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Estimation of combining ability and heterosis by using diallel mating design in *Kabuli* genotypes of chickpea

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Abstract

An experiment consisting of six parents and 15 hybrids (developed by using 6 x 6 half diallel mating design) in kabuli chickpea was laid out in RBD design with three replications to estimate combining ability and heterosis. The ANOVA (Analysis of Variance) for different characters revealed highly significant differences among genotypes for all traits under study. The estimates of SCA variance were found to be higher than the GCA variance for all the characters under consideration, indicating good prospects for exploitation of non-additive gene action for grain yield and its components under study. Estimates of the ratio of *gca* variances to the *sca* variances for all the characters is less than one indicating the preponderance of non-additive gene effects (dominance and epistasis) in controlling the expression of all the characters under study. Line KAK2 was identified as good general combiner for plant height, canopy width, number of secondary branches per plant, number of pods per plant, pod length, grain yield per plant, biological yield per plant, 100 seed weight and harvest index. High estimates of heterosis over better parent, mid parent and standard check was exhibited by three crosses viz., PKC1 × HK4, KAK2 × HK4 and JGK1 × HK4.

Keywords: Chickpea, kabuli, diallel, GCA, SCA and heterosis

Introduction

Chickpea (*Cicer arietinum* L.) with 2n = 2x = 16 stands as third most important food legume among the essential sustenance legumes grown worldwide after dry bean and dry pea. Chickpea is said to be one of the first grain legumes domesticated by humans in the old world (Van der Maesen, 1972)^[9]. It belongs to the family Fabaceae and sub family Faboideae and is only cultivated species of the genus Cicer. Chickpea is classified into two distinct types: the desi type with pink flowers, anthocyanin pigmentation on stems small, angular, dark coloured seeds and the kabuli type with large, white flowers, lacking anthocyanin pigmentation on stems, smooth coated, beige seeds. This classification overlaps, to a particular extent, with the macrosperma and microsperma races proposed by (Moreno and Cubero, 1978)^[6] utilizing quantitative as well as qualitative characters. Information on genetic frameworks governing the inheritance of traits, combining ability and hybrid vigour helps not just in the identification of superior parents for breeding programmes but also helps in the identification of potential crosses for further exploitation. For a successful breeding programme, it is also a pre-requisite to evaluate nature of gene action implicated in expression of the various agronomical vital traits and determining the potentiality of the parents in hybrid combinations. In this respect, the information of combining ability is rather important in identifying the parents for their utilization in crop improvement programme. It additionally gives essential and fundamental information concerning nature of gene action that governs expression of the character being referred to and thus helps in deciding upon the future breeding strategy. Heterosis breeding in crop plants has been the best approach among different specialized choices accessible to the geneticists and plant breeders for improvement of productivity in crop plants. This phenomenon though not completely understood genetically up until now, has yet empowered the plant researchers to enhance the performance of several economic traits. Heterosis in chickpea has been perceived as a method for improving yield and other critical traits. The extent of heterosis especially for yield is of ultimate significance, and if the heterosis is of high magnitude, it can accomplish high productivity and in this manner high yield levels.

Material and Methods

The present investigation was undertaken with six Kabuli chickpea genotypes (PG071, PKC1, KAK2, JGK1, GNG1969 and HK4) which were crossed in a half diallel fashion to produce fifteen F₁'sduring rabi season 2014-15 and were evaluated in the following year during rabi season 2015-16 in a Randomized Complete Block Design with three replication. Observations were recorded for days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, Plant canopy width, Pod length, number of seeds per pod, 100 seed weight, Harvest index (%), grain yield per plant and biological yield per plant. The combining ability analysis for parental genotypes and their crosses were carried out following method 2 and model I (fixed effect model) of Griffing (1956) [3]. Heterosis was computed for each character as suggested by Hayes et al. (1955)^[4] and Fonseca and Paterson (1968)^[2]. For testing the significance of heterosis, the method proposed by Panse and Sukhatme (1961)^[8] were followed.

Results and Discussion

The analysis of variance showed highly significant differences among the parents for each of the thirteen characters, showing the presence of sufficient genetic variation in all the six parents and their F1's under the study (Table 1). The analysis of variance for combining ability indicated that mean squares due to GCA and SCA were significant for all the characters studied (Table 2). This highlighted the importance of both additive and non-additive gene action for the expression of the traits. The magnitude of the non-additive (SCA) variance was found to be higher than additive (GCA) variance for all the characters studied (Table 2). Estimates of the ratio of GCAvariances to the SCA variances for all the characters is less than one indicating the preponderance of non-additive gene effects (dominance and epistasis) in controlling the expression of all the characters under study. These results were in agreement with the findings of Pandey and Tiwari (1985)^[7]; Ambadabade et al. (2014); Jadhav and Gawande (2016)^[5].

The overall estimates of GCAeffects revealed (Table 3) that none of the parent was good general combiner for all the attributes studied. However, parental line KAK2 was identified as good general combiner for plant height, canopy width, number of secondary branches per plant, number of pods per plant, pod length, grain yield per plant, biological yield per plant, 100 seed weight and harvest index. Parental line PKC1 appeared as good general combiner for days to maturity, number of primary branches per plant, number of pods per plant and pod length; KAK2 for plant height, canopy width, number of secondary branches per plant, number of pods per plant, pod length, grain yield per plant ,biological yield per plant 100 seed weight and harvest index; JGK1for days to 50 % flowering, days to maturity; GNG1969 for days to 50% flowering, number of primary branches per plant, number of secondary branches per plant, number of pods per plant and number of seeds per pod .Parent HK4 was found to be a good general combiner for pod length, grain yield per plant, biological yield per plant,100 seed weight and harvest index.

Thus among the parental lines, KAK2 can be ranked as the best parent as it had a good general combining ability for maximum number (9) of yield attributes including grain yield per plant. Parent PG071 had good GCAfor maximum number (8) of yield attributes after KAK2 followed by HK4, which showed good GCAfor 5 yield attributes

None of the crosses was found having significantSCA effects for all the traits. Significant positive or negative SCA effects were observed in F_1 generation for yield and various yield attributing traits. Cross PG071 × PKC1 was identified as the best cross for canopy width, number of pods per plant and number of seeds per pod, as per SCA effect and *per se* performance. The cross PKC1 × HK4 had highest SCA effect and *per se* performance for days to maturity, pod length, grain yield per plant and harvest index. Cross KAK2 × GNG1969 was identified as best cross for number of secondary branches per plant based on highest SCA effect and *per se* performance.

Heterosis

The percentage of heterosis over mid parent (relative heterosis), better parent (heterobeltiosis) and standard check variety (standard heterosis) were estimated for all the 15 hybrids for thirteen biometrical characters and were presented in (Table 4). The results of heterosis for yield per plant indicated that, high estimates of heterosis over better parent, mid parent and standard check was exhibited by three crosses PKC1 × HK4, KAK2 × HK4 and JGK1 × HK4. The cross KAK2 × HK4 also expressed significant heterosis for plant height, number of secondary branches, number of pods per plant, number of seeds per pod and 100 seed weight over all the three parents. HK4 for canopy width, number of secondary branches, pod length, grain yield per plant, 100 seed weight and harvest index.

Character	Mean sum squares			бĘ	CV (0/)
Character	Replication	Treatment	Error	5. E	CV (70)
Degree of freedom	01	20	20		
Days to 50 % flowering	0.21	34.78**	1.41	0.84	1.60
Days to maturity	2.38	166.42**	2.73	1.16	1.17
Plant height (cm)	10.78	125.63**	6.15	1.75	7.99
Canopy width (cm)	0.11	18.39**	0.40	0.44	3.26
Number of primary branches per plant	0.02	0.63**	0.04	0.15	7.28
Number of secondary branches per plant	0.07	0.77**	0.07	0.19	8.48
Number of pods per plant	2.16	90.65**	2.29	1.07	4.68
Pod length (cm)	0.03	10.58**	0.37	0.43	2.83
Number of seeds per pod	0.02	0.03**	0.007	0.06	8.03
Grain yield per plant (g)	2.62	4.01**	0.83	0.64	10.47
Biological yield per plant (g)	6.16	82.77**	13.21	2.57	12.48
100 seed weight (g)	0.97	34.58**	0.53	0.51	2.82
Harvest index (%)	5.32	73.11**	6.32	1.77	7.98

Table 1: Analysis of variance for thirteen characters in chickpea

** Significant at 1% level of probability, * significant at 5% level of probability

	Table 2: Analysi	is of v	variance fo	r combining	ability for	or different	characters
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Character.	Mean sum s	quares Source of va	riation			
Character	GCA	SCA	Error	σ ² gca	σ ² sca	σ²gca/σ²sca
Degree of Freedom	5	15	20			-
Days to 50 % flowering	44.74**	31.46**	1.41	1.66	30.05	0.06
Days to maturity	218.24**	149.14**	2.73	8.64	146.41	0.06
Plant height (cm)	150.90**	117.20**	6.15	4.21	111.05	0.04
Canopy width (cm)	29.25**	14.77**	0.40	1.81	14.37	0.13
Number of primary branches per plant	1.01**	0.86**	0.66	0.01	0.81	0.01
Number of secondary branches per plant	2.03**	1.65**	0.07	0.04	1.57	0.03
Number of pods per plant	131.20**	77.12**	2.29	6.76	74.83	0.09
Pod length (cm)	12.32**	10.00**	0.37	0.29	9.64	0.03
Number of seeds per pod	0.04**	0.03**	0.007	0.0006	0.03	0.02
Grain yield per plant (g)	4.824**	3.74**	0.83	0.13	2.92	0.05
Biological yield per plant (g)	95.10**	78.66**	13.21	2.05	65.45	0.03
100 seed weight (g)	38.04**	33.43**	0.53	0.58	32.90	0.02
Harvest index (%)	87.99**	68.15**	6.32	2.48	61.83	0.04

** Significant at 1% level of probability * significant at 5% level of probability δ^2_{gca} = variance of GCA δ^2_{sca} = Variance of SCA

Table 3: Summary	table for g	general combining	ability of	parents of	chickpea
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	Characters													
Parents	Days to 50 % flowering	Days to maturity	Plant height (cm)	Canopy width (cm)	Number of primary branches per plant	Number of secondary branches per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	Grain yield per plant(g)	Biological yield per plant(g)	100 seed weight(g)	Harvest index (%)	Overall good
PG071	Α	Р	G	G	G	А	G	G	А	G	G	Р	G	08
PKC1	Р	G	Α	Р	G	Р	G	G	А	Р	А	Р	А	04
KAK2	А	Р	G	G	А	G	G	G	А	G	G	G	G	09
JGK1	G	G	Р	Р	Р	А	Р	Р	Р	Р	Р	Р	Р	02
GNG1969	G	Р	Α	Р	G	G	G	Α	G	А	А	Р	Р	05
HK4	Р	Р	Α	Р	А	Р	Р	G	А	G	G	G	G	05

Table 4: Percentage increase or decrease of the F1 over mid parent (relative heterosis), better parent (heterobeltiosis) and standard parent (economic heterosis)

	Days to 50 % flowering			Days to maturity			Plant height (cm)			Canopy width (cm)			
Crosses	He	eterosis o	ver	Н	eterosis o	ver	Heterosis over			He	eterosis o	ver	
CIUSSES	Mid	Better	Standard	Mid	Better	Standard	Mid	Better	Standard	Mid	Better	Standard	
	parent	parent	parent	parent	parent	parent	parent	parent	parent	parent	parent	parent	
PG071 x PKC	1.97	-2.51*	-2.51**	8.34**	0.68**	12.74**	16.28**	12.20**	19.32**	25.06**	8.35**	2.56**	
PG071 x KAK2	-5.92**	-10.06**	-10.06**	4.91**	-0.68**	11.19**	-8.54*	-11.27**	-5.64**	-12.28**	-14.62**	-14.62**	
PG071 x JGK-1	10.79**	6.20**	-3.14**	13.19**	2.06	14.28**	-49.23**	-58.22**	-55.57**	35.44**	7.30**	1.58*	
PG071x GNG1969	-1.92	-13.33**	-13.33**	-4.56*	-5.05**	7.41**	-12.89**	-14.45**	-5.64	-8.36**	-16.49**	-20.94**	
PG071 x HK4	6.08**	3.97**	-1.25**	-6.27**	-6.75**	5.48**	15.30**	2.91	9.44**	-10.95**	-21.08**	-25.29**	
PKC1 x KAK2	-12.57**	-12.57**	-12.57**	20.07**	17.76**	17.76**	-33.47**	-33.85**	-33.85**	-27.18**	-38.33**	-38.33**	
PKC1 x JGK-1	-8.21**	-7.58**	-15.72**	8.71**	5.22**	1.15	-29.46**	-40.22**	-40.90**	13.15**	1.70*	-29.44**	
PKC1x GNG1969	5.08**	-2.51*	-2.51**	9.96**	1.70	15.05**	-13.82**	-18.28**	-9.87**	7.65**	1.77*	-20.75**	
PKC1 x HK4	-5.16**	-7.54**	-7.54**	-7.89**	-14.81**	-3.62*	12.76**	3.99	2.82	-9.57**	-11.89**	-35.57**	
KAK2 x JGK-1	-3.42**	-11.32**	-11.32**	20.32**	14.28**	14.28**	28.09**	8.03**	8.03**	-3.81**	-25.29**	-25.29**	
KAK2x GNG1969	-0.33	-7.54**	-7.54**	7.24**	1.02	14.28**	-36.01**	-39.00**	-32.72**	-32.66**	-40.11**	-40.11**	
KAK2 x HK4	1.29	-1.25	-1.25	5.43**	-0.68	12.35**	26.51**	16.07**	16.07**	-16.21**	-27.47**	-27.47**	
JGK-1x GNG1969	7.80**	6.61**	-8.80**	4.56*	-6.14**	6.17**	-8.30*	-25.60**	-17.94**	18.10**	1.01	-21.34**	
JGK-1 x HK4	7.74**	1.32	-3.77**	6.46**	-4.43*	8.10**	-37.34**	-42.90**	-52.32**	22.46**	7.56**	-21.34**	
GNG1969 x HK4	7.31**	1.98	-3.14*	-3.07	-3.07	9.65**	-26.20**	-35.16**	-28.49**	0.52	-2.53**	-24.11**	

**Significant at 1% level of probability *significant at 5% level of probability

	Number	of primary per plant	y branches	Num brai	Number of secondary branches per plant			Number of pods per plant			Pod length (cm)			
Crosses	I	Heterosis ov	ver	Heterosis over			Heterosis over			Heterosis over				
	Mid	Better	Standard	Mid	Better	Standard	Mid	Better	Standard	Mid	Better	Standard		
	parent	parent	parent	parent	parent	parent	parent	parent	parent	parent	parent	parent		
PG071 x PKC	24.19**	16.66**	6.94**	-15.06**	-27.05**	-16.21**	43.98**	20.48**	42.04**	5.84**	4.24**	2.07**		
PG071 x KAK2	-10.14**	-13.88**	-13.88**	-33.33**	-37.64**	-28.37**	-7.82**	-14.81**	0.42	-6.30**	-7.27**	-7.27**		
PG071 x JGK-1	-20**	-27.27**	-33.33**	-30.88**	-44.70**	-36.48**	-29.21**	-39.34**	-28.49**	-14.90**	-20.59**	-22.24**		
PG071x GNG1969	26.56**	22.72**	12.5**	18.98**	10.58**	27.02**	22.38**	8.19**	27.55**	7.20**	-2.12**	-4.15**		
PG071 x HK4	9.83**	1.51**	-6.944**	-46.85**	-55.29**	-48.64**	-36.68**	-47.50**	-38.11**	-20.74**	-25.90**	-27.44**		
PKC1 x KAK2	-9.23**	-18.05**	-18.05**	-22.96**	-29.72**	-29.72**	14.01**	2.27	2.27	-7.22**	-7.64**	-9.56**		
PKC1 x JGK-1	-3.57**	-6.89**	-25**	8.92**	0	-17.56**	12.22**	9.06**	-8.23**	-4.02**	-13.72**	-13.72**		
PKC1x GNG1969	-10**	-12.90**	-25**	-32.83**	-38.35**	-39.18**	3.80	-2.58	-11.78**	10.90**	2.67**	-2.49**		
PKC1 x HK4	3.50**	1.72**	-18.05**	-27.73**	-29.50**	-41.89**	18.69**	17.35**	-6.81**	15.17**	9.23**	3.74**		

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KAK2 x JGK-1	-39.68**	-47.22**	-47.22**	-12.00**	-25.67**	-25.67**	-28.25**	-33.94**	-33.94**	-7.98**	-10.46**	-14.96**
KAK2x GNG1969	7.46**	0	0	55.10**	54.05**	54.05**	15.84**	10.36**	10.36**	10.57**	2.12**	0
KAK2 x HK4	4.68**	-6.94**	-6.94**	31.81**	17.56**	17.56**	41.07**	25.28**	25.28**	-20.51**	-26.40**	-26.40**
JGK-1x GNG1969	-12.06**	-17.74**	-29.16**	17.74**	0	-1.35**	-28.44**	-30.98**	-37.5**	-8.65**	-10.78**	-24.32**
JGK-1 x HK4	-10.90**	-9.25**	-31.94**	-13.76**	-18.96**	-36.48**	4.68*	0.62	-15.34**	10.30**	10.08**	-6.23**
GNG1969 x HK4	27.11**	20.96**	4.16**	25.19**	12.32**	10.81**	26.02**	17.01**	5.96**	7.92**	5.19**	-10.39**

	Number	Number of seeds per pod			Grain yield per plant (g)		Biological yield per plant (g)		100 seed weight (g)			Harvest index (%)			
Crosses	He	eterosis o	over	H	eterosis o	ver	H	eterosis o	ver	He	terosis o	ver	He	terosis o	ver
	Mid	Better	Standard	Mid	Better	Standard	Mid	Better	Standard	Mid	Better	Standard	Mid	Better	Standard
PG071 x PKC	33.33**	27.27**	27.27**	6.49**	-5.20**	-24.42**	6.45	-12.75**	-26.85**	1.57	- 11.94**	-16.23**	-14.33**	-18.72**	-42.50**
PG071 x KAK2	-9.09**	-9.09**	-9.09**	-11.79**	-20.73**	-20.73**	- 31.79**	-37.30**	-37.30**	-1.16	-3.57**	-3.57**	-30.02**	-40.26**	-40.26**
PG071 x JGK-1	-9.09**	-9.09**	-9.09**	16.32**	-1.15	-21.19**	- 16.92**	-34.20**	-44.83**	-21.68**	- 30.37**	-33.76**	5.89	-4.74	-32.62**
PG071x GNG1969	21.73**	16.66**	27.27**	12.69**	5.20**	-16.12**	- 36.69**	-39.13**	-48.96**	-40.90**	- 43.17**	-45.94**	3.57	0	-29.26**
PG071 x HK4	-4.76**	-9.09**	-9.09**	-33.16**	-39.43**	-40.55**	- 28.99**	-32.63**	-37.05**	-35.00**	- 36.18**	-37.01**	-25.61**	-30.43**	-43.47**
PKC1 x KAK2	-4.76**	-9.09**	-9.09**	3.40**	-16.12**	-16.12**	-3.79	-26.12**	-26.12**	-2.10**	- 16.88**	-16.88**	-16.03**	-31.36**	-31.36**
PKC1 x JGK-1	-4.76**	-9.09**	-9.09**	45.31**	37.77**	-14.28**	50.23**	43.76**	-22.96**	18.05**	14.69**	-15.09**	19.60**	13.03**	-28.22**
PKC1x GNG1969	9.09**	0	9.09**	5.96**	0.66	-30.41**	- 18.77**	-31.27**	-46.80**	1.33	-9.05**	-20.12**	25.63**	23.38**	-18.75**
PKC1 x HK4	10**	10**	0	32.18**	7.98**	5.99**	25.95**	-0.910	-7.41*	23.69**	5.59**	4.22**	51.85**	35.25**	9.89**
KAK2 x JGK-1	-9.09**	-9.09**	-9.09**	-1.77**	-23.50**	-23.50**	- 13.05**	-35.23**	-35.23**	-0.55	-13.47*	-13.47**	-8.29*	-28.22**	-28.22**
KAK2x GNG1969	- 13.04**	- 16.66**	-9.09**	12.26**	-5.02**	-5.06**	21.36**	7.65*	7.65*	-17.71**	- 22.72**	-22.72**	-7.52*	-23.31**	-23.31**
KAK2 x HK4	14.28**	9.09**	9.09**	6.23**	5.25**	5.25**	- 35.17**	-37.30**	-37.30**	2.61**	1.94*	1.94*	-15.27**	-23.22**	-23.22**
JGK-1x GNG1969	- 13.04**	- 16.66**	-9.09**	20.29**	8.66**	-24.88**	20.76**	-1.41	-23.69**	15.34**	6.28**	-6.65**	-0.89	-7.90**	-39.35**
JGK-1 x HK4	-4.76**	-9.09**	-9.09**	32.69**	4.03**	2.11**	- 23.54**	-41.74**	-45.56**	9.39**	-4.27**	-5.51**	53.52**	30.16**	5.75**
GNG1969 x HK4	18.18**	8.33**	18.18**	-5.78**	-19.71**	-21.19**	- 11.52**	-19.11**	-24.42**	-17.84**	- 22.36**	-23.37**	-14.65**	-22.74**	-37.23**

**Significant at 1% level of probability *significant at 5% level of probability

Table 5: Heterotic cr	rosses for variou	s characters
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S. No.	Character	Promising parents (per se)	Good general combiners (gca)	Promising cross (per se)	Good specific crosses (sca)	Heterotic crosses (over mid, better and standard parent)
1	Days to 50 % flowering	JGK1, GNG1969	GNG1969, JGK-1	PKC1 × JGK1	PKC1 × KAK2, PG071 × GNG1969, PKC1 × HK4, PKC1 × JGK-1	PKC1 × JGK1, PKC1 × KAK2 PKC1 × HK4
2	Days to maturity	JGK 1, PKC 1	JGK-1, PKC1	$PKC1 \times HK4$	PKC1 × HK4, PG071 × GNG1969, PG071 × HK4	$PKC1 \times HK4$
3	Plant height (cm)	GNG1969, PG071	PG071,KAK2	$\begin{array}{c} \text{PG071} \times \text{PKC1, KAK2} \times \\ \text{HK4} \end{array}$	KAK2 × JGK1, KAK2 × HK4, PG071 × PKC1, PG071 × HK4	PG071 × PKC1, KAK2 × JGK1, KAK2 × HK4
4	Canopy width (cm)	KAK 2, PG071	PG071, KAK2	$PG071 \times PKC1$	PG071 × PKC1, PG071 × JGK-1, JGK-1 × HK4, JGK-1 × GNG1969	PG071 × PKC1, PG071 × JGK1
5	Number of primary branches per plant	KAK 2, PG071	PG071, PKC1	$PG071 \times GNG1969$	PG071 × PKC1, PG071 × GNG1969, GNG1969 × HK4	PG071 × PKC1, PG071 × GNG1969, GNG1969 × HK4
6	Number of secondary branches per plant	PG071, GNG1969	GNG1969, KAK2	KAK2 × GNG1969	KAK2 × GNG1969, KAK2 × HK4 PG071 × GNG1969	KAK2 × GNG1969, PG071 × GNG1969, KAK2 × HK4
7	Number of pods per plant	PG071, KAK 2	PG071,GNG1969,KAK2	PG071 × PKC1 KAK2 × HK4	PG071 × PKC1, PG071 × GNG1969, GNG1969 × HK4, JGK-1 × HK4, KAK2 × HK4	PG071 × GNG1969, PG071 × PKC1, KAK2 × HK4, GNG1969 × HK4
8	Pod length (cm)	KAK2, PG071	PKC1,KAK2, PG071	PKC1 × HK4	JGK1 × HK4, PKC1 × HK4, KAK2 × GNG1969, PG071 × PKC1,	PKC1 × HK4, PG071 × PKC1
9	Number of seeds per pod	GNG1969	GNG1969	PG071 × GNG1969, PG071 × PKC1, KAK2 × HK4, GNG1969 × HK4	PG071 × PKC1, PG071 × GNG1969, KAK2 × HK4, GNG1969 × HK4	PG071 × PKC1, PG071 × GNG1969, KAK2 × HK4, GNG1969 × HK4
10	Grain yield per plant (g)	KAK2, HK4	KAK2, HK4, PG071	PKC1 × HK4, KAK2 × HK4	PKC1 × HK4, JGK1 × HK4, KAK2 × HK4, PKC1 × JGK-1	PKC1 × HK4, KAK2 × HK4JGK1 × HK4
11	Biological yield per plant (g)	КАК2, НК4	KAK2, PG071, HK4	KAK2 × GNG1969, PKC1 × HK4	PKC1 × HK4, PKC1 × JGK1, KAK2 × GNG1969, JGK-1 × GNG1969	KAK2 × GNG1969
12	100 seed weight (g)	KAK 2, HK4	KAK2, HK4	$\begin{array}{c} \text{KAK2} \times \text{HK4, PKC1} \times \\ \text{HK4,} \end{array}$	JGK1 \times GNG1969, PKC1 \times HK4, GNG1969 \times HK4, KAK2 \times HK4	$PKC1 \times HK4, KAK2 \times HK4$
13	Harvest index (%)	KAK 2, HK4	PG071, HK4, KAK2	PKC1 × HK4, JGK1 × HK4	PKC1 × HK4, JGK1 × HK4, PKC1 × GNG1969, PG071 × GNG1969	PKC1 × HK4, JGK1 × HK4

Conclusion

Thus it is concluded that among six parents taken for diallel analysis, KAK2 was considered as best parent of yield attributes including grain yield per plant followed by parental line PG071 that showed good GCA for eight yield attributes. These promising parents for various traits could be utilized in future breeding programmes in order to create large genetic variability and to isolate true breeding lines with desirable combination of yield attributes. Among crosses, PKC1 x JGK1 (P x G) and PKC1 x HK4 (G x P) were identified as outstanding crosses for days to flowering and days to maturity, respectively. These crosses can be exploited for isolating early maturity lines. Three crosses viz. PKC1 x HK4 (P x G), KAK2 x HK4 (G x G) and JGK1 x HK4 (P x G) showed significantly high mean performance, good SCA effects and heterosis over mid, better and check parents for grain yield per plant. These crosses were also found superior for other yield components traits. Promising cross combinations based on mean performance, SCA effects and heterosis can be exploited for isolating superior recombinants in the advanced generations. On the basis of cross combinations showing highest heterosis in desired direction and best SCA estimates for most of the characters, it is evident that crosses showing high extent of heterosis have high SCA estimates. This indicated that manifestation of heterosis depends upon SCA estimates. Hence, these crosses could be utilized in future breeding programme.

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