



## Research Article

# HETEROSIS AND INBREEDING DEPRESSION FOR GRAIN YIELD ATTRIBUTING TRAITS IN COWPEA

(*Vigna unguiculata* (L.) Walp.)

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**Abstract:** The present investigation was conducted at Pulse & Castor Research Station, Navsari Agricultural University, Navsari during *kharif* - 2020 with a view to study the heterosis and inbreeding depression in four crosses (each having P1, P2, F1, F2, BC1 and BC2 generations) of cow pea through a compact family block design with three replications. The analysis of variance between crosses revealed that the mean square due to crosses were significant for all the characters except for days to flowering in cross NCK-13-07 x NCK-15-09 and grain yield per plant in cross NCK-13-11 x GC-3. For grain yield and its attributes, positive and highly significant relative heterosis, heterobeltiosis and inbreeding depression were found for all the crosses. Significant positive heterosis for grain yield per plant and its related traits followed by significant inbreeding depression indicated major role of non-additive gene actions in the inheritance of grain yield per plant and its attributes. For grain yield per plant only cross III (NCK-13-11 x NCK-15-09) exhibited positive and highly significant relative heterosis as well as heterobeltiosis, which also showed significant heterosis for days to flowering, plant height, pods per plant and pod length. So, these characters should be given due consideration while improving yield.

**Keywords:** Heterosis, Inbreeding depression, Cowpea

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## Introduction

Pulses are extremely important source of plant protein (20 to 30 %) for the poorest of the world's poor and play a significant role in restoring and enriching soil fertility by fixing atmospheric nitrogen. Pulses contain in their grains nearly about three times the amount of storage proteins found in cereals.

Cowpea [*Vigna unguiculata* (L) Walp.] is diploid with chromosome number of 2n=22 is one of the oldest sources of human food. It belongs to the order *Fabales*, family *Fabaceae*, subfamily *Faboideae*, tribe *Phaseoleae*, subtribe *Phaseolinae* and genus *Vigna*. All cultivated cowpeas are grouped under *V. unguiculata* subspecies *unguiculata*, which is subdivided into four major groups, i.e. *Unguiculata*, *Biflora*, *Sesquipedalis* and *Textilis* [1,2]; Ng and Marechal [3]. Cowpea is a highly self pollinated because of cleistogamous nature of flower. Significant out crossing can occur in some environment, possibly associated with pollen transfer by bumblebees.

Cowpea is comparatively a cheaper source of quality protein, phosphorus, iron, vitamins and an excellent substitute for meat, eggs and other protein rich foods. Dry cowpea seeds are an important source of affordable protein (~25%), fiber (6.3%), low fat (1.9%), carbohydrate (63.6%), thiamine (0.00074%), riboflavin (0.00042%) and niacin (0.00281%). The protein found in cowpea seed is rich in the amino acids like lysine and tryptophan compared to cereal grains however; it is deficient in methionine and cysteine when compared to animal proteins. Therefore, cowpea seed is being valued as a nutritional supplement to cereals and an extender of animal proteins [4].

About two-thirds of the production and more than three-fourths of the area of production is spread over the vast Sudan Savannah and Sahelian zones of Sub-Saharan Africa. The major cowpea growing countries are Nigeria, Burkina Faso, Ghana, Kenya, Uganda, Malawi, Tanzania, India, Sri Lanka, Burma, Bangladesh,

Philippines, Indonesia, Thailand etc. In India it is mainly grown in Rajasthan, Gujarat, Maharashtra, Central India and some region of Southern India.

Information related to heterosis and inbreeding depression to identify potential crosses which can offer chances of isolating transgressive segregates is important in self-pollinated crops. In the present study an attempt was made to estimate the extent of heterosis for grain yield and yield attributes in cowpea. In addition, inbreeding depression was also estimated for yield and yield attributes. The relative ranking of most heterotic crosses for different characters was quite different with change, indicating appreciable influence of environment in the expression of various traits.

## Materials and Methods

The present investigation was carried out during *kharif*-2020, at College Pulse & Castor Research Station, Navsari Agricultural University, Navsari located at 22°57' N latitude and 72°54' E longitudes at an altitude of 11.98 m above the mean sea level. The crossing program was initiated during *kharif*-2018 to produce four F1 hybrids among four selected genotypes, while backcrossing and selfing of F1 was done in summer-2019 and *kharif*-2019 to obtain BC1, BC2 and F2 generations of respective crosses [Table-1]. Six generations (P1, P2, F1, F2, BC1 and BC2) of each of the four crosses were sown during *kharif*-2020 in compact family block design with three replications.

Each replication was divided in four compact blocks. Each four crosses consisting of six generations were randomly allotted to the blocks. Six generations of each cross were randomly allotted to each plot within a block. Each plot consisted of one line of parents and F1s, two lines of the backcrosses and four lines of the F2 generations of each cross.

Inter row spacing was 45 cm and intra row spacing was 10 cm. Recommended agronomic as well as plant protection measures were timely adopted for successful rising of the good crop.

The crossing work was started, when the crop commenced flowering, the buds of appropriate size are selected and emasculation was done during evening hours followed by pollination on next day morning.

Ten plants from each of the P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, 40 plants from F<sub>2</sub> were randomly selected per replication and observations were recorded on single plant basis. Protein content from dry seeds were determined by estimating the nitrogen content as per the Kjeldhal's method [5] and multiplying the nitrogen content with a factor 6.25 and expressed on per cent basis for each genotype.

Mean values obtained from the observations recorded on representative plants and samples for quantitative and biochemical characters for each entry in each family main and sub- plots were used for statistical computation.

## Results and Discussion

The manifestation of heterosis, heterobeltiosis and inbreeding depression are presented in [Table-2]. The results revealed significant positive and negative mid parent and better parent's heterosis in many crosses for different characters studied. The high values for heterotic effects also indicated that the parents used for the study were widely diverse.

The estimates of relative heterosis (RH) in four crosses ranged from -5.63 per cent (NCK-13-11 x NCK-15-09) to -1.34 per cent (NCK-13-11 x GC-3). As negative heterosis is desirable for days to flowering because this will make the hybrids to mature earlier as compared to parents. However, in this study only one cross (NCK-13-11 x NCK-15-09) depicted significant and negative relative heterosis as well as heterobeltiosis in desired direction. Two cross NCK-13-07 x GC-3 and NCK-13-11 x GC-3 showed significant and positive inbreeding depression. Similar results were reported by Rashwan, (2010) [6], Patel *et al.*, (2013b) [7], Nautiyal *et al.*, (2015) [8], Pandey and Singh [9] and Pathak *et al.*, (2017) [10].

A perusal of data presented in [Table-2] revealed that only one out of four crosses i.e. NCK-13-11 x GC-3 manifested significant negative relative heterosis (RH), which is desirable for days to maturity. Looking for inbreeding depression, it was found positive significant in crosses NCK-13-07 x NCK-15-09 (3.94 %) and NCK-13-11 x NCK-15-09 (3.79 %) which is desirable for days to maturity. As far as heterobeltiosis is concerned, the cross NCK-13-11 x GC-3 (-3.90%) depicted significant negative heterobeltiosis which was desirable for early maturity, while crosses NCK-13-07 x NCK-15-09 (3.97 %) and NCK-13-11 x NCK-15-09 (3.28 %) were showed significant heterosis in undesirable direction. Similar results were reported by Patel *et al.*, (2013b) [7], Nautiyal *et al.*, (2015) [8], Pandey and Singh [9], Pathak *et al.*, (2017) [10] and Gupta, *et al.*, (2020) [11].

The heterosis over mid parent and better parents in desired direction with respect to plant height was recorded by three hybrids viz., NCK-13-07 x GC-3, NCK-13-11 x NCK-15-09 and NCK-13-11 x GC-3. While cross NCK-13-07 x NCK-15-09 recorded heterosis as well as heterobeltiosis in negative direction. Significant heterosis in desirable directions were also reported by Pandey and Singh [9], Pathak *et al.*, (2017) [10], Gupta, *et al.*, (2020) [11], Usha Kumari, *et al.*, (2010) [12].

For pods per plant, the hybrids with positive heterosis directly contributes to the grain yield hence this trait would be highly desirable. In the present investigation, only one crosses (NCK-13-11 x NCK-15-09) recorded highly significant heterosis, rest crosses reported negative relative heterosis. While all the crosses showed significant negative heterobeltiosis for the clusters per plant. Significant inbreeding depression were found cross NCK-13-11 x NCK-15-09 and cross NCK-13-11 x GC-3. Positive significant heterosis results also reported by Rashwan (2010) [6], Patel, *et al.*, (2013b) [7], Pandey and Singh [9], Gupta, *et al.*, (2020) [11], Usha Kumari, *et al.*, (2010) [12], and Get, *et al.*, (2021) [13].

For pod length, two crosses NCK-13-11 x NCK-15-09 and NCK-13-11 x GC-3 showed highly significant heterosis as well as heterobeltiosis, while cross I and II (NCK-13-07 x NCK-15-09 and NCK-13-07 x GC-3) recorded negative significant heterosis and heterobeltiosis. Significant positive inbreeding depression were found in cross I and III (NCK-13-07 x NCK-15-09 and NCK-13-11 x NCK-15-09) and negative inbreeding depression in cross II (NCK-13-07 x GC-3). Positive

significant heterosis results for pod length also reported Patel, *et al.*, (2013b) [7], Get, *et al.*, (2021) [13] and by Patel, *et al.*, (2009) [14].

The grain yield is very complex trait. It is multiplicative end product of several basic components of yield. Many workers have reported wide range of variation in the expression of heterosis for grain yield. Three out of four crosses under this study depicted significant positive relative heterosis (NCK-13-07 x NCK-15-09, NCK-13-11 x NCK-15-09 and NCK-13-11 x GC-3) and significant heterobeltiosis was found only in cross III (NCK-13-11 x NAK-15-09). The crosses showed significant relative heterosis also showed significant inbreeding depression. Similar results were also reported by several earlier workers viz., Pathak, *et al.*, (2017) [10], Gupta, *et al.*, (2020) [11], Get, *et al.*, (2021) [13], Raut, *et al.*, (2017) [15], Risha, *et al.*, (2017) [16], Patel, *et al.*, (2013a) [17], Yadav, *et al.*, (2010) [18]. Two crosses (cross II and cross IV) exhibited the positive and highly significant relative heterosis and heterobeltiosis for protein content. While rests crosses were recorded negative heterosis and heterobeltiosis. Three crosses (cross I, cross II and cross III) showed positive and significant inbreeding depression for this trait, while cross IV recorded negative inbreeding depression so transgressive segregants might be help to select better genotypes for this character. Patel, *et al.*, (2009), Pathak, *et al.*, (2017) and Gupta, *et al.*, (2020) were also observed similar results.

Table-1 The F<sub>1</sub> hybrids were developed

Cross	Generation	Details
I	NCK-13-07(♀) × NCK-15-09(♂)	
	P <sub>1</sub>	NCK-13-07
	P <sub>2</sub>	NCK-15-09
	F <sub>1</sub>	(NCK-13-07 × NCK-15-09)
	F <sub>2</sub>	(NCK-13-07 × NCK-15-09) selfed
	BC <sub>1</sub>	(NCK-13-07 × NCK-15-09) × NCK-13-07
	BC <sub>2</sub>	(NCK-13-07 × NCK-15-09) × NCK-15-09
II	NCK-13-07(♀) × GC-3(♂)	
	P <sub>1</sub>	NCK-13-07
	P <sub>2</sub>	GC-3
	F <sub>1</sub>	(NCK-13-07 × GC-3)
	F <sub>2</sub>	(NCK-13-07 × GC-3) selfed
	BC <sub>1</sub>	(NCK-13-07 × GC-3) × NCK-13-07
	BC <sub>2</sub>	(NCK-13-07 × GC-3) × GC-3
III	NCK-13-11(♀) × NCK-15-09(♂)	
	P <sub>1</sub>	NCK-13-11
	P <sub>2</sub>	NCK-15-09
	F <sub>1</sub>	(NCK-13-11 × NCK-15-09)
	F <sub>2</sub>	(NCK-13-11 × NCK-15-09) selfed
	BC <sub>1</sub>	(NCK-13-11 × NCK-15-09) × NCK-13-11
	BC <sub>2</sub>	(NCK-13-11 × NCK-15-09) × NCK-15-09
IV	NCK-13-11(♀) × GC-3(♂)	
	P <sub>1</sub>	NCK-13-11
	P <sub>2</sub>	GC-3
	F <sub>1</sub>	(NCK-13-11 × GC-3)
	F <sub>2</sub>	(NCK-13-11 × GC-3) selfed
	BC <sub>1</sub>	(NCK-13-11 × GC-3) × NCK-13-11
	BC <sub>2</sub>	(NCK-13-11 × GC-3) × GC-3

## Conclusion

In general, heterosis followed by presence of inbreeding depression was observed in cross I (NCK-13-07 x NCK-15-09) for days to maturity and grain yield per plant; in cross II (NCK-13-07 x GC-3) for protein content; in cross III (NCK-13-11 x NCK-15-09) for days to maturity, pods per plant, pod length and grain yield per plant; in cross IV (NCK-13-11 x GC-3) for grain yield per plant indicated that positive and significant heterosis over mid-parent and better parent along with positive inbreeding depression may be attributed to major contribution from dominance (h) and additive x additive (i) gene effects and selection will be effective only in latter generations.

Table-2 Estimates of relative heterosis (R.H %), heterobeltiosis (H.B %) and inbreeding depression (I.D %) for days to flowering, days to maturity, plant height (cm), pods per plant, pod length (cm), grain yield per plant (g) and protein content (%) in four crosses of cowpea

Particulars	Days to flowering		Days to maturity		Plant height (cm)		Pods per plant		Pod length (cm)		Grain yield/plant (g)		Protein content (%)	
Cross I (NCK-13-07 x NCK-15-09)														
	Estimates	SE	Estimates	SE	Estimates	SE	Estimates	SE	Estimates	SE	Estimates	SE	Estimates	SE
RH %	-2.01	±0.48	2.95*	±0.85	-8.47**	±1.61	-42.29**	±0.61	-41.91**	±0.36	35.14**	±1.18	-2.03**	±0.06
HB %	-1.04	±0.55	3.97**	±0.93	-29.08**	±2.11	-65.16**	±1.00	-61.95**	±0.51	5.68	±1.38	-4.46**	±0.07
ID %	1.25	±0.49	3.94**	±0.87	-0.46	±1.60	-3.76	±0.45	12.68**	±0.37	35.11**	±1.15	5.14**	±0.06
Cross II (NCK-13-07 x GC-3)														
RH %	-2.28	±0.45	-2.47	±1.34	30.51**	±2.17	-11.78*	±0.92	-42.35**	±0.57	11.80	±1.46	14.49**	±0.10
HB %	-1.33	±0.50	-0.99	±1.45	11.05**	±2.86	-41.83**	±1.53	-61.41**	±0.73	-9.20	±1.97	1.25*	±0.15
ID %	2.52*	±0.40	-2.37	±1.33	4.25	±2.10	8.08	±0.63	-28.45**	±0.65	-4.78	±1.42	19.34**	±0.11
Cross III (NCK-13-11 x NCK-15-09)														
RH %	-5.63**	±0.43	3.20	±1.37	18.81**	±2.47	35.68**	±0.74	17.09**	±0.28	28.81**	±1.17	-17.78**	±0.04
HB %	-5.09**	±0.46	3.28**	±0.91	17.17**	±2.76	-7.66**	±0.92	14.34**	±0.30	26.32**	±1.39	-21.50**	±0.05
ID %	-0.32	±0.37	3.79**	±0.75	-1.70	±2.46	45.38**	±0.73	10.85**	±0.28	26.70**	±1.18	0.68*	±0.05
Cross IV (NCK-13-11 x GC-3)														
RH %	-1.34	±0.43	-4.92**	±1.21	8.72**	±1.24	-3.28	±0.49	13.38**	±0.32	8.95*	±1.30	11.56**	±0.12
HB %	0.09	±0.47	-3.90*	±1.33	5.03*	±1.69	-27.14**	±0.74	10.05**	±0.34	4.32	±1.48	6.89**	±0.12
ID %	2.42*	±0.89	0.44	±1.04	-1.98	±1.34	7.77**	±0.39	3.03	±0.32	8.63*	±1.20	-6.16**	±0.15

I: NCK-13-07 x NCK-15-09, II: NCK-13-07 x GC-3, III: NCK-13-11 x NCK-15-09, IV: NCK-13-11 x GC-3

Significant positive heterosis for grain yield per plant and its related traits followed by significant inbreeding depression indicated major role of non-additive gene actions in the inheritance of grain yield per plant and its attributes. These findings are similar to those of Yadav, *et al.*, (2010), Patel, *et al.*, (2013a), Nautiyal, *et al.*, (2015), Pathak, *et al.*, (2017) and Gupta, *et al.*, (2020).

Heterosis followed by absence of inbreeding depression were recorded in cross I (NCK-13-07 x NCK-15-09) for plant height and pods per plant; in cross II (NCK-13-07 x GC-3) for plant height and seeds per pod; in cross III (NCK-13-11 x NCK-15-09) for days to flowering, plant height and seeds per pod; in cross IV (NCK-13-11 x GC-3) for days to maturity, plant height and pod length indicated that absence of inbreeding depression and increase in performance of F<sub>2</sub> was accompanied by fixation of genes *i.e.*, additive gene action.

**Application of research:** Overall grain yield per plant only cross III (NCK-13-11 x NCK-15-09) exhibited positive and highly significant relative heterosis as well as heterobeltiosis, which also performed well for days to flowering, plant height, pods per plant and pod length. Thus, heterosis in grain yield was observed due to heterosis for component characters *viz.*, days to flowering, plant height, pods per plant and pod length which resulted in increased yield. So, these characters should be given due consideration while improving yield.

**Research Category:** Heterosis and Inbreeding

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**Author Contributions:** All authors equally contributed

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**Study area / Sample Collection:** College Pulse & Castor Research Station, Navsari

**Cultivar / Variety / Breed name:** Cowpea (*Vigna unguiculata* (L.) Walp.)

**Conflict of Interest:** None declared

**Ethical approval:** This article does not contain any studies with human participants or animals performed by any of the authors.

Ethical Committee Approval Number: Nil

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