cross 65-8B x 69B-882 for PHM, HFP and SPP while cross 69B – 882 x PACH showed good combination for NPB and NPP. However, none of the crosses showed combination of SCA effects for all the desirable traits simultaneously.

The results of mid and better parents heterosis for the crosses employed in this study are shown in Table 4.

The five crosses recorded both positive and negative mid and better parents heterosis for the twelve traits evaluated. Very high positive heterosis was obtained for the characters measured except for LFN, NPP and SWP which were mostly negative. The highest mid and better parents positive heterosis were recorded for NPB (266.67% and 83.33 respectively) in 65-8B x PACH, followed by HFP (139.10 mid-parent; 109.21 better parent) in 65-8B x 69B-882 and TSW (72.69 mid-parent; 22.59 better parent) in

S530 x PACH. Crosses 65-8B x PACH had significant positive heterosis for nine out of the characters studied, followed by 65-8B x 69B-882 for seven characters and S530 x PACH for five characters. Cross 65-8B x PACH had the highest significant positive better parent heterosis for NSP, NPB and PHM, S530 x PACH was best for TSW and POC while 65-8B x C-K2 was best for LOP and 65-8B x 69B-882 the best for PPC.

Fatty acids profile of the five parents along with their crosses (Table 5) revealed five principal fatty acids. Palmitic (PAL) and stearic (STE) acids ranged from 2.15% and 3.13% in 65-8B x PACH to 8.79% and 9.56% respectively in PACH while Oleic (OLE) acids varied from 33.13% in C-K2 to 40.84% in 65-8B x 69B-882. Linoleic (LIN) acid ranged from 42.20% to 52.08% with the lowest value occurring in PACH and the highest in 65-8B x PACH while Linolenic (LIL) varied from 0% in PACH to 9.39% in S530. The highest oil content was observed in S530 x PACH (57.58%) and the lowest in S530 (53.20%) while the highest level of unsaturated fatty acids was obtained in 65-8B x PACH (94.45%) and the lowest in PACH (79.81%). Cross 65-8B x PACH had the best oil quality with the highest level of linoleic acid (52.08%) and unsaturated fatty acids (UFA = 94.45%), followed by 65-8B x 69B-882 and 69B-882 x PACH with 91.17%.

4. Discussion

In breeding programmes, Griffing's method of diallel analysis has proven to be very useful in the identification of parents for hybrid combinations. The present investigation has revealed that the ratio of GCA to SCA mean squares was less than unity for all the traits studied except for TSW and SWP. This is indicative of the predominance of non-additive gene action for most traits, suggesting the possibility of exploiting heterosis breeding for their improvement. However, TSW and SWP were under additive gene action and can be improved effectively by any methods of pure line breeding.

In related works on sesame, non-additive gene actions were reported for NPP [20, 21], PHM [22, 23, 24,20] while additive gene action was reported for PHM by Preveenkumar et al. [21]. Non-additive gene action had also been recorded for NPB [20], LOP [21, 25], and SPP [21].

Table 1. Estimates of the mean squares of general and specific combining abilities for twelve traits assessed in sesame parent accessions and its F1 crosses

Characters	Mean sum of squares		
	GCA	SCA	GCA/SCA
PHM	1410.42**	2806.36**	0.50
HFP	682.50**	890.04**	0.77
NPB	7.49**	18.62**	0.40
LFN	503.51**	858.88**	0.66
NPP	109.94ns	298.33**	0.37
LOP	1.58**	1.85**	0.85
SPP	653.26**	929.25**	0.70
TSW	3.70**	2.62**	1.41
SWP	11.10**	7.39**	1.50
NSP	429926.59*	820669.42**	0.52
POC	466.91**	836.05**	0.56
PPC	51.75**	90.57**	0.57

GCA = General combining ability; SCA = Specific combining ability

PHM = Plant height at first fruit(s) maturity; HFP = Height to first pod; NPB = Number of primary branches; LFN = Length of the fruiting nodes, NPP = Number of pods per plant; LOP = Length of pods; SPP = Number of seeds per pod; TSW = 1000-seed weight; NSP = Number of seeds per plant; POC = Percentage oil content; PPC = Percentage protein content.

Table 2. General combining ability (GCA) effects for vegetative and yield attributes in five parent accessions of sesame

Parents	Characters											
	PHM	HFP	NPB	LFN	NPP	LOP	NSP	TSW	SWP	SPP	POC	PPC
S530	-15.37**	-16.24**	0.75*	0.87**	-4.61*	-0.50**	-10.86**	-0.84**	-1.57**	-312.95*	-8.21**	-2.24**
65-8B	13.33**	10.07**	-0.62*	3.26*	-1.15**	0.44**	10.20**	0.70**	0.41**	2.34**	8.07**	2.52**
C-K2	-14.96**	-0.78**	1.18**	-14.18**	-1.67**	-0.52**	-9.77**	-0.73**	-1.07**	-172.97**	-7.96**	-3.26**
PACH	11.92**	3.38*	-1.39**	8.54**	5.93**	0.20**	6.14**	0.53**	0.95**	262.74*	8.42**	2.74**
69B-882	5.08*	3.57*	0.07**	1.52**	1.50**	0.38**	4.28**	0.33**	1.28**	220.85*	-0.32**	0.25**
S.E. (gi)±	1.83	1.49	0.28	1.63	1.87	0.01	0.56	0.04	0.30	102.89	0.05	0.05
S.E. (gj ± gj)	2.90	2.35	0.44	2.57	2.95	0.02	0.88	0.06	0.47	162.69	0.08	0.07

PHM = Plant height at first fruit(s) maturity; HFP = Height to first pod; NPB = Number of primary branches; LFN = Length of the fruiting nodes, NPP = Number of pods per plant; LOP = Length of pods; SPP = Number of seeds per pod; TSW = 1000-seed weight; NSP = Number of seeds per plant; POC = Percentage oil content; PPC = Percentage protein content.

Table 3. Specific combining ability (SCA) effects for vegetative and yield attributes five successful crosses studied

Crosses	Characters											
	PHM	HFP	NPB	LFN	NPP	LOP	NSP	TSW	SWP	SPP	POC	PPC
S530 x PACH	15.61**	10.54*	-2.35**	5.07**	-0.87**	1.07**	22.87**	2.19**	1.75*	125.70**	20.46**	6.79**
65 – 8B x C – K2	33.17**	18.99**	1.05**	14.18**	1.08**	1.11**	26.62**	1.12**	0.92**	232.50**	18.54**	4.96**
65 – 8B x PACH	20.84**	9.50*	1.22**	11.34*	0.28**	0.36**	11.17**	0.26*	1.09**	249.50**	3.45**	2.78**
65 – 8B x 69B - 882	35.59**	42.00**	1.96*	-6.41**	1.50**	0.72**	22.71**	1.15**	1.68*	286.20**	10.67**	6.14**
69B – 882 x PACH	13.01*	10.85*	4.33**	2.16**	5.42**	0.01**	7.53**	-0.74**	-1.47**	285.30**	10.71**	3.45**
S.E. (Sij)±	4.73	3.84	0.72	4.20	4.82	0.03	1.44	0.10	0.77	265.67	0.13	0.12
S.E. (Sij ± Ski)	7.10	5.76	1.08	6.30	7.23	0.05	2.16	0.15	1.15	398.50	0.20	0.18

PHM = Plant height at first fruit(s) maturity; HFP = Height to first pod; NPB = Number of primary branches; LFN = Length of the fruiting nodes, NPP = Number of pods per plant; LOP = Length of pods; SPP = Number of seeds per pod; TSW = 1000-seed weight; NSP = Number of seeds per plant; POC = Percentage oil content; PPC = Percentage protein content.

Table 4. Estimates of percentage heterosis based on mid-parent values (MP), and better-parent values (BP) for characters measured on five crosses

F ₁ Progenies	Plant height (cm)		Height of first capsule (cm)		No of primary branches		length of the fruiting nodes (cm)	
	MP	BP	MP	BP	MP	BP	MP	BP
S530 x PACH	-22.22±2.94**	-25.22±2.83**	-11.88± 7.43	-27.25±6.13*	-100.00±0.00	-100.00±0.00	-27.87±3.93**	-38.74±3.34**
65 – 8B x C – K2	11.12±3.55*	1.53±3.24	25.19±1.61**	-7.42±1.19**	-23.33±17.95	-57.41±9.97**	-7.10±9.81	-25.03±7.92*
65 – 8B x PACH	27.61±5.42**	16.45±4.95*	51.02±12.14*	31.93±10.61*	266.67±169.97	83.33±84.98	10.18±18.07	3.99±17.05
65 – 8B x 69B - 882	28.61±3.13**	11.94±2.72*	139.10±5.75**	109.21±5.03**	69.23±43.17	10.00±28.06	-45.31±2.96**	-52.57±2.57**
69B – 882 x PACH	8.41±10.89	2.87±10.34	27.58±14.10	27.34±14.08	30.00±46.37	-35.00±23.18	-5.53±22.61	-13.68±20.66
F ₁ Progenies	No of capsules per plant		Capsule length (cm)		1000-seed weight (g)		No of seeds per capsule	
	MP	BP	MP	BP	MP	BP	MP	BP
S530 x PACH	-45.35±14.27*	-51.50±12.66*	16.98±4.06*	14.81±3.98*	72.69±3.37**	22.59±2.39**	17.71±4.83*	15.78±4.75*
65 – 8B x C – K2	-46.42±10.02**	-59.43±7.58**	28.04±1.14**	17.09±1.05**	19.09±1.35**	-0.95±1.12	36.96±1.09**	35.80±1.08**
65 – 8B x PACH	-22.33±9.82	-40.00±7.58**	22.62±1.81**	15.81±1.71**	10.87±5.71	10.52±5.69	39.33±1.94**	39.12±1.93**
65 – 8B x 69B - 882	-27.78±7.40*	-41.90±5.95**	7.95±1.32**	-11.89±1.08**	15.64±2.54**	2.33±2.25	35.55±1.75**	17.81±1.52**
69B – 882 x PACH	-31.93±24.91	-35.50±23.60	-22.49±3.56**	-39.46±2.78**	-36.77±9.20*	-43.74±8.18**	-21.49±7.70*	-31.85±6.68**
F ₁ Progenies	Seed yield per plant (g)		No of seeds per plant		Percentage oil content		Percentage protein content	
	MP	BP	MP	BP	MP	BP	MP	BP
S530 x PACH	5.64±31.86	-27.63±21.82	-32.20±21.25	-37.94±19.45	6.32±0.32**	4.46±0.35**	9.27±1.05**	3.85±1.09*
65 – 8B x C – K2	-8.60±17.54	-19.28±15.49	-26.97±13.55	-44.34±10.32*	0.85±0.18**	0.84±0.14**	-1.06±0.77	-1.88±0.50*
65 – 8B x PACH	20.96±22.08	-6.14±17.13	9.03±13.51	-14.00±10.66	3.15±0.33**	3.13±0.33**	21.43±0.75**	19.76±0.93**
65 – 8B x 69B - 882	7.50±11.40	-26.12±7.84*	-5.25±9.81	-30.41±7.20*	1.36±0.39*	0.41±0.21	24.77±1.26**	21.25±0.85**
69B – 882 x PACH	-60.13±18.70*	-66.54±15.69*	-44.76±19.46	-49.96±17.63*	2.06±0.21**	1.09±0.20**	8.58±0.70**	6.96±0.65**

* Standard error used to determine whether each estimate is significantly greater than zero (with D.F. = 4)

Table 5. Fatty acid profile of the total lipids in the oil of five sesame parent accessions and their crosses

Fatty Acids	S530	65-8B	C-K2	PACH	69B-882	S530xPACH	65-8BxPACH	65-8x69B-882	65-8BxC-K2	69B-882xPACH
CAP x 10 ⁻⁴	0.20g	2.72c	3.45b	0.54e	0.31f	-	1.41d	0.32f	5.69a	0.31f
LAU x 10 ⁻⁴	0.25i	2.08c	3.91b	0.53e	0.34g	1.14d	0.21h	0.42f	6.43a	0.31h
MYR	0.95b	0.63b	1.26b	1.83a	1.16b	0.81b	0.26c	0.24c	2.07a	1.02b
PAL	4.06h	7.65d	5.06f	8.79a	8.28c	6.47e	2.15i	2.66g	8.35b	4.24g
PAT x 10 ⁻⁴	3.86i	25.31c	49.49b	6.62f	4.51g	15.81d	2.11j	8.06e	81.68a	3.92h
STE	4.49f	4.88e	4.38g	9.56a	5.06d	7.27b	3.13h	5.96c	7.24b	4.48f
OLE	35.28f	36.21e	33.13h	37.61c	36.82d	38.99b	33.22h	40.84a	33.24h	35.15g
LIN	45.87d	46.79c	48.85b	42.20i	42.41h	43.48g	52.08a	45.08e	43.78f	45.88d
LIL	9.39a	3.86h	7.31d	-	6.28e	3.48i	9.15c	5.25g	5.31f	9.24b
ARA x 10 ⁻⁴	1.66e	1.83d	21.51b	0.40h	0.55g	0.60e	0.25i	2.46c	35.51a	1.60f
BEH x 10 ⁻⁴	-	-	-	-	-	-	-	1.61	-	-
LIG x 10 ⁻⁴	0.13a	-	1.42b	0.29d	0.14e	-	0.11f	1.24c	2.35a	0.11f
POC (%)	53.20	55.09	55.08	55.12	54.07	57.58	56.84	55.32	55.34	55.42
UFA (%)	90.54	86.86	89.30	79.81	85.51	85.95	94.45	91.17	82.34	90.27
SFA (%)	9.46	13.14	10.70	20.19	14.49	14.05	5.55	8.83	17.66	9.73
UFA/SFA	9.57	6.61	8.35	3.95	5.90	6.12	17.02	10.33	4.66	9.28

Fatty acid means on the same row followed by different letters are significantly different at 0.05 probability level according to Duncan Multiple Range test.

CAP = Capric acid; LAU = Lauric acid; MYR = Myristic acid; PAL = Palmitic acid; PAT = Palmitoleic acid; STE = Stearic acid; OLE = Oleic acid; LIN = Linoleic acid; LIL = Linolenic acid; ARA = Arachidic acid; BEH = Behenic acid; LIG = Lignoceric acid; POC = Percentage oil content; UFA = % Unsaturated fatty acids; SFA = % Saturated fatty acids; S/UF = Ratio of saturated to unsaturated fatty acids.

On the contrary, additive gene effect was recorded for LOP [26] while both additive and non-additive gene actions were recorded for this same trait by Singh [27].

TSW had been reported to be governed by additive gene effect [24,27,28], which is also similar to the finding in the present work. However, the work of Preveen Kumar et al. [21] is at variance to this report on TSW as it was discovered to be governed by non-additive gene action. According to Kavitha et al. [29] and Preveen Kumar et al. [21], POC was influenced by non-additive gene effect but in another study [30], additive component was recorded for this same trait. Seed yield was observed in this study to be governed by additive gene interaction contrary to the findings of Ragiba & Reddy [22], Manivaran and Ganesan [31], Krishnah et al. [32], Mothilal and Manoharan [23], Vidhyavathi et al. [24], Thiyagu et al. [20] and Preveen Kumar et al. [21]. In another report however, both additive and non-additive gene action were recorded for seed yield [33,27].

Estimates of GCA effects for traits studied in five parents have revealed that none had good general combining ability for all the traits. Nevertheless, parents' 65-8B and 69B-882 are good general combiner for four of the characters each while S530 was the lowest general combiner. Since none of the parents showed desirable combining ability for majority of the component characters, multiple crosses involving more than two parents would be an appropriate technique to be employed in the development of hybrids and or selection of superior recombinants in the segregating generation [11].

Estimates of the SCA effects have shown that S530 x PACH exhibited maximum and significant seed yield along with significant positive SCA effects for PHM, LOP, NSP, TSW, POC and PPC. Cross 65-8B x 69B-882 also exhibited high SCA effect for seed yield along with significant positive SCA effects for PHM, LOP, NSP, TSW, POC and PPC. Four of the five crosses except 69B-882 x PACH were involved more frequently in the crosses exhibiting significant

positive SCA effects and therefore should be exploited as high yielding hybrids.

On heterosis, crosses such as 65-8B x PACH and 65-8B x 69B-882 expressed significant positive mid and better parents' heterosis for PHM which is in agreement with the report of the earlier workers [34, 14, 35, 36]. Crosses S530 x PACH, 65-8B x C-K2 and 65-8B x PACH revealed significant positive mid and better parents heterosis for LOP whereas, only S530 x PACH showed significant positive heterosis for TSW while heterosis for NSP was also significantly positive in four crosses. Mothilal and Ganesan [35], Padmasundai and Kamala [36] reported significant positive heterosis for TSW and NSP.

Significant positive mid and better parents' heterosis were observed for percentage oil and protein contents. Moreover, on the basis of mid and better parents heterosis, cross 65-8B x PACH showed combination of favourable heterosis for plant height, length of pod, number of seeds per pod, percentage oil and protein content while S530 x PACH combined favourable heterosis for plant height at maturity, height of first pod, length of fruiting nodes, length of pods, 1000-seed weight, number of seeds per pod, percentage oil and protein contents. Simultaneously, these two crosses were also observed to be good specific combiners for most desirable traits.

Of interest is the cross 65-8BxPACH which exhibited tremendous improvement in oil quality based on high level of linoleic acid and percentage of unsaturated fatty acids. The beneficial effect of sesame oil in lowering the cholesterol levels and hypertension [37,38], and its potential in reducing the incidence of certain cancers [39,40] have been reported. This health benefits of sesame oil hinged on the linoleic acid constituent, a fatty acid that is essential to human and has been shown to be tremendously improved in this report. Therefore, advance selection for lines with superior oil quality in the segregating population of cross 65-8BxPACH of sesame is currently being pursued for development into newly improved cultivar.

4. Conclusion

This study has shown that parents 65-8B and 69B-882 are good general combiners and the crosses S530 x PACH and 65-8B x PACH are good specific combiners. These two crosses have been shown to combine heterosis for favourable characters through diallel mating. Generally, the parents involved in these crosses identified as promising were low x high, medium x low and medium x high general combiners for seed yield and other characters. In addition, Cross 65-8BxPACH has been identified to have shown high level of linoleic acid with high percentage of unsaturated fatty acids. This cross is presently being advanced into higher generation with a view to select superior lines for oil quality through recurrent selection.

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