

**GENETIC AND PHYSIOLOGICAL STUDIES FOR
SEED YIELD AND YIELD ATTRIBUTING TRAITS
IN COWPEA [*Vigna unguiculata* (L.) Walp.]**

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PALB-3055

**DEPARTMENT OF GENETICS AND PLANT BREEDING
UNIVERSITY OF AGRICULTURAL SCIENCES
GKVK, BENGALURU-560065**

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SEED YIELD AND YIELD ATTRIBUTING TRAITS
IN COWPEA [*Vigna unguiculata* (L.) Walp.]**

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Thesis submitted to the

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in partial fulfillment of the requirements for the award of the degree of

DOCTOR OF PHILOSOPHY

in

GENETICS AND PLANT BREEDING

BENGALURU

OCTOBER, 2016

**Affectionately
dedicated to my
parents, Family
and
Chinnu**

**DEPARTMENT OF GENTICS AND PLANT BREEDING
UNIVERSITY OF AGRICULTURAL SCIENCES
BENGALURU**

CERTIFICATE

This is to certify that the thesis entitled “Genetic and physiological studies for seed yield and yield attributing traits in cowpea [*Vigna unguiculata* (L.) Walp.]” submitted by **Mr. LOKESH, G, Y.**, for the degree of **DOCTOR OF PHILOSOPHY in GENETICS AND PLANT BREEDING** to the University of Agricultural Sciences, Bengaluru, is a record of research work done by him during the period of study in this university under my guidance and supervision and the thesis has not previously been formed the basis of the award of degree, diploma, associateship, fellowship or any other similar titles.

Bengaluru
25th October, 2016


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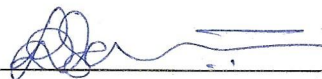


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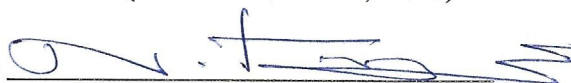
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(LOKESH, G. Y.)

Genetic and Physiological studies for seed yield and yield attributing traits in Cowpea [*Vigna unguiculata* (L.) Walp.]

LOKESH, G. Y.

ABSTRACT

Investigation was carried out in cowpea at Dry Land Agriculture Project, GKVK, UAS, Bangalore during 2008-2010 to study the variability and five generation mean analysis for days to first flowering, days to maturity, plant height, primary branches and secondary branches per plant, pods per plant, pod length, seeds per pod, seed yield per plant and test weight in three crosses of cowpea viz., IT-38956-1 $\times$ KBC-2, IT-38956-1 $\times$ CP-12 and KBC-2 $\times$ CP-12. In addition, the genetic variability parameters and character association studies for the two physiological traits viz., specific leaf area and spad chlorophyll meter reading were studied in the F_3 for the cross IT-38956-1 $\times$ KBC-2. The mean and variance in three F_2 populations of ten quantitative characters indicated wide variability for plant height, days to maturity, pod length, seeds per pod and seed yield per plant. Moderate to high GCV, PCV, genetic advance and heritability were observed for plant height, secondary branches per plant, pods per plant, seeds per pod and seed yield per plant in all three crosses. Significant and high positive correlation for seed yield per plant with secondary branches per plant, pods per plant, pod length and seeds per pod were observed in all three crosses. Five generation analysis in three crosses indicated non-additive gene action. Minimum number of effective factors ranged from one to five pairs. Potence ratio indicated the presence of over-dominance and partial dominance in maximum traits. SLA and SCMR has showed weak association with the seed yield.

October, 2016

Department of Genetics and Plant Breeding
UAS, GKVK, Bengaluru-65

Niranjana Murthy

Major Advisor

**“ಅಲಸಂದೆಯ ಜೀಜ ಮತ್ತು ಜೀಜದ ಗುಣಧರ್ಮಗಳ ಮೇಲೆ ಅನುವಂಶಿಕ ಮತ್ತು ಶಾರೀರಿಕ
ಪ್ರಭಾವಗಳ ಅಧ್ಯಯನ”**

ಲೋಕೇಶ್. ಜಿ. ವೈ

ಪ್ರಬಂಧ ಸಾರಂಶ

ಪ್ರಸ್ತುತ ಅಧ್ಯಯನವನ್ನು ಅಲಸಂದೆಯಲ್ಲಿ ವೃತ್ತಾಸ ವಿಶ್ಲೇಷಣೆ ಮತ್ತು ಐದನೇ ತಲೆಮಾರಿನ ಅಧ್ಯಯನವನ್ನು ಮೂರು ಸಂಕರಣಗಳಾದ ಐಟಿ-೩೮೯೫೬-೧ X ಕೆಬಿಸಿ-೨, ಐಟಿ-೩೮೯೫೬-೧ X ಸಿಪಿ-೧೨ ಮತ್ತು ಕೆಬಿಸಿ-೨ X ಸಿಪಿ-೧೨ ಗಳಲ್ಲಿ ವಿವಿಧ ಗುಣಲಕ್ಷಣಗಳಾದ ಗಿಡದಲ್ಲಿನ ಮೊದಲ ಹೂವು, ಗಿಡದ ಎತ್ತರ, ಮಾಗುವಿಕೆಯ ಅವಧಿ, ಗಿಡದ ಎತ್ತರ, ಪ್ರತಿ ಗಿಡದಲ್ಲಿನ ಪ್ರಾಥಮಿಕ ಗೋಂಚಲುಗಳು, ಪ್ರತಿ ಗಿಡದಲ್ಲಿನ ದ್ವಿತೀಯ ಗೋಂಚಲುಗಳು, ಪ್ರತಿ ಗಿಡದಲ್ಲಿನ ಕಾಯಿಗಳು, ಕಾಯಿಯ ಉದ್ದ, ಪ್ರತಿ ಕಾಯಿಯಲ್ಲಿನ ಬೀಜಗಳು, ಪ್ರತಿ ಗಿಡದ ಬೀಜದ ಇಳುವರಿ ಮತ್ತು ನೂರು ಬೀಜದ ತೂಕ ಇವುಗಳಲ್ಲಿ ಮತ್ತು ಐಟಿ-೩೮೯೫೬-೧ X ಕೆಬಿಸಿ-೨ ಸಂಕರಣದಲ್ಲಿ ಸಸ್ಯ ಶಾರೀರಿಕ ಗುಣಲಕ್ಷಣಗಳಾದ ಎಸ್.ಎಲ್.ಎ ಮತ್ತು ಎಸ್.ಸಿ.ಎಂ.ಅರ್ ಗಳಲ್ಲಿ ಪ್ರಸ್ತುತ ಅಧ್ಯಯನವನ್ನು ಒಣ ಬೇಸಾಯ ಸಂಶೋಧನಾ ಪ್ರಯೋಜನೆ ಕೃ.ವಿ.ವಿ., ಬೆಂಗಳೂರು ಪ್ರಾಯೋಗಿಕ ತಾಕುಗಳಲ್ಲಿ ೨೦೦೮-೨೦೧೦ ರ ಸಾಲಿನಲ್ಲಿ ಅಧ್ಯಯನವನ್ನು ಕೈಗೊಳ್ಳಲಾಯಿತು. ಗಿಡದ ಎತ್ತರ, ಮಾಗುವಿಕೆಯ ಅವಧಿ, ಕಾಯಿಯ ಉದ್ದ, ಪ್ರತಿ ಕಾಯಿಯಲ್ಲಿನ ಬೀಜಗಳು ಮತ್ತು ಪ್ರತಿ ಗಿಡದ ಇಳುವರಿ ಇ ಗುಣಲಕ್ಷಣಗಳು ವ್ಯಾಪಕ ಬಿನ್ನಾಭಿಪ್ರಾಯವನ್ನು ಎರಡನೆಯ ಪೀಳಿಗೆಯ ಮಧ್ಯಮ ಮತ್ತು ಪರಿಮಾಣಾತ್ಮಕ ವಿಶ್ಲೇಷಣೆಯಲ್ಲಿ ಕಂಡು ಬಂದಿದೆ. ಗುಣಲಕ್ಷಣಗಲ್ಲಿರುವ ವೈವಿಧ್ಯತೆಯನ್ನು ಸೂಚಿಸುವ ಪಿ.ಸಿ.ವಿ ಮತ್ತು ಜಿ.ಸಿ.ವಿ ಯು ಮಧ್ಯದಿಂದ ಹೆಚ್ಚು ವ್ಯಾಪ್ತಿಯ ಗಿಡದ ಎತ್ತರ, ದ್ವಿತೀಯ ಗೋಂಚಲುಗಳು ಪ್ರತಿ ಗಿಡದಲ್ಲಿ, ಪ್ರತಿ ಗಿಡಕ್ಕೆ ಕಾಯಿಗಳು, ಕಾಯಿಗಳ ಉದ್ದ ಮತ್ತು ನೂರು ಬೀಜದ ತೂಕ ಈ ಗುಣಲಕ್ಷಣಗಳಲ್ಲಿ ಕಂಡುಬಂದಿರುತ್ತದೆ. ದ್ವಿತೀಯ ಗೋಂಚಲುಗಳು ಪ್ರತಿ ಗಿಡದಲ್ಲಿ, ಪ್ರತಿ ಗಿಡಕ್ಕೆ ಕಾಯಿಗಳು, ಪ್ರತಿ ಕಾಯಿಗಳ ಉದ್ದ ಮತ್ತು ಪ್ರತಿ ಕಾಯಿಯಲ್ಲಿನ ಬೀಜಗಳು ಬೀಜದ ಇಳುವರಿಯ ಮೇಲೆ ಪರಸ್ಪರ ಮಹತ್ವ ಪೂರ್ಣ ಧನಾತ್ಮಕ ಸಂಬಂಧವನ್ನು ಎಲ್ಲಾ ಮೂರು ಸಂಕರಣಗಳಲ್ಲಿ ಹೊಂದಿವೆ. ಮೂರು ಸಂಕರಣಗಳ ಎರಡನೆಯ ತಲೆಮಾರಿನ ಐದು ಪೀಳಿಗೆಯ ವಿಶ್ಲೇಷಣೆಯಲ್ಲಿ ಅಲ್ಲದ-ಸಂಯೋಜನೆಯ ವಂಶವಾಹಿನಿಯ ಕ್ರಮವು ಎಲ್ಲಾ ಮೂರು ಸಂಕರಣಗಳಲ್ಲಿ ಕಂಡುಬಂದಿವೆ. ಎಲ್ಲಾ ಮೂರು ಸಂಕರಣಗಳಲ್ಲಿ ಕನಿಷ್ಠ ಒಂದರಿಂದ ಐದು ಪರಿಣಾಮಕಾರಿ ವಂಶವಾಹಿಗಳು ಪ್ರತಿ ಗಿಡದ ಬೀಜದ ಇಳುವರಿ ಮೇಲೆ ನಿಯಂತ್ರಣ ಹೊಂದಿದೆ. ಐಟಿ-೩೮೯೫೬-೧ X ಕೆಬಿಸಿ-೨ ಸಂಕರಣದಲ್ಲಿ ಸಸ್ಯ ಶಾರೀರಿಕ ಗುಣಲಕ್ಷಣಗಳಾದ ಎಸ್.ಎಲ್.ಎ ಮತ್ತು ಎಸ್.ಸಿ.ಎಂ.ಅರ್ ಗಳು ಬೀಜದ ಇಳುವರಿಯ ಮೇಲೆ ದುರ್ಬಲ ಸಂಬಂಧವನ್ನು ಹೊಂದಿದೆ.

ಅಕ್ಟೋಬರ್, ೨೦೧೬

ಸಂಯೋಜಿತ ಸಮರ್ಥ ಬೆಳೆಗಳ ಪ್ರಯೋಜನೆ
ಕೃಷಿ ವಿಶ್ವವಿದ್ಯಾಲಯ, ಬೆಂಗಳೂರು

ಡಾ|| ನಿರಂಜನ ಮೂರ್ತಿ
ಪ್ರಮುಖ ಸಲಹೆಗಾರರು

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A decorative red border shaped like a scroll, with a vertical section on the left and horizontal sections at the top and right, each ending in a small circular scroll detail.

Introduction

I INTRODUCTION

Cowpea (*Vigna unguiculata* (L). Walp) belongs to the family leguminosae, sub family papilionaceae having chromosome number $2n=22$. The, classification and nomenclature of taxa at the interspecific level still debated (Verdcourt, 1970). The cultivated species in cowpea is sub divided in to three sub species *i.e.* cowpea (sub species *ungi-culata*), catjung (sub species *catjung*) and yardlong bean (sub species *sesquipedalis*).

Cowpea is an annual herb with strong tap root system with different growth habit *i.e.*, erect, semi erect, trailing or climbing, bushy annual with glabrous stem. The trifoliate leaves arise alternatively and terminal leaflet is frequently longer and greater leaf area than that of a symmetrical lateral leaves. Flowers are racemose or indeterminate inflorescence at the distal ends of peduncles which are in leaf axil. The flower is typical with five sepals in gamo sepalous condition containing five petals in polypetalous condition. The flowers are born on short peduncle and corolla varies in colour from white to purple.

Cowpea is an important versatile legume grown in tropics, sub tropics of Asia, Africa, central and southern America, parts of the southern Europe and Asia. It is difficult to estimate the precise area and productivity of cowpea as it is generally grown as mixed crop and most of the countries do not maintain separate records of cowpea. Nigeria contributes about 31 per cent of world area and 46.06 per cent of production.

In India, cowpea is grown as a sole crop, inter crop, mixed crop and in agroforestry combinations. The area of cultivation of cowpea in India is 1.3 million hectares of area in Asian region. Cowpea is considered as a minor pulse crop in India and mainly cultivated in the states of Rajasthan, Gujrat, Karnataka, Tamil Nadu, Maharastra and few parts in other states and it is estimated to be cultivated in other states.

In Karnataka, cowpea is grown in almost all the districts, with an area of 0.78 lakh hectares with a production of 0.22 lakh tones. The productivity is only 302 kg/ha during the year 2012-13(Source: Directorate of Economics and Statistics, Govt of Karnataka)

Cowpea is also cultivated in many regions of India and also elsewhere in the world. Cowpea cultivated as pulse and vegetable crop which is good source of protein (22.24 %), carbohydrate (56.66 %), crude fiber (5.9-7.3 %), fat (1.3-1.5 %), phosphorous (0.14 to 0.6 %), calcium (0.076 to 0.104 %) and iron (0.005 %). Cowpea seed is used as a nutritious component in human diet, cheap livestock feed, and the matured pods are used as a vegetable. The tender green leaves are also used as vegetable, especially by small-scale farmers in rural areas. Cowpea is used as a vegetable because of its good palatability, high nutrition and is relatively free of anti- metabolites and other toxins. The seeds also contain small proportion of β -carotene, thiamin, riboflavin, vitamin -A, niacin, folic acid and ascorbic acid.

Cowpea is a hardy crop is known for its drought tolerance, Its wide and droopy leaves keep soils and soil moisture conserved due to shading effect. Initial fast growth with fast penetrating root system and strong stomatal sensitivity justify its initial establishment in soil moisture deficit conditions. Cowpea was grown in residual moisture condition can yield in the range of 25-30 quintals of seed per hectare.

Development of cultivars with early maturity, acceptable grain quality, resistance to some important diseases and pest has significantly increased the yield and cultivated area of cowpea (Ehlers and Hall, 1996). Grain yield is a complex trait and is influenced by many other important yield contributing characters controlled by polygenes and environmental factors. Any breeding program aiming at increasing yield consider the association between yield and its attributes through estimation of genotypic and phenotypic correlation, which help in a great deal in formulating selection indices to aid crop improvement programs. Understanding of the variability existing in a crop is also very much necessary to formulate and accelerate breeding program (Johnson *et al.*, 1955).

Though, cowpea is a highly self-pollinated crop, tremendous genetic variability is available in the crop. In addition to selection, hybridization has been followed to get the recombinants with high seed yield coupled with the superior agronomic traits. The heterotic response over mid as well as better parents could be informative to identify true

heterotic cross combinations. Heterosis for seed yield and other characters in grain legumes were first reported by Pal (1945).

The genetic coefficient of variation together with heritability estimates give the reliable picture of the amount of genetic gain that can be expected from selection. According to Lush (1940), heritability in broad sense represents the functioning of the genotype as a whole. Burton and Devane (1953) suggested that genotypic coefficient of variation, together with heritability estimates, would give reliable indication of the extent of improvement expected from selection and further explained that expected genetic advance under a particular system provides true practical information needed by a breeder.

Yield is a complex entity and is associated with a number of component characters. These characters are interrelated and such interdependence of the contributory factors often affect their direct relationship with yield thereby making correlation coefficient unreliable to formulate effective selection indices. It is however, desirable to know the degree to which different component characters are correlated among themselves as well as seed yield both at genotypic and phenotypic levels.

However, farmers-traditional cultivars are known to be well adapted to the low input conditions, but generally poor in yield and highly susceptible to the major diseases and pests. These production constraints are the main target of cowpea breeding program both at the international national levels in sub-Sahara Africa. Although, past research efforts have brought some improvement into farmer's yield.

The effective crop improvement programme is very essential to assess the genetic variability for the desired trait or trait of interest. It is also important to understand the association of seed yield and with other related traits. To develop drought tolerant genotypes combined with agronomically superior traits, it is essential to recombine the traits through hybridization and isolation of genetically superior recombinants. It is very important to know the genetic aspects and physiological basis of seed yield and related traits associated with the drought tolerance.

Keeping these aspects in view, to know the extent of variability, heritability and character association for the physiological parameters such as specific leaf area and the SPAD chlorophyll meter reading (SCMR) for seed yield in the one single cross of cowpea and also to know the extent of variability, heritability, character association and gene action for the seed yield and yield attributing characters in three crosses of cowpea the present investigation was taken up in the Dry Land Agriculture Project, GKVK, UAS, Bangalore with the following objectives.

Keeping these aspects the following objectives were formulated.

1. To estimate the extent of variability, heritability and genetic advance in F_2 generation of three cowpea crosses (IT-38956-1 $\times$ KBC-2, IT-38956-1 $\times$ CP-12 and KBC-2 $\times$ CP-12).
2. Correlation studies for seed yield and yield related characters in F_2 generation in three crosses of cowpea (IT-38956-1 $\times$ KBC-2, IT-38956-1 $\times$ CP-12 and KBC-2 $\times$ CP-12).
3. To study the nature of gene action for seed yield and their attributing characters through five generation mean analysis in three crosses of cowpea (IT-38956-1 $\times$ KBC-2, IT-38956-1 $\times$ CP-12 and KBC-2 $\times$ CP-12).
4. To quantify the extent of variability and character association of quantitative and physiological traits in F_3 generation of cowpea cross IT-38956-1 $\times$ KBC-2.

A decorative red border shaped like a scroll, with a vertical strip on the left and a horizontal strip on the right, framing the title text.

Review of Literature

II REVIEW OF LITERATURE

Cowpea [*Vigna unguiculata* (L). Walp] is a leguminosces crop belonging to family papilinoceae. According to Vavilov (1951), India and Ethiopia are primary centers of origin. Maximum diversity among the related species of cowpea is found in Africa.

Survey of the variability and understanding of genetic makeup of the crop are important for crop improvement programmes. Limited availability of high productive varieties, with higher tolerance to biotic and abiotic stress are the major hindrance to increase the production, Hence, an attempt to collect the information on these factors will be useful in crop improvement activities. The available related literature to the present study was reviewed and presented here under the following headings.

2.1 Heterosis and inbreeding depression

2.2 Variability, heritability and genetic advance

2.3 Gene action

2.4 Path and combining ability

2.5 Drought tolerance

2.1 Heterosis and inbreeding depression

2.1.1 Heterosis

The effect of manifestation of heterosis has been one of the most interesting themes in the science of genetics. Commercial exploitation of heterosis in autogamous crop like cowpea at present it has not become possible due to absence of stable male sterility and low recovery of crossed seeds in manually attempted crosses. Nevertheless, information on nature and magnitude of heterosis is useful, while selecting crosses for further evaluation and selection. The character wise review of literature on percentage heterosis over mid parent (MP) and better parent (BP) is presented in Table 1. The salient observations of the same are presented below.

Table 1: Review of literature on heterosis in cowpea

Sl. No.	Character	No of Crosses studied	Range of Heterosis (%)		References
			Over Better Parent	Over mid Parent	
1	Days to first flower initiation	5	1.0 to 1.50	-0.45 to -8.00	Khanum (2001)
		28	-16.55 to 40.74	-18.2 to 23.77	Patel <i>et al.</i> (2009)
		15	3.0	-0.72	Bhawan Pandey and Singh (2015)
2	Days to maturity	4	-8.10 to 6.80	4.47 to 6.67	Ningappa (1979)
		6	-14.12 to 3.64	-14.55 to 5.82	Chikkadevaiah <i>et al.</i> (1980)
		42	-2.83 to 7.08	-6.41 to 3.89	Marangappanavar (1984)
		45	-2.46 to 13.23	-6.35 to 9.60	Kabi Raj (1986)
		21	-13.55 to 0.84	-10.91 to 3.93	Arun Kumar (1989)
		45	-5.80 to 15.20	-10.20 to 6.20	Sawant <i>et al.</i> (1994)
		8	-5.99 to 9.22	-6.98 to 4.18	Shakarad (1989)
		27	-3.01 to 9.64	-1.83 to 10.98	Madhusudan (1994)
		3	0.03 to 1.63	-0.74 to 2.59	Balaraju (1997)
		5	-5.5 to 10.00	-18.00 to 6.80	Khanum (2001)
		28	36.70 to 36.87	-11.71 to 22.90	Patel <i>et al.</i> (2009)
3	Plant height (Cm)	6	-49.57 to 6.37	-38.17 to 12.36	Chikkadevaiah <i>et al.</i> (1980)
		6	67 (maximum)	--	Doto and Whillington (1981)
		42	-6.75 to 31.42	-7.62 to 37.06	Marangappanavar (1984)
		45	-7.34 to 74.63	-24.88 to 48.48	Kabi Raj (1986)
		21	-25.48 to 15.78	-19.07 to 21.19	Arun Kumar (1989)
		45	-67.25 to 75.00	-51.22 to 98.24	Savithramma (1991b)
		45	-45.30 to 63.40	-25.40 to 73.40	Sawant <i>et al.</i> (1994)
		8	-14.60 to 1.19	-9.70 to 0.90	Shakarad (1989)
		27	-83.17 to 57.82	-73.86 to 141.60	Madhusudan (1994)
		3	-8.99 to 43.95	-0.04 to 60.36	Balaraju (1997)
		5	14.78 to 54.6	-58.98 to 2.35	Khanum (2001)
		28	52.30 to 55.44	-28.91 to 36.65	Patel <i>et al.</i> (2009)
		15	6.20	-9.54	Bhawan Pandey and Singh (2015)

Sl. No.	Character	No of Crosses studied	Range of Heterosis (%)		References
			Over Better Parent	Over mid Parent	
4	Primary branches per plant	4	-57.85 to 15.68	-33.29 to 11.96	Ningappa (1979)
		42	-26.58 to 44.83	-14.58 to 15.27	Marangappanavar (1984)
		45	-24.87 to 128.65	-2.77 to 143.34	Srikantaradhya (1984)
		45	-24.11 to 27.27	-9.09 to 37.36	Kabi Raj (1986)
		21	-3.89 to 59.64	-11.27 to 62.61	Arun Kumar (1989)
		45	-45.09 to 34.21	-37.31 to 48.14	Savithramma (1991)
		45	-0.00 to 50.00	-3.90 to 85.60	Sawant <i>et al</i> (1994)
		8	-13.04 to 17.76	-2.85 to 32.47	Shakarad (1989)
		27	-16.28 to 219.23	-10.00 to 232.00	Madhusudan (1994)
		3	-17.05 to -20.84	-12.05 to -30.10	Balaraju (1997)
5	Secondary branches per plant	36	-32.21 to 152.24	-15.92 to 171.54	Bhushana (1996)
		3	-28.99 to 43.55	-22.22 to 57.96	Balaraju (1997)
		5	-0.58 to 6.75	-0.38 to 6.63	Khanum(2001)
6	Pods per plant	1	—	39.9	Kheradnam and Nicknejad (1975)
		45	-48.89 to 152.83	-25.61 to 166.49	Bhaskaraiah (1977)
		90	31.5	-55.4	Bhaskaraiah <i>et al</i> (1980)
		42	-16.53 to 123.84	-39.14 to 150.06	Marangappanavar (1984)
		45	-13.60 to 238.54	-3.86 to 207.59	Srikantaradhya (1984)
		45	-31.02 to 88.27	-26.13 to 94.95	Kabi Raj (1986)
		21	-13.00 to 89.00	-2.00 to 128.00	Patil and Shete (1987)
		21	-22.77 to 134.75	-1.94 to 182.00	Arun Kumar (1989)
		45	-3.10 to 122.60	-17.70 to 132.50	Sawant <i>et al</i> (1994)
		8	-2.46 to 103.69	2.59 to 112.01	Shakarad (1989)
		3	3.74 to 54.21	16.15 to 32.70	Balaraju (1997)
		5	-9.34 to 19.45	-2.42 to 26.92	Khanum(2001)
		28	-29.31 to 85.67	-19.14 to 39.03	Patel <i>et al</i> (2009)
		15	12.78	16.33	Bhawan Pandey and Singh (2015)

Sl. No.	Character	No of Crosses studied	Range of Heterosis (%)		References
			Over Better Parent	Over mid Parent	
7	Pod length(cm)	25	-31.9 to 81.6	-16.9 to 95.2	Sanghwan and Lodhi (1995)
		10	-15.00 to 27.16	-7.71to 30.53	Singh and Jain (1972)
		45	-18.89 to 36.95	-13.96 to 43.80	Bhaskaraiah (1977)
		90	2.4	10.3	Bhaskaraiah <i>et al.</i> (1980)
		6	-27.14 to 36.45	-0.97 to 47.99	Chikkadevaiah <i>et al.</i> (1980)
		21	-17.00 to 11.00	-12.00 to 19.00	Patil and Shete (1987)
		21	-20.14 to 24.46	-14.53 to 29.80	Arun Kumar (1989)
		45	-27.36 to 43.22	- 18.14 to 46.87	Savithramma (1991)
		45	-15.90 to 14.00	-1.90 to 19.90	Sawant <i>et al</i> (1994)
		8	-13.5 to 35.6	-7.94 to 8.28	Shakarad (1989)
		25	-15.26 to 14.04	0.00 to 44.2	Sanghwan and Lodhi (1995)
		3	-7.12 to 3.79	9.39 to 12.87	Balaraju (1997)
		5	2.14 to 8.00	1.82 to 5.39	Khanum(2001)
		28	-14.45 to 28.61	11.85 to 17.81	Patel <i>et al</i> (2009)
		15	35.36	40.24	Bhawan Pandey and Singh (2015)
8	Seeds per pod	10	-15.26 to 14.04	-11.02 to 39.61	Singh and Jain (1972)
		1	--	-4.3	Kheradnam <i>et al.</i> (1975)
		45	-35.55 to 19.54	-20.09 to 36.11	Bhaskaraiah (1977)
		4	-25.45 to 10.06	-10.03 to 18.48	Ningappa (1979)
		90	-8.0	1.6	Bhaskaraiah <i>et al</i> (1980)
		21	-15.00 to 7.00	-10.00 to 18.00	Patil and Shete (1987)
		45	-22.83 to 19.15	-12.06 to 34.53	Arun Kumar (1989)
		45	Average	Low	Sawant <i>et al.</i> (1994)
		8	-8.00 to 11.29	- 8.02 to 15.07	Shakarad (1989)
		27	-25.00 to 20.4	-12.8 to 22.8	Sanghwan and Lodhi (1995)
		25	-28.30 to 23.85	-18.28 to 37.61	Madhusudan (1994)
		3	0.33 to 1.01	4.97 to 19.61	Balaraju (1997)
		28	-33.27 to 30.75	8.03 to 16.33	Patel <i>et al.</i> (2009)
		15	35.36	40.24	Bhawan Pandey and Singh (2015)

Sl. No.	Character	No of Crosses studied	Range of Heterosis (%)		References
			Over Better Parent	Over mid Parent	
9	Hundred seed weight(g)	45	-38.83 to 22.83	-27.13 to 28.73	Bhaskaraiah (1977)
		4	-25.69 to 12.48	-10.76 to 14.29	Ningappa (1979)
		90	-8.6	-0.2	Bhaskaraiah <i>et al.</i> (1980)
		6	-53.28 to 24.10	-37.94 to 2.14	Chikkadevaiah <i>et al.</i> (1980)
		42	-32.44 to 14.66	-13.41 to 22.95	Marangappanavar (1984)
		45	-20.32 to 11.62	-10.65 to 15.17	Kabi Raj (1986)
		21	-27.00 to 23.00	-21.00 to 38.00	Patil and Shete (1987)
		21	-13.47 to 49.52	-10.67 to 60.00	Arun Kumar (1989)
		45	-40.80 to 20.30	-14.90 to 31.40	Sawant <i>et al.</i> (1994)
		8	-25.14 to -0.34	-21.12 to 5.86	Shakarad (1989)
		25	-50.3 to 127.7	-31.7 to 36.30	Sanghwan and Lodhi (1995)
		3	-11.67 to 4.90	-6.90 to 4.97	Balaraju (1997)
		28	-23.49 to 35.04	9.10 to 16.69	Patel <i>et al.</i> (2009)
10	Seed yield per plant(g)	90	6.0	-42.8	Bhaskaraiah <i>et al.</i> (1980)
		6	-45.58 to 6.61	-32.50 to 20.35	Chikkadevaiah <i>et al.</i> (1980)
		42	-16.81 to 199.21	-42.45 to 213.23	Marangappanavar (1984)
		45	-27.20 to 320.15	-11.35 to 365.12	Srikantaradhya (1984)
		45	-42.51 to 83.27	-24.19 to 109.35	Kabi Raj (1986)
		21	-27.00 to 79.00	-0.7 to 131.00	Patil and Shete (1987)
		21	-11.75 to 445.51	-15.40 to 471.90	Arun Kumar (1989)
		45	-7.50 to 130.00	-18.20 to 140.50	Sawant <i>et al.</i> (1994)
		8	-7.95 to 86.09	-5.68 to 117.62	Shakarad (1989)
		25	-28.8 to 84.00	-11.90 to 127.7	Sanghwan and Lodhi (1995)
		42	-38.36 to 69.54	-24.76 to 93.04	Aravindhan and Vijendra Das (1996)
		3	-28.34 to 9.76	-14.70 to 28.47	Balaraju (1997)
		28	-28.48 to 60.00	11.11 to 23.77	Patel <i>et al.</i> (2009)
		15	42.70	52.14	Bhawan Pandey and Singh (2015)

Days to first flower initiation

Khanum (2001) observed low better parent heterosis (1.00 to 1.50 per cent) and negative mid parent heterosis (-0.45 to -0.80 per cent) for this trait and also the range of heterosis was -18.02 to 23.77 per cent and -16.55 to 40.74 per cent over mid parent and better parent respectively reported by Patel *et al.* (2009).

Kadam *et al.* (2013) observed the range of heterosis from -28.63 per cent to 4.28 per cent over better parent and -21.53 to 12.98 per cent over standard heterosis.

The heterosis ranged from -23.27 to 27.85 per cent over mid parent, 2.20 to 39.84 per cent over better parent and -8.27 to 23.45 per cent over standard heterosis as reported by Bhawana padey and Singh (2015).

Days to maturity

Low heterosis for days to maturity was reported by Ningappa (1979), Chikkadevaiah *et al.* (1980), Arun Kumar (1989), Sawant *et al.* (1994), Balaraju (1997) and Khanum (2001), Girish (2005) and Patel *et al.* (2009).

Plant height

Out of nine reports available for plant height, heterosis ranged from negative to positive, only one report indicated the positive heterosis (Khanum., 2001).

Kajal *et al.*, 2013 reported that the range of heterosis from -35.66 to 18.81 for mid parent, -21.92 to 35.36 for better parent and -15.78 to 47.78 for standard check.

Kadam *et al.*, 2013 observed the range of heterosis from -39.32 to 77.54 per cent over better parent and -43.22 to 83.64 per cent over standard heterosis.

The heterosis ranged from -23.39 to 81.86 per cent over mid parent, -14.43 to 222.37 per cent over better parent and -52.81 to 77.77 per cent over standard heterosis as reported by Bhawana padey and Singh (2015).

Primary branches

For primary branches, out of ten reports available, only one (Balaraju., 1997) indicated the absence of positive heterosis. While, all other reports were same where, heterosis ranged from positive to negative.

Secondary branches

All the three reports of Bhushana (1996), Balaraju (1997) and Khanum (2001) on heterosis for secondary branches showed the range of heterosis from negative to significantly high positive.

Pods per plant

For pods per plant, Balaraju (1997) indicated highly significant positive heterosis and other eleven reports indicated the range of heterosis from negative to positive. Kajel *et al.*(2013) reported that the range of heterosis from -17.28 to 58.24 for mid parent, -19.73 to 57.48 for better parent and -24.14 to 29.07 for standard check.

Kadam *et al.* (2013) observed the range of heterosis from -34.08 per cent to 17.68 per cent over better parent and -35.36 to 3.05 per cent over standard heterosis.

The heterosis ranged from -13.02 to 17.75 per cent over mid parent, -50.22 to 20.25 per cent over better parent and -40.21 to 13.22 per cent over standard heterosis as reported by Bhawana padey and Singh (2015).

Pod length

A wide range of positive heterosis was reported for pod length by several researchers, such as Bhaskaraiah *et al.* (1980), Girish *et al.* (2006), Kumar R *et al.* (2009), Inuwa *et al.* (2012), Kumar P *et al.* (2013), Tigga K., *et al.* (2014) and Kharde *et al.* (2014)

Kadam *et al.* (2013) observed the range of heterosis from -11.33 per cent to 25.68 per cent over better parent and -17.83 to 28.43 per cent over standard heterosis and range

of heterosis from -14.97 to 35.79 per cent for mid parent, -19.49 to 32.31 per cent for better parent and -10.77 to 33.31 for standard check.

The heterosis ranged from -35.63 to 70.10 per cent over mid parent, -56.87 to 65.85 per cent over better parent and -6.12 to 90.19 per cent over standard heterosis as reported by Bhawana padey and Singh (2015).

Seeds per pod

For seeds per pod, out of twelve reports only one report by Sawant *et al.* (1994) indicated the absence of heterosis and other eleven reports indicated wide range of heterosis. Kajel *et al.*, 2013 reported that the range of heterosis from -13.41 to 52.26 for mid parent, -21.45 to 50.41 for better parent and 6.94 to 60.45 for standard check.

Kadam *et al.* (2013) observed the range of heterosis from -16.32 per cent to 38.58 per cent over better parent and -17.06 to 37.35 per cent over standard heterosis.

The heterosis ranged from -4.09 to 38.46 per cent over mid parent, -30.08 to 28.57 per cent over better parent and -10.02 to 34.24 per cent over standard heterosis as reported by Bhawana padey and Singh (2015).

Hundred seed weight

Heterosis for test weight was noticed by several workers in which the heterosis ranged from negative to positive (-53.8 to 24.10 per cent by Chikkadevaiah *et al.*, 1980 and -10.67 to 60 per cent by Arun Kumar, 1989).

Kadam *et al.* (2013) observed the range of heterosis from -27.35 per cent to 20.66 per cent over better parent and -13.45 to 54.62 per cent over standard heterosis.

Seed yield per plant

The wide range of heterosis over both midparent heterosis and heterobeltiosis have been reported by many workers (Arun Kumar, 1989; Girish *et al.*, 2006; Kumar R *et al.*, 2009; Inuwa *et al.*, 2012; Kumar P *et al.*, 2013; Tigga K *et al.*, 2014 and Kharde *et*

al., 2014. The heterosis ranged from 8.60 to 67.85 per cent over mid parent, -1.26 to 50.52 per cent over better parent and 8.52 to 74.48 per cent over standard heterosis as reported by Bhawana padey and Singh (2015).

2.1.2 Inbreeding depression

Ningappa (1979) reported non-significant positive inbreeding depression for number of primary branches, number of seeds per pod, seed yield, test weight, while significant inbreeding depression was observed only for number of pods per plant. Balaraju (1997) observed negative to positive inbreeding depression values for days to maturity, plant height, primary branches, secondary branches and test weight. Whereas, positive inbreeding depression was observed for number of pods per plant, pod length, number of seeds per pod and seed yield. Khanum (2001) and Girish *et al.* (2006), Ramesh Kumar *et al.* (2009), Inuwa *et al.* (2012) Kumar P *et al.* (2013), Tigga K *et al.* (2014), Kharde *et al.* (2014) observed negative to positive inbreeding depression for all the characters studied (Table 2).

2.2 Variability, heritability and genetic advance

Planning and execution of a breeding programme for the improvement of quantitative traits depends mainly upon the magnitude of genetic variability and divergence present in the material. The progress made to derive such information on genetic variability in cowpea is reviewed and listed in Table 3.

2.2.1 Variability

A comprehensive character wise review on phenotypic and genotypic coefficient of variation is presented in Table 3.

Days to first flowering

For days to first flowering, the genotypic coefficient of variation (GCV) ranged from 3.45 to 9.13 per cent, while phenotypic coefficient of variation (PCV) ranged from 3.6 to 8.5 per cent as reported by Girish (2000) and Venkatesan *et al.* (2003).

Table 2: Review of literature on inbreeding depression in cowpea [*Vigna unguiculata* (L.) Walp.]

Sl. No.	Character	Method of Study	F ₁ to F ₂	F ₂ to F ₃	References
1	Days to first flower initiation	Generation mean analysis	-15.97 to 2.00	-0.4 to 1.37	Khanum (2001)
2	Days to maturity	Generation mean analysis	-6.18 to 2.78 -9.60 to 10.15	-1.94 to 2.60 -5.46 to 4.93	Balaraju (1997) Khanum (2001)
3	Plant height	Generation mean analysis	-23.22 to 42.43 -50.24 to 89.64	-32.8 to 4.17 -109.36 to 34.25	Balaraju (1997) Khanum (2001)
4	Primary branches	Generation mean analysis	Non significant -23.22 to 42.43 -50.24 to 62.67	- -32.8 to 4.17 -52.69 to 52.22	Ningappa (1979) Balaraju (1997) Khanum (2001)
5	Secondary branches	Generation mean analysis	-13.07 to 46.45	-13.68 to 2.04	Balaraju (1997)
6	Number of pods per plant	Generation mean analysis	Significant 3.58 to 44.09 10.96 to 45.70	- -40.90 to 11.97 -64.12 to 6.23	Ningappa (1979) Balaraju (1997) Khanum (2001)
7	Pod length	Generation mean analysis	4.95 to 16.69 -100.23 to 18.38	-2.73 to 1.44 -7.71 to 11.08	Balaraju (1997) Khanum (2001)
8	Number of seeds per pod	Generation mean analysis	Non significant 4.96 to 8.20	- -14.73 to -3.04	Ningappa (1979) Balaraju (1997)
9	100 seed weight	Generation mean analysis	Non significant -1.11 to 8.20	- -3.04 to 3.62	Ningappa (1979) Balaraju (1997)
10	Seed yield per plant	Generation mean analysis	Non significant 13.83 to 29.98	- -24.69 to 12.87	Balaraju (1997)

Table 3: Review of literature on genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and heritability (h^2), genetic advance in cowpea [*Vigna unguiculata* (L.) Walp.]

Sl. No.	Character	Material used For study	GCV (%)	PCV (%)	Heritability (%)	Genetic advance	References
1	Days to first flowering	5 F ₂ s 100 genotypes 25 genotypes 11 F ₂ s 40 genotypes 30 genotypes 72 genotypes	3.45 4.9 –5.74 9.13 6.40 5.34 1.5683 9.59	3.69 5.2 –6.03 8.58 3.48 5.95 2.7294 10.26	87.05 88.8-92.1 88.51 6.40 80.39 33.0160 87.33	6.6 6.26 –11.3 7.83 2.14 9.86 1.85 18.46	Girish(2000) Khanum (2001) Venkatesan <i>et al.</i> (2003) Subbaiah <i>et al.</i> (2013) Pravin kumar <i>et al.</i> (2013) Eswaran <i>et al.</i> (2007) Kumar R <i>et al.</i> (2009)
2	Days to 50 % flowering	100 genotypes 50 genotypes 22 genotypes 30 genotypes	2.88 15.94 23.103 2.23	3.10 16.18 23.115 3.66	86.53 97.10 99.89 37.19	5.5 16.54 46.845 2.80	Girish(2000) Selvam <i>et al.</i> (2000) Kiran Tigga <i>et al.</i> (2014) Eswaran <i>et al.</i> (2007)
3	Days to maturity	40 varieties 154 varieties 43 genotypes 6 F ₁ 's 42 F ₁ 's 4 F ₁ 's 50 genotypes 49 purelines 7 parents and F ₁ 's 5 F ₂ 's 3 F ₂ 's 100 genotypes 5 F ₂ 's 72 genotypes 22 genotypes	5.52 9.31-9.65 4.48 -- 5.61 -- 5.36 6.72 4.74 4.86 1.72-2.3 2.66 0.29 –5.44 8.43 27.588	-- -- 6.39 -- 5.84 -- 6.64 7.38 5.27 4.86 2.06-2.52 3.19 4.4-9.42 8.91 27.639	78.29 73.30-89.20 49.2 Low 92.39 76.25-88.89 65 82.88 81.01 99.84 69.90-83.30 69.34 0.01-96.5 89.69 99.627	10.06 13.82-15.04 6.48 -- 8.03 2.40-3.20 9.09 9.28 5.66 8.47 2.96 –4.32 4.5 0.02-9.07 16.46 55.845	Singh and Mehndiratta (1969) Sohoo <i>et al.</i> (1971) Sreekumar <i>et al.</i> (1979) Chikkadevaiah <i>et al.</i> (1980) Marangappanavar (1984) Patil and Shete (1987) Apte <i>et al.</i> (1987) Patil and Baviskar (1987) Thiyagarajan (1989) Madhusudan (1994) Balaraju (1997) Girish (2000) Khanum (2001) Kumar R <i>et al.</i> (2009) Tigga K <i>et al.</i> (2014)

Sl. No.	Character	Material used For study	GCV (%)	PCV (%)	Heritability (%)	Genetic advance	References
4	Plant height	154 varieties	14.25-19.52	--	67.80-72.50	11.83-15.76	Sohoo <i>et al.</i> (1971)
		25 varieties	34.43	--	66.51	47.95	Tikka <i>et al.</i> (1977)
		12 varieties	51.20	51.95	97.2	37.51	Lakshmi and Goud (1977)
		50 genotypes	41.49	--	83.18	43.47	Angadi <i>et al.</i> (1979)
		40 genotypes	10.28	25.95	15.72	0.087	Pandita <i>et al.</i> (1982)
		40 genotypes	13.19	17.98	53.80	--	Dharmalingam and Kadambavanasundram (1984)
		42 F ₁ 's	14.13	14.33	97.16	9.26	Marangappanavar (1984)
		4 F ₁ 's	--	--	56.81- 87.32	4.07-11.24	Patil and Shete (1987)
		50 genotypes	24.75	47.32	27.35	12.72	Apte <i>et al.</i> (1987)
		7 parents and F ₁ 's	18.83	22.86	67.85	40.33	Thiyagarajan (1989)
		4 F ₁ 's	31.85	46.61	46.70	18.81	Savithramma (1991a)
		5 F ₂ 's	37.40	38.27	95.51	59.86	Madhusudan (1994)
		3 F ₂ 's	16.27-33.77	34.96-54.62	19.67-93.33	14.87-67.27	Balaraju(1997)
		100 genotypes	21.8	22.43	94.80	43.79	Girish (2000)
		50 genotypes	44.8	54.69	67.10	58.90	Selvam <i>et al.</i> (2000)
		5F ₂ 's	59.3-133.6	61.5-134.09	93.0-99.40	45.6-12.96	Khanum (2001)
		20 genotypes	46.82	47.07	98.93	85.28	Venkatesan <i>et al.</i> (2003)
		72 genotypes	35.28	35.71	97.60	71.81	Kumar R <i>et al.</i> (2009)
		11 F ₂ 's	5.49	--	59.46	40.48	Subbaiah <i>et al.</i> (2013)
		40 genotypes	11.66	--	96.88	23.65	Kumar P <i>et al.</i> (2013)
5	Primary Branches	40 varieties	5.52	--	78.29	10.06	Singh and Mehndiratta (1969)
		154 varieties	9.31-9.65	--	73.30-89.20	13.82-15.04	Sohoo <i>et al.</i> (1971)
		43 genotypes	4.48	6.39	49.2	6.48	Sreekumar <i>et al.</i> (1979)
		6 F ₁ 's	--	--	Low	--	Chikkadevaiah <i>et al.</i> (1980)
		42 F ₁ 's	5.61	5.84	92.39	8.03	Marangappanavar (1984)
		4 F ₁ 's	--	--	76.25-88.89	2.40-3.20	Patil and Shete (1987)

Sl. No.	Character	Material used For study	GCV (%)	PCV (%)	Heritability (%)	Genetic advance	References
		50 genotypes	5.36	6.64	65	9.09	Apte <i>et al.</i> (1987)
		49 purelines	6.72	7.38	82.88	9.28	Patil and Baviskar (1987)
		7 parents and F ₁ 's	4.74	5.27	81.01	5.66	Thiyagarajan (1989)
		5 F ₂ 's	4.86	4.86	99.84	8.47	Madhusudan (1994)
		3 F ₂ 's	15.12-32.4	33.54-45.36	18.2-58.45	13.43-47.90	Balaraju(1997)
		100 genotypes	21.84	22.43	94.80	43.79	Girish (2000)
		50 genotypes	32.09	45.39	50.00	0.95	Selvam <i>et al.</i> (2000)
		5 F ₂ 's	10.6-32.37	22.60-81.00	7.7-92.30	2.84-85.4	Khanum (2001)
		20 genotypes	17.30	19.10	82.50	1.07	Venkatesan <i>et al.</i> (2003)
		72 genotypes	20.83	24.91	69.94	35.89	Kumar R <i>et al.</i> (2009)
		40 genotypes	10.43	--	4.88	1.10	Kumar P <i>et al.</i> (2013)
		22 genotypes	7.619	--	19.787	7.049	Tigga K <i>et al.</i> (2014)
6	Secondary branches	7 parents and F ₁ 's	13.70	23.85	33	2.19	Thiyagarajan (1989)
		3 F ₂ 's	20.76-47.09	48.99-76.04	15.19-68.38	16.66-69.01	Balaraju(1997)
		100 genotypes	20.39		82.83	38.21	Girish (2000)
7	Pods per plant	154 varieties	49.66-69.44	--	83.24-94.83	19.34-32.50	Sohoo <i>et al.</i> (1971)
		25 varieties	84.94	--	94.46	33.00	Tikka <i>et al.</i> (1977)
		12 varieties	20.93	32.36	41.91	4.05	Lakshmi and Goud (1977)
		8 genotypes	13.4	27.10	24.45	4.19	Singh <i>et al.</i> (1977)
		50 genotypes	81.58	--	93.69	23.68	Angadi <i>et al.</i> (1979)
		60 F ₃ 's	2.30	3.70	38.70	6.40	Vaid and Singh (1983)
		80 F ₄ 's	1.90	3.60	27.40	4.70	Vaid and Singh (1983)
		40 genotypes	29.92	41.08	53.01	--	Dharmalingam and Kadamaba-Vanasundaram (1984)
		42 F ₁ 's	38.10	41.04	86.18	23.77	Marangappanavar (1984)
		4 F ₁ 's	--	--	44.96-64.25	3.43-6.53	Patil and Patil (1987)
		50 genotypes	10.07	26.94	13.97	1.04	Apte <i>et al.</i> (1987)

Sl. No.	Character	Material used For study	GCV (%)	PCV (%)	Heritability (%)	Genetic advance	References
		49 purelines	20.78	25.07	68.73	12.44	Patil and Baviskar (1986)
		7 parents and F ₁ 's	11.71	23.02	25.88	2.66	Thiyagarajan (1989)
		4 F ₁ 's	33.44	35.54	88.51	8.23	Madhusudan (1994)
		5 F ₂ 's	12.22	31.3	15.23	1.78	Savithramma (1991a)
		3 F ₂ 's	40.94-66.83	57.54-70.27	36.47-90.46	50.93-130.94	Balaraju(1997)
		100 genotypes	27.85	29.50	89.13	54.15	Girish (2000)
		50 genotypes	26.85	52.51	26.10	2.22	Selvam <i>et al</i> (2000)
		5F ₂ 's	31.3-38.90	33.7-40.23	19.9-93.6	0.8-17.97	Khanum (2001)
		72 genotypes	23.88	27.98	72.83	41.98	Kumar R <i>et al.</i> (2009)
		20 genotypes	27.98	29.07	88.69	4.76	Venkatesan <i>et al.</i> (2003)
		11 F ₂ 's	17.97	18.26	96.49	53.61	Subbaiah <i>et al.</i> (2013)
		60 genotypes	14.88	--	55.26	22.79	Kumar P <i>et al.</i> (2013)
		22 genotypes	16.319	--	18.103	--	Tigga <i>et al.</i> (2014)
8	Pod length	154 varieties	18.82-19.61	--	75.90-87.00	5.47-5.89	Sohoo <i>et al.</i> (1971)
		25 varieties	29.75	--	95.03	6.40	Tikka <i>et al.</i> (1977)
		12 varieties	16.27	16.68	95.40	4.76	Lakshmi and Goud (1977)
		50 genotypes	46.74	--	94.22	13.70	Angadi <i>et al.</i> (1979)
		40 genotypes	4.69	8.28	32.16	0.75	Pandit <i>et al.</i> (1982)
		60 F ₃ 's	0.80	1.70	23.80	1.10	Vaid and Singh (1983)
		50 F ₄ 's	1.00	1.70	34.00	1.40	Vaid and Singh (1983)
		40 genotypes	14.04	15.02	87.37	--	Dharmalingam and Kadamabavanasundaram (1984)
		42 F ₁ 's	16.77	17.06	96.59	4.76	Marangappanavar (1984)
		50 genotypes	10.21	12.92	62.45	2.30	Apte <i>et a.l</i> (1987)
		49 purelines	8.98	10.71	70.28	2.39	Patil and Baviskar (1987)
		7 parents andF ₁ 's	4.42	5.25	70.84	1.31	Thiyagarajan (1989)
		45 F ₁ 's	10.29	14.16	52.79	1.97	Savithramma (1991a)
		5 F ₂ 's	3.98	11.40	12.17	0.41	Madhusudan (1994)

Sl. No.	Character	Material used For study	GCV (%)	PCV (%)	Heritability (%)	Genetic advance	References
		3 F ₂ 's	3.97-11.80	10.32-12.57	10.44-89.13	2.64-22.94	Balaraju (1997)
		100 genotypes	12.29	13.59	81.79	22.9	Girish (2000)
		50 genotypes	12.6	15.15	69.20	2.6	Selvam <i>et al</i> (2000)
		5 F ₂ 's	9.81-14.67	11.58-15.61	69.90-88.40	3.6-19.17	Khanum (2001)
		20 genotypes	20.85	21.17	97.02	5.30	Venkatesan <i>et al.</i> (2003)
		72 genotypes	22.46	22.95	95.76	41.98	Kuamr R <i>et al.</i> (2009)
		11 F ₂ 's	26.33	--	90.87	42.78	Subbaiah <i>et al.</i> (2013)
		60 genotypes	9.33	--	78.03	16.98	Kumar <i>et al.</i> (2013)
9	Seeds per pod	25 varieties	19.15	--	86.28	0.02	Tikka <i>et al.</i> (1977)
		12 varieties	12.34	14.66	70.11	2.66	Lakshmi and Goud (1977)
		8 genotypes	5.69	13.18	18.63	0.82	Singh <i>et al.</i> (1977)
		50 genotypes	30.48	--	72.41	6.81	Angadi <i>et al.</i> (1979)
		43 genotypes	12.53	2.60	40.60	16.45	Sreekumar <i>et al.</i> (1979)
		60 F ₃ 's	1.80	19.67	44.50	2.10	Vaid and Singh (1983)
		50 F ₄ 's	1.40	2.10	37.50	1.30	Vaid and Singh (1983)
		40 genotypes	12.88	16.09	64.60	--	Dharmalingam and Kadamaba-Vanasundaram (1984)
		42 F ₁ 's	8.84	9.18	92.72	2.19	Marangappanavar (1984)
		50 genotypes	11.97	14.76	65.84	2.31	Apte <i>et al.</i> (1987)
		49 purelines	6.07	10.51	33.33	1.08	Patil and Baviskar (1987)
		7 parents and F ₁ 's	6.55	7.77	71.24	1.77	Thiyagarajan (1989)
		45 F ₁ 's	7.93	15.16	27.42	0.90	Savithramma (1991)
		5 F ₂ 's	8.63	13.98	38.14	1.51	Madhusudan (1994)
		3 F ₂ 's	7.79-13.78	11.79-17.62	19.54-88.60	7.10-23.18	Balaraju (1997)
		100 genotypes	14.36	16.18	78.80	26.28	Girish (2000)
		50 genotypes	10.2	18.22	31.30	1.18	Selvam <i>et al.</i> (2000)
		20 genotypes	14.7	15.64	88.75	2.83	Venkatesan <i>et al.</i> (2003)
		72 genotypes	12.03	13.14	83.79	22.69	Kumar R <i>et al.</i> (2009)

Sl. No.	Character	Material used For study	GCV (%)	PCV (%)	Heritability (%)	Genetic advance	References
		60 genotypes	7.75	10.44	55.15	11.86	Kumar P <i>et al.</i> (2013)
		22 genotypes	12.966	--	61.074	20.952	Tigga K <i>et al.</i> (2014)
10	Hundred seeds weight	154 varieties	14.56-26.95	--	62.22-71.80	2.39-4.75	Sohoo <i>et al.</i> (1971)
		25 varieties	18.78	--	96.02	5.52	Tikka <i>et al.</i> (1977)
		12 varieties	12.23	20.87	93.78	3.80	Lakshmi and Goud (1977)
		8 genotypes	18.41	16.84	24.97	2.07	Singh <i>et al.</i> (1977)
		50 genotypes	51.9	--	98.92	11.19	Angadi <i>et al.</i> (1979)
		43 genotypes	23.5	25.02	96.49	49.69	Sreekumar <i>et al.</i> (1979)
		60 F ₃ 's	0.50	1.20	15.10	0.30	Vaid and Singh (1983)
		40 genotypes	16.01	17.33	85.38	--	Dharmalingam and Kadamaba-Vanasundaram (1984)
		42 F ₁ 's	23.86	24.85	93.14	4.67	Marangappanavar (1984)
		50 genotypes	19.84	21.852	82.47	4.08	Apte <i>et al.</i> (1987)
		49 purelines	17.43	18.28	90.94	3.17	Patil and Baviskar (1987)
		7 parents and F ₁ 's	9.47	10.37	83.39	2.18	Thiyagarajan (1989)
		45 F ₁ 's	21.11	22.74	83.00	3.60	Gowda <i>et al.</i> (1991)
		5 F ₂ 's	10.13	14.07	51.87	1.10	Madhusudan (1994)
		3 F ₂ 's	5.91-11.52	10.45-12.72	24.11-84.30	5.97-21.50	Balaraju(1997)
		100 genotypes	43.35	44.74	93.90	86.55	Girish (2000)
		50 genotypes	22.49	30.00	56.20	4.00	Selvam <i>et al.</i> (2000)
		20 genotypes	27.60	27.70	99.31	5.51	Venkatesan <i>et al.</i> (2003)
		72 genotypes	35.01	35.58	96.78	36.729	Eswaran <i>et al.</i> (2007)
		60 genotypes	11.09	21.21	99.26	70.95	Kumar R <i>et al.</i> (2009)
		30 genotypes	17.82	11.62	90.99	21.79	Kumar P <i>et al.</i> (2013)
		22 genotypes	21.145	13.46	99.344	42.743	Tigga <i>et al.</i> (2014)

Sl. No.	Character	Material used For study	GCV (%)	PCV (%)	Heritability (%)	Genetic advance	References
11	Seed yield per plant	25 Varieties	61.59	--	70.02	22.50	Tikka <i>et al.</i> (1977)
		12 varieties	33.26	48.24	47.53	6.59	Lakshmi and Goud (1977)
		8 genotypes	23.69	47.41	24.96	3.77	Singh <i>et al.</i> (1977)
		50 genotypes	60.50	--	90.96	17.55	Angadi <i>et al.</i> (1979)
		43 genotypes	32.50	49.33	43.42	44.11	Sreekumar <i>et al.</i> (1979)
		40 genotypes	32.92	32.97	91.62	0.62	Pandita <i>et al.</i> (1982)
		60 F ₃ 's	2.50	3.40	54.50	5.40	Vaid and Singh (1983)
		50 F ₄ 's	2.60	3.50	57.80	5.70	Vaid and Singh (1983)
		40 genotypes	24.16	40.53	35.52	--	Dharmalingam and Kadamba- vanasundram (1984)
		4 F ₁ 's	34.32	35.56	93.15	14.51	Marangappanavar (1984)
		50 genotypes	--	--	53.06-74.22	1.69-2.89	Patil and Patil (1986)
		49 purelines	13.12	31.80	17.03	1.46	Apte <i>et al.</i> (1987)
		7 parents and F ₁ 's	18.32	25.49	51.62	9.17	Patil and Baviskar (1987)
		45 F ₁ 's	14.09	25.61	30.25	5.15	Thiyagarajan (1989)
		5 F ₂ 's	22.54	52.64	18.34	6.32	Savithramma (1991a)
		3 F ₂ 's	84.78	86.53	96.00	41.01	Madhusudan (1994)
		100 genotypes	51.98-57.75	59.57-71.77	64.75-78.73	93.41-101.28	Balaraju(1997)
		50 genotypes	17.07	17.11	99.58	35.22	Girish (2000)
		20 genotypes	34.01	51.32	43.90	2.99	Selvam <i>et al.</i> (2000)
		72 genotypes	77.65	77.68	99.92	40.75	Venkatesan <i>et al.</i> (2003)
		30 genotypes	30.23	46.755	75.22	54.03	Kumar R <i>et al.</i> (2009)
		5 F ₂ 's	29.073	34.86	85.319	55.37	Eswaran <i>et al.</i> (2007)
		60 genotypes	35.32	36.02	96.17	186.89	Subbaiah <i>et al.</i> (2013)
		22 genotypes	22.12	25.58	74.77	39.40	Kumar P <i>et al.</i> (2013)
		35 genotypes	34.094	13.46	53.174	50.739	Tigga K <i>et al.</i> (2014)

Kumar R. *et al.* (2009) reported on PCV and GCV which ranged from 10.26 to 9.59 per cent respectively. Tigga K *et al.* (2014) reported the range of PCV and GCV from 23.15 to 23.10 per cent with the narrow difference between them and also the range of PCV and GCV from 16.65 to 14.70 per cent as reported by Kharde *et al.* (2014).

Olawale M A and Bukola O M (2016) reported on GCV and PVC values which ranged from 10.3 and 11.5 respectively for days to flowering.

Days to maturity

For days to maturity, the GCV ranged from 0.29 to 9.65 per cent while, the PCV ranged from 2.06 to 9.42 per cent. In general, several researchers have reported low GCV and PCV for this trait (Khanum, 2001 and Balaraju, 1997). The range of PCV and GCV ranged from 27.63 to 27.58 per cent as reported by Tigga K *et al.* (2009) and also the range varied from 8.91 to 8.43 per cent respectively for PCV and GCV as reported by Kumar R *et al.* (2009).

Olawale M A and Bukola O M (2016) reported on GCV and PVC values which ranged from 10.8 and 11.9 per cent respectively for days to flowering.

Plant height

The values of GCV for plant height ranged from 10.28 to 133.66 per cent where as, PCV ranged from 14.33 to 134.09 per cent. Low to high GCV and moderate to high PCV have been reported by several workers for this character (Pandita *et al.* (1982), Khanum, 2001 and Marangappanavar, 1984). High GCV and PCV were observed which ranged from 27.94 to 23.09 as reported by Tigga K *et al.* (2009). Shashidhar K *et al.* (2010) reported on PCV and GCV which ranged from 20.8 and 20.20 respectively. Similar types of results have been reported by Kumar R *et al.* (2009) and Khandre *et al.* (2014).

Tudu D *et al.* (2015) reported GCV value of 66.56 per cent and PCV value of 5.28 per cent for days to maturity.

Primary branches per plant

For primary branches per plant, the GCV values varied from 4.48 to 32.37 per cent (Sreekumar *et al.*, 1979 and Khanum, 2001). The PCV was 4.86 to 81.00 per cent as reported by Madhusudan, 1994 and low to high GCV and PCV were observed by various investigators.

Secondary branches per plant

Only three reports (Thiyagarajan, 1989; Balaraju, 1997 and Girish, 2000) are available on secondary branches in cowpea and in which GCV values ranged from 13.7 to 47.09 per cent and PCV from 22.40 to 76.04 per cent.

Pods per plant

The GCV values for pods per plant ranged from 1.90 to 84.94 per cent, While PCV values were from 3.6 to 70.27 per cent, as reported by several authors (Vaid and Singh, 1983; Tikka *et al.*, 1977; Balaraju, 1997; Tigga K *et al.*, 2009; Kumar R *et al.*, 2009; Shashidar K *et al.*, 2010; Olayiwola and Soremi., 2014; Kharde *et al.*, 2014 and Tudu D *et al.*, 2015).

Olawale M A and Bukola O M (2016) reported on GCV and PVC values which ranged from 36.6 and 39.8 per cent respectively for pods per plant.

Pod length

For pod length, the least GCV and PCV of 0.80 and 1.70 per cent have been reported by Vaid and Singh (1983), while the highest GCV was 46.74 per cent (Angadi *et al.*, 1979) and PCV was 21.17 per cent (Venkatesan *et al.*, 2003). Shashidhar K *et al.* (2010) reported on PCV and GCV which ranged from 10.48 to 10.16 respectively. Tudu D *et al.*, (2015) reported GCV value of 24.84 per cent and PCV value of 25.22 per cent.

Olawale M A and Bukola O M (2016) reported on GCV and PVC which ranged from 18.6 and 20.5 per cent respectively for pod length.

Seeds per pod

GCV value of 1.40 per cent (Vaid and Singh., 1983) to 30.48 per cent (Angadi *et al.*, 1979) and PCV of 2.10 to 19.67 per cent (Vaid and Singh., 1983) for number of seeds per pod have been reported for number of seeds per pod.

Shashidhar K *et al.* (2010) reported on PCV and GCV which ranged from 15.64 to 14.68 respectively. Olayiwola and Soremi., 2014 reported the PCV and GCV values of 11.35 and 4.16 per cent respectively.

Tudu D *et al.* (2015) reported GCV value of 7.51 per cent and PCV value of 9.70 per cent for days to maturity.

Olawale M A and Bukola O M (2016) reported on GCV and PVC which ranged from 23.4 and 26.9 per cent respectively for seeds per pod.

Hundred seed weight

Low to high GCV (0.50 - 51.90 per cent) and PCV value (1.20 - 44.74 per cent) for test weight have been reported by several scientists (Vaid and Singh., 1983; Angadi *et al.*, 1979; Girish, 2000; Shashidhar K *et al.*, 2010; Olayiwola and Soremi., 2014 and Olawale M A and Bukola O M., 2016.) respectively.

Seed yield per plant

For seed yield per plant, the GCV ranged from 2.50 to 84.78 per cent and PCV from 3.40 to 86.53 per cent as observed by Vaid and Singh (1983); Madhusudan (1994) has reported very low to high GCV and PCV for this character. Shashidhar K *et al.* (2010) reported on PCV and GCV which ranged from 38.83 to 35.48 respectively. Olayiwola and Soremi., 2014 reported the PCV value of 60.76 per cent and GCV value of 38.82 per cent respectively.

Olawale M A and Bukola O M (2016) reported on GCV and PVC which ranged from 15.9 and 16.7 per cent respectively for seed yield.

2.2.2 Heritability and Genetic advance

A brief character wise listing of literature on heritability and genetic advance is presented in Table 3 while a summary of the same is presented below.

Days to first flowering

For days to first flowering studies indicated heritability range from 87.05 to 92.1 per cent and genetic advance from 6.26 to 11.3 per cent (Girish, 2000 and Khanum, 2001). Heritability value of 99.62 per cent and genetic advance value of 55.85 per cent as reported by Tigga K *et al.*, (2014)

Olawale M A and Bukola O M (2016) reported the heritability value of 86 per cent for days to flowering.

Days to 50 % flowering

Heritability values for this trait ranged from 86.53 to 97.10 per cent and genetic advance from 5.5 to 16.54 per cent (Girish, 2000 and Selvam *et al.*, 2000).

Days to maturity

For days to maturity in cowpea, several studies indicated the range of heritability from 0.01 to 99.84 per cent and genetic advance of 0.02 to 15.40 per cent (Khanum, 2001, Madhusudan, 1994 and Sohoo *et al.*, 1971). Tigga K *et al.* (2014) reported the heritability and genetic advance values of 99.62 and 55.85 per cent respectively.

Olawale M A and Bukola O M (2016) reported the heritability value of 82 per cent for days to maturity.

Plant height

Low (15.72 per cent) to high (99.40 per cent) heritability and very low (0.087 per cent) to high (85.28 per cent) genetic advance were reported by various authors for plant height (Pandita *et al.*, 1982; Khanum, 2001 and Venkatesan *et al.*, 2003). Shashidhar K *et al.* (2010) reported the heritability of 96 per cent and genetic advance of 39.96 per cent.

Tigga K *et al.*, (2014) reported the heritability and genetic advance values of 68.29 and 38.92 per cent respectively.

High heritability and very high genetic advance (94.65 and 147.64 per cent) were reported by Tudu D *et al.*, (2015) for plant height.

Primary branches

For number of primary branches per plant, a range of 7.7 to 99.84 per cent heritability and 0.60 to 47.49 per cent genetic advance were reported by Khanum (2001) and Madhusudan (1994). Tigga K *et al.* (2014) reported the heritability and genetic advance values of 19.78 and 7.04 per cent respectively.

High heritability and very low genetic advance (64.74 and 1.11 per cent) were reported by Tudu D *et al.* (2015) for primary braches per plant.

Secondary branches

Only three reports are available on secondary branches which indicated 15.19 to 82.83 per cent of heritability and 2.19 to 69.01 per cent of genetic advance (Thiyagarajan, 1989; Balaraju, 1997 and Girish, 2000).

Pods per plant

In general, low to high heritability (13.97 to 94.83 per cent by Apte *et al.*, 1987) and Sohoo *et al.*, 1971) and genetic advance (0.8 to 130.94 per cent by Khanum, 2001 and Balaraju, 1997) for number of pods per plant was observed. Shashidhar *et al.* (2010) reported the high heritability of 90.42 per cent and high genetic advance of 70.84 per cent.

High heritability and very low genetic advance (81.36 and 3.21 per cent) were reported by Tudu D *et al.* (2015) for pods per plant and Tigga K *et al.* (2014) reported the heritability and genetic advance values of 18.10 and 14.15 per cent respectively. Olayiwola and Soremi., 2014 reported the heritability of 94 per cent and genetic advance of 47.17 per cent respectively.

Olawale M A and Bukola O M (2016) reported the heritability value of 85 per cent for pods per plant.

Pod length

As reported by various workers, indicated heritability of 10.44 to 97.02 per cent and genetic advance of 0.41 to 22.94 per cent has been reported for pod length by Balaraju, 1997; Venkatesan *et al.*, 2003 and Madhusudan, 1994 and Tigga K *et al.*, 2014 reported the heritability and genetic advance values of 76.93 and 25.49 per cent respectively. Shashidhar K *et al.*, 2010 reported the heritability of 89.02 per cent and genetic advance of 22.06 per cent.

High heritability and low genetic advance (97.01 and 10.18 per cent) were reported by Tudu D *et al.* (2015) for pod length and Olawale M A and Bukola O M (2016) reported the heritability value of 82 per cent for pod length.

Seeds per pod

Low to high heritability (18.63 to 92.72 per cent) was observed by Singh *et al* (1977) and Marangappanavar (1984). Genetic advance of 0.02 to 26.28 per cent was observed for number of seeds per pod as reported by Tikka *et al.* (1977), Girish (2000) and Shashidhar K *et al.* (2010) reported the heritability of 98.04 per cent and genetic advance of 31.98 per cent respectively Olayiwola and Soremi., 2014 reported the heritability of 13 per cent and 3.14 per cent respectively. Tigga K *et al.* (2014) reported the heritability and genetic advance values of 61.07 and 20.95 per cent respectively.

High heritability and very low genetic advance (60.14 and 1.48 per cent) were reported by Tudu D *et al.* (2015) for seeds per pod.

Olawale M A and Bukola O M (2016) reported the heritability value of 75 per cent for seeds per pod.

Hundred seed weight

The range of heritability was from 15.10 to 99.31 per cent and 0.30 to 86.55 per cent of genetic advance have been reported by various researchers (Vaid and Singh,

1983; Venkatesan *et al.*, 2003; Girish, 2000 and Shashidhar K *et al.* (2010) reported the heritability of 91.22 per cent and genetic advance of 20.34 per cent respectively. Olayiwola and Soremi., 2014 reported the heritability of 72 per cent and genetic advance of 21.39 per cent respectively and Tigga K *et al.* (2014) reported the heritability and genetic advance values of 99.34 and 42.74 per cent respectively.

Olawale M A and Bukola O M (2016) reported the heritability value of 91 per cent for hundred seed weight.

Seed yield per plant

For seed yield per plant, the range of heritability was from 17.03 to 99.58 per cent as reported by Apte *et al.* (1987) and Girish (2000) and genetic advance was between 0.62 and 101.28 per cent, as studied by earlier breeders Pandita *et al.* (1982) and Balaraju (1997). Shashidhar K *et al.* (2010) reported the high heritability of 94.64 per cent and high genetic advance of 74.57 per cent. Tigga K *et al.* (2014) reported the heritability and genetic advance values of 53.17 and 50.73 per cent respectively and Olayiwola and Soremi., 2014 reported the heritability of 41.11 per cent and genetic advance of 51.09 per cent respectively.

Olawale M A and Bukola O M (2016) reported the heritability value of 82 per cent for seed yield.

2.3 Gene action

Literature available on gene action in cowpea is given character wise in Table 4 and the salient observations on the same are presented below.

Days to first flowering

Predominance of additive gene action was reported for days to first flowering in cowpea (Khanum, 2001).

Days to maturity

The predominance of additive gene effect for days to maturity was reported by Kabi Raj (1986), Patil and Bhapkar (1989), Madhusudan (1994), Shakarad *et al.* (1989),

Table 4: Review of literature on gene action in cowpea [*Vigna unguiculata* (L.) Walp.]

Sl. No.	Character	Method of study	Predominance of gene action (in that order)	References
1	Days to first flowering	Generation mean analysis Line $\times$ Tester Generation mean analysis	Additive Additive Additive	Khanum (2001) Subbaiah <i>et al.</i> (2013) Girish (2005)
2	Days to Maturity	Generation mean analysis Line $\times$ tester and diallel Line $\times$ Tester Diallel Diallel Line $\times$ tester and diallel Line $\times$ Tester Line $\times$ Tester Line $\times$ Tester Line $\times$ Tester Generation mean analysis Generation mean analysis Line $\times$ Tester Generation mean analysis Line $\times$ Tester	Dominance Additive $\times$ Additive Additive Additive Additive and dominance Non additive Additive and dominance Additive Additive Additive Dominance Dominance $\times$ Dominance Dominance Dominance Additive	Ningappa (1979) Marangappanavar (1984) Kabi Raj (1986) Patil and Bhapkar (1986) Patil and Patil (1986) Singh and Dabas (1986) Arun Kumar (1989) Madhusudhan (1994) Shakarad <i>et al.</i> (1995) Bhushana (1996) Balaraju(1997) Khanum(2001) Yadav <i>et al.</i> (2004) Girish (2006) Subbaiah <i>et al.</i> (2013)
3	Plant height	Line $\times$ Tester Diallel Diallel Diallel Generation mean analysis	Additive and dominance Additive and dominance Additive and dominance Additive and over dominance Additive	Marangappanavar (1984) Kabi Raj N (1986) Patil and Patil (1986) Arun Kumar (1989) Thiyagarajan <i>et al.</i> (1989)

Sl. No.	Character	Method of study	Predominance of gene action (in that order)	References
		Line × Tester Line × Tester Line × Tester Generation mean analysis Generation mean analysis Generation mean analysis Line × Tester Line × Tester	Additive Additive and dominance Additive Additive Additive Additive × Additive Additive × Dominance Additive	Madhusudhan (1994) Shakarad <i>et al.</i> (1995) Bhushana (1996) Balaraju(1997) Khanum(2001) Yadav <i>et al.</i> (2004) Girish (2005) Subbaiah <i>et al.</i> (2013)
4	Primary Branches	Generation mean analysis Line × Tester Diallel Diallel Generation mean analysis Generation mean analysis Line × tester Line × Tester Line × Tester Generation mean analysis Generation mean analysis Generation mean analysis	Additive × Dominance dominance × Dominance Additive and dominance Additive and dominance and Additive × Additive Additive and non- additive Additive and partial dominance Dominance and dominance × dominance Additive Additive Epistasis Additive and dominance	Ningappa (1979) Marangapanavar (1984) Srikantaradhya (1984) Kabi Raj (1986) Patil and Patil (1987) Thiyagarajan <i>et al.</i> (1989) Madhusudhan (1994) Shakarad (1995) Bhushana (1996) Balaraju(1997) Khanum(2001) Girish (2006)
5	Secondary branches	Generation mean analysis Line × tester Generation mean analysis Generation mean analysis	Additive Dominance Additive Additive	Thiyagarajan <i>et al.</i> (1990) Bhushana (1996) Balaraju(1997) Girish (2005)

Sl. No.	Character	Method of study	Predominance of gene action (in that order)	References
6	Pods per plant	Generation mean analysis Line × Tester Diallel Diallel Diallel Diallel Diallel Line × tester and diallel Diallel Generation mean analysis Diallel Line × tester Line × Tester Line × Tester Generation mean analysis Line × Tester Generation mean analysis Generation mean analysis	Additive, dominance, Additive × Additive and Additive × Dominance Additive Additive and epistatic Dominance, Additive × Additive, Additive × Dominance Additive and non-additive Additive and dominance Dominance, additive × additive, Additive × Dominance Non additive Dominance Additive Additive Dominance Dominance Additive Dominance Additive	Ningappa (1979) Marangappanavar (1984) Marangappanavar (1984) Srikantaradhya (1984) Kabi Raj (1986) Patil and Bhapkar (1986) Patil and Patil (1986) Singh and Dabas (1986) Arun Kumar (1989) Thiagarajan <i>et al.</i> (1989) Savithamma (1991a) Madhusudhan (1994) Shakarad <i>et al.</i> (1995) Bhushana (1996) Balaraju (1997) Khanum (2001) Yadav <i>et al.</i> (2004) Girish (2005) Subbaiah <i>et al.</i> (2013)
7	Pod Length	Line × tester and diallel Diallel Diallel Diallel Generation mean Analysis Diallel	Dominance, additive and Epistatic Additive, additive × additive Additive, non additive Additive Additive Dominance	Marangappanavar (1984) Srikantaradhya (1984) Kabi Raj (1986) Patil and Patil (1986) Patil and Patil (1987) Arun Kumar (1989)

Sl. No.	Character	Method of study	Predominance of gene action (in that order)	References
		Generation mean Analysis Generation mean Analysis Line $\times$ Tester Line $\times$ Tester Generation mean analyses Generation mean analysis Line $\times$ Tester	Additive Additive, additive $\times$ additive Dominance Dominance Dominance Additive Dominance $\times$ Dominance	Thiyagarajan <i>et al.</i> (1990) Hazra <i>et al.</i> (1993) Madhusudhan (1994) Bhushana (1996) Balaraju (1997) Khanum (2001) Subbaiah <i>et al.</i> (2013)
8	Seeds per pod	Generation mean analysis Line $\times$ tester and diallel Diallel Diallel Generation mean analysis Diallel Diallel Line $\times$ Tester Line $\times$ Tester Generation mean analysis Line $\times$ Tester Generation mean analysis	Dominance and Epistasis Additive, Dominance and Epistasis Additive, Dominance and Epistasis Additive and non-additive Additive and Additive $\times$ Additive Additive dominance Additive Additive Additive Dominance $\times$ Dominance Additive Dominance $\times$ Dominance	Ningappa (1979) Marangappanavar (1984) Srikantaradhya (1984) Kabi Raj (1986) Patil and Patil (1987) Arun Kumar (1989) Savithamma (1991) Madhusudhan (1994) Bhushana (1996) Balaraju(1997) Yadav <i>et al.</i> (2004) Girish (2006)
9	Hundred seed weight	Generation mean analysis Generation mean analysis Diallel Line $\times$ tester and diallel Diallel Generation mean analysis	Additive, additive $\times$ additive Dominance $\times$ Dominance Additive and dominance Additive and dominance Additive Additive	Ningappa (1979) Jatsara (1980) Kabi Raj (1986) Singh and Dabas (1986) Patil and Patil (1986) Patil and Patil (1987)

Sl. No.	Character	Method of study	Predominance of gene action (in that order)	References
		Diallel Generation mean Analysis Diallel Line × Tester Line × Tester Generation mean Analysis Generation mean analysis	Additive × Additive Additive and dominance Additive and additive × additive Additive Additive Dominance Additive × Additive	Arun Kumar (1989) Thiyagarajan <i>et al.</i> (1989) Savithramma (1991a) Madhusudhan (1994) Bhushana (1996) Balaraju (1997) Girish (2005)
10	Seed yield per plant	Generation mean analysis Line × tester and diallel Diallel Diallel Diallel Line × tester and diallel Generation mean analysis Diallel Diallel Line × Tester Line × Tester Line × Tester Generation mean analysis Generation mean analysis	Additive × additive and dominance × dominance Dominance Additive × Additive Dominance Additive dominance Non additive Additive Dominance Dominance Dominance Additive Dominance Additive × Additive Additive × Additive	Ningappa (1979) Marangappanavar (1984) Srikantaradhya (1984) Kabi Raj (1986) Patil and Patil (1986) Singh and Dabas (1986) Patil and Patil (1987) Arun Kumar (1989) Savithramma (1991a) Madhusudhan (1994) Shakarad <i>et al.</i> (1995) Bhushana (1996) Balaraju (1997) Girish (2005)

Bhushana (1996), while Patil and Patil (1987) and Arun Kumar (1989) reported the predominant role of additive gene effects followed by dominance for the expression of this trait. The trait was also reported to be under the control of dominance (Ningappa, 1979 and Khanum, 2001), additive $\times$ additive (Marangappanavar, 1984) and non additive (Singh and Dabas., 1986 and Balaraju, 1997) gene actions.

Plant height

Additive gene effect followed by dominance was observed for the plant height by Marangappanavar, 1984; Kabi Raj, 1986; Patil and Patil, 1986 and Shakarad *et al.*, 1995.

The trait was also under the control of over dominance gene action (Arun Kumar, 1989) and additive (Thiyagarajan *et al.*, 1990; Madhusudan, 1994; Bhushana, 1996; Balaraju, 1997 and Khanum, 2001) effect.

Primary branches

Marangappanavar (1984), Srikantaradhya (1984), Patil and Patil (1987), Bhushana (1996) and Khanum (2001) reported additive gene effect followed by dominance for primary branches per plant. Others reported as additive and non additive Kabi Raj (1986) and additive (Madhusudan, 1994) gene effects for this trait. Ningappa (1979) observed additive $\times$ dominance type of gene action for this trait, while Srikantaradhya (1984) reported additive $\times$ additive type of epistasis. Dominance $\times$ dominance type of gene action also was reported in another cross of cowpea by Ningappa (1979), Thiyagarajan *et al.* (1990) and Balaraju (1997).

Secondary branches

Thiyagarajan *et al.* (1990) and Balaraju (1997) reported on the preponderance of additive gene effect. Whereas, Bhushana (1996) has reported dominance gene effect for the inheritance of this traits.

Pods per plant

Number of pods per plant was found to be under the control of additive gene action as reported by Ningappa (1979), Marangappanavar (1984), Kabi Raj (1986),

Thiyagarajan *et al.* (1990) and Savithramma (1991). This trait was also under the control of non-additive gene action as reported by Kabi Raj (1986), Singh and Dabas, (1986), Balaraju (1997) and Khanum, (2001), additive $\times$ additive and additive $\times$ dominance (Ningappa, 1979; Srikantardhya, 1984 and Patil and Patil, 1986) gene effects.

Pod length

The predominant role of additive gene effect for pod length was reported by Marangappanavar (1984), Kabi Raj (1986), Patil and Patil (1986), Patil and Baviskar (1987), Thiyagarajan *et al.* (1990) and Balaraju (1997). The trait was also under the control of dominance in another cross of Marangappanavar (1984), Arun Kumar (1989), Madhusudhan (1994), Bhushana (1996). Additive gene action followed by additive $\times$ additive gene action were also reported by Srikantaradhya (1984), Hazra *et al.* (1993), while dominance $\times$ dominance by Hazra *et al.* (1993) and Khanum (2001).

Seeds per pod

Dominance effects followed by epistasis was observed for number of seeds per pod by Ningappa (1979), Marangappanavar (1984), Arun Kumar (1989) and Balaraju (1997). The predominant role of additive gene effect was evidenced from the study of Marangappanavar (1984), Srikantaradhya (1984), Savithramma (1991), Madhusudan (1994) and Bhushana (1996). Additive $\times$ Additive (Patil and Patil, (1987) and non additive (Kabi Raj, 1986) gene actions were also reported for this trait.

Hundred seed weight

Test weight was reported to be controlled by additive gene effect (Ningappa, 1979; Singh and Dabas, 1986; Patil and Patil, 1986; Savithramma, 1991; Madhusudan, 1994 and Balaraju, 1997). However, additive followed by dominance gene effect were reported by Jatsara (1980); Kabi Raj (1986) and Arun Kumar (1989). Additive $\times$ dominance effect was observed by Ningappa (1979). Whereas, Bhushana (1996) observed the importance of only dominance gene action.

Seed yield per plant

The importance of dominance gene action for seed yield per plant was reported by Marangappanavar (1984), Kabi Raj (1986), Patil and Patil (1986), Arun Kumar (1989), Savithramma (1991), Madhusudan (1994) and Bhushana (1996). However, Patil and Patil, 1986; Patil and Patil, 1987 and Shakarad *et al.*, 1995 reported preponderance of additive gene effects. Additive $\times$ additive gene effects were reported by Ningappa, (1979), Srikantaradhya (1984) and Balaraju (1997).

Whereas, dominance $\times$ dominance gene action was also found to influence the inheritance of this trait in cowpea was reported by Ningappa (1979).

2.4 Character association

Grain yield in any crop depends on many component characters which influence yield either jointly or single and either directly or indirectly through other related characters. Selection for yield on the basis of *per se* performance alone may not be effective compared to selection based on the component character associated with it which is biometrically determined by correlation and path analysis. Understanding the nature and extent of association of these components with seed yield and amongst themselves is an essential pre-requisite for formulating sound breeding programme.

The concept of correlation was given by Fisher (1918) and Wright (1921). The information on correlation is of great importance when simultaneous selection is to be carried out for more than one character to achieve the required improvement in seed yield.

The correlation coefficient analysis measures the mutual relationship between various characters and it determines the component traits on which selection can be relied upon to effect the improvement. The Association of characters can be expressed as phenotypic correlation and genotypic correlation coefficient.

Phenotypic correlation is the observable correlation between two variables and includes both genotypic and environmental effects. Genotypic correlation on the other

hand, is the inherent association between two variables which may be either due to pleiotropic action of genes or linkage, more likely both or developmentally induced relationships.

A brief review of the nature of correlation of different characters on yield in cowpea reported by several workers are presented below.

The literature reviewed indicated that, characters such, days to maturity, plant height, primary branches, pods per plant, pod length, seeds per pod and 100-seed weight were found to be positively correlated with seed yield. Few workers also reported negative correlation of days to 50 per cent flowering, days to physiological maturity, plant height, pods per pod and 100-seed weight with seed yield

2.4.1 Yield contributing characters in cowpea

Yield is considered as “dependent character” (effect) which is influenced by many “independent characters” (causes). When such a cause and effect relationship exists, each cause would have a direct effect (path coefficient) and number of indirect effects through other characters on the dependent character yield. The major yield components in cowpea are pod numbers, seeds per pod and hundred seed weight. These in turn are influenced by number of other traits like plant height, number of clusters per plant, pod length, etc. Any change in yield has to be brought from a change in one or more of these components (Grafius, 1969). The details of character association was reported by several workers are tabulated in the Table 5 and Table 6.

2.5 Path coefficient analysis

Path coefficient analysis, which is simply a standardized partial regression was developed by Wright (1921) and later developed by Dewey and Lu (1959). Path coefficient analysis permits the paring of correlation coefficient into direct and indirect effects and gives a more realistic relationship of the character and helps in identifying the effects components. The available literature on path analysis on seed yield with their component traits in cowpea was briefly reviewed.

Table 5: Summary of review of literature on correlation of different yield attributing characters with seed yield per plant in cowpea (*Vigna unguiculata* L. Walp)

Character	Nature of association	Material used	Reference
Plant height	Positive	F ₃ and F ₄ of 12 crosses F ₄ of 2 crosses 8 Parents and their 28 F ₁ s and F ₂ s F ₂ of single cross F ₂ of 28 cross 35 genotypes 30 genotypes 14 genotypes 168 genotypes 9 genotypes 65 genotypes	Kalaiyarasi and Palaniswamy (1999) Kalaiyarasi and Palaniswamy (2001) Yadav <i>et al.</i> (2004) Belkher <i>et al.</i> (2003) Neema and Palaniswamy (2003) Patil (2006) Eswaran <i>et al.</i> (2007) Kumari U R <i>et al.</i> (2010) Gitanjali <i>et al.</i> (2013) Madhavi <i>et al.</i> (2014) Singh <i>et al.</i> (2014)
	Negative	15 genotypes	Tudu D <i>et al.</i> (2014)
Days to maturity	Negative	14 geneotypes	Kumari U R <i>et al.</i> (2010)
Days to flowering	Positive	45 geneotypes 22 geneotypes 30 F ₁ s 30 genotypes 168 genotypes	Singh and Verma (2002) Singh <i>et al.</i> (2010) Mittal and Singh (2005) Eswaran <i>et al.</i> (2007) Gitanjali <i>et al.</i> (2013)
	Negative	50 genotypes 30 genotypes 14 genotypes 9 genotypes 15 genotypes	Mittal and Singh (2005) Eswaran <i>et al.</i> (2007) Usha Kumari <i>et al.</i> (2010) Madhavi <i>et al.</i> (2014) Tudu <i>et al.</i> (2014)
Pod length	Positive	F ₂ s of 28 crosses 8 parents and their 28 F ₁ s and F ₂ s 37 genotypes 6 genotypes 26 genotypes 35 genotypes 30 genotypes 7 parents and 21 F ₁ s	Neema and Palaniswamy (2003) Yadav <i>et al.</i> (2004) Kutty <i>et al.</i> (2005) Pekson and Artk (2004) Anbumalarmathi <i>et al.</i> (2005) Patil (2006) Suganthi and Murugan (2008) Romanus <i>et al.</i> (2008)

Character	Nature of association	Material used	Reference
		F ₂ s of single cross 168 genotypes 9 genotypes 65 genotypes	Asish (2009) Gitanjali <i>et al.</i> (2013) Madhavi <i>et al.</i> (2014) Singh <i>et al.</i> (2014)
Seed per pod	Positive	F ₄ of 2 crosses F ₂ s of 5 crosses 8 parents and their 28 F ₁ s and F ₂ s 26 genotypes 35 genotypes 15 genotypes 7 parents and 21 F ₁ s F ₃ of single cross F ₂ of single cross 14 genotypes 168 genotypes 9 genotypes	Kalaiyarasi and Palaniswamy (2001) Malarvizhi and Rangaswamy (2003) Yadav <i>et al.</i> (2004) Anbumalarmathi <i>et al.</i> (2005) Patil <i>et al.</i> (2006) Tudu <i>et al.</i> (2014) Romanus <i>et al.</i> (2008) Padi and Ehlers (2008) Asish (2009) Kumari U <i>et al.</i> (2010) Gitanjali <i>et al.</i> (2013) Madhavi <i>et al.</i> (2014)
Pods per plant	Positive	14 genotypes 65 genotypes	Kumari U <i>et al.</i> (2010) Singh <i>et al.</i> (2014)
Hundred seed weight	Positive	F ₄ of 2 crosses F ₂ of single cross 50 genotypes 6 genotypes 30 F ₁ s 26 genotypes 35 genotypes F ₂ of single cross 168 genotypes 9 genotypes	Kalaiyarasi and Palaniswamy (1999) Belkher <i>et al.</i> (2003) Kumari <i>et al.</i> (2003) Pekson and Artk (2004) Mittal and Singh (2005) Anbumalarmathi <i>et al.</i> (2005) Patil <i>et al.</i> (2006) Asish (2009) Gitanjali <i>et al.</i> (2013)
	Negative	14 genotypes	Kumari U <i>et al.</i> (2010)

Table 6: Summary of review of literature on correlation among different yield attributing traits in cowpea (*Vigna unguiculata* L. Walp)

Character	Nature of association	Character correlated	Reference
Plant height	Positive	Pod length	Naidu <i>et al.</i> (1996) Kalaiyarasi and Palaniswamy (1999) Venkatesan <i>et al.</i> (2003) Neema and Palaniswamy (2003) Madhavi <i>et al.</i> (2014) Singh <i>et al.</i> (2014)
		Seeds per pod	Neema and Palaniswamy (2003) Madhavi <i>et al.</i> (2014) Singh <i>et al.</i> (2014)
		Test weight	Parmar <i>et al.</i> (2003) Madhavi <i>et al.</i> (2014)
		Pods per plant	Kumari U <i>et al.</i> (2010)
	Negative	Pods per plant	Neema and Palaniswamy (2003) Singh <i>et al.</i> (2014)
		Braches per plant	Singh <i>et al.</i> (2014)
Days to flowering	Positive	Plant height	Naidu <i>et al.</i> (1996), Tyagi <i>et al.</i> (2000) Parmar <i>et al.</i> (2003)
		Days to maturity	Parmar <i>et al.</i> (2003), Romanus <i>et al.</i> (2008)
		Pods per plant	Tyagi <i>et al.</i> (2000)
		Seeds per pod	Singh <i>et al.</i> (1998) Kumar <i>et al.</i> (2001) Romanus <i>et al.</i> (2008)
		Pod Length	Kumar <i>et al.</i> (2001), Romanus <i>et al.</i> (2008)
	Negative	Plant height	Singh and verma (2002)
		Pods per plant	Kutty <i>et al.</i> (2003) Madhavi <i>et al.</i> (2014)
		Pod length	Madhavi <i>et al.</i> (2014)
		Seeds per pod	Madhavi <i>et al.</i> (2014)
		Hundred seed weight	Madhavi <i>et al.</i> (2014)
		Seed yield	Madhavi <i>et al.</i> (2014)

Character	Nature of association	Character correlated	Reference
Pods per plant	Positive	Seeds per pod	Singh <i>et al.</i> (1998)
	Negative	Plant height	Singh <i>et al.</i> (1998) Venkatesan <i>et al.</i> (2003) Chuhan <i>et al.</i> (2003) Neema and Palaniswamy (2003) Singh <i>et al.</i> (2014)
		Seeds per pod	Mathur (1995)
		Test weight	Singh <i>et al.</i> (1998) Kutty <i>et al.</i> (2003)
		Days to maturity	Kumari U <i>et al.</i> (2010)
Pod length	Positive	Pods per plant	Madhavi <i>et al.</i> (2014) Singh <i>et al.</i> (2014)
		Seeds per pod	
		Hundred seed weight	
		Seed yield	
		Plant height	Singh <i>et al.</i> (2014)
Seeds per pod	Positive	Plant height	Kalaiyarasi and Palaniswamy (1999) Chuhan <i>et al.</i> (2003) Usha Kumari <i>et al.</i> (2010) Madhavi <i>et al.</i> (2014) Singh <i>et al.</i> (2014)
		Pod length	Mathur (1995) Naidu <i>et al.</i> (1996) Biradar <i>et al.</i> (1991) Singh <i>et al.</i> (1998) Kalaiyarasi and Palaniswamy (1999) Tyagi <i>et al.</i> (2000) Kumar <i>et al.</i> (2001) Kutty <i>et al.</i> (2003) Chuhan <i>et al.</i> (2003) Tyagi <i>et al.</i> (2000) Kumari U <i>et al.</i> (2010) Madhavi <i>et al.</i> (2014)
		Pods per plant	Kumari U <i>et al.</i> (2010) Madhavi <i>et al.</i> (2014)

Character	Nature of association	Character correlated	Reference
Test weight	Positive	Plant height	Kalaiyarasi and Palaniswamy (1999) Tyagi <i>et al.</i> (2000) Kumar <i>et al.</i> (2001) Singh and Verma (2002) Venkatesan <i>et al.</i> (2003) Kumari U <i>et al.</i> (2010) Madhavi <i>et al.</i> (2014)
		Pods per plant	Biradar <i>et al.</i> (1991) Kalaiyarasi and Palaniswamy (1999) Kumari U <i>et al.</i> (2010) Madhavi <i>et al.</i> (2014)
		Seeds per pod	Naidu <i>et al.</i> (1996) Singh and Verma (2002) Usha Kumari <i>et al.</i> (2010) Madhavi <i>et al.</i> (2014)
	Negative	Pod Length	Tamilselvam and Das (1994) Naidu <i>et al.</i> (1996) Singh <i>et al.</i> (1998) Kalaiyarasi and Palaniswamy (1999) Kumar <i>et al.</i> (2001) Singh and Verma (2002) Madhavi <i>et al.</i> (2014)
		Pods per plant	Singh and Verma (2002) Chuhan <i>et al.</i> (2003) Venkatesan <i>et al.</i> (2003) Asish (2009)
		Seeds per pod	Kalaiyarasi and Palaniswamy (1999) Venkatesan <i>et al.</i> (2003)
		Days to maturity	Kumari U <i>et al.</i> (2010)

Chikkadevaiah (1980) observed the direct effect of plant spread, pods per plant and seeds per pod on seed yield in a study consisting of various cowpea genotypes.

Patil and Bhapkar *et al.* (1989) while studying path coefficient analysis reported that pods per plant, 100 seed weight and seeds per pod had greatest positive direct effect on yield in a study consisting of various cowpea genotypes.

The highest positive direct effect on grain yield was recorded by pod yield and lowest by pod length. The indirect effect was maximum for pod length via pod yield. The direct effect of pod yield on grain yield and the genotypic correlation between pod yield and grain were almost equal, this study was conducted by Neema and Palinisamy (2001)

2.6 Drought tolerance

The majority of the studies on drought tolerance in the cowpea are through the box screening or through the laboratory techniques but the use of physiological traits such as specific leaf area and SCMR readings were very rare.

Presently, only a few studies have been reported in the selection of cowpea varieties on the basis of their tolerance to water stress. The strategy is to screen cowpea genotypes on the basis of their tolerance to water stress which was based on the assessment of shoot dry matter and leaf area under well watered and drought treatments in the field conditions. These studies allow identifying cowpea genotypes showing tolerance to water stress.

A large number of cowpea germplasm accessions have been evaluated for drought tolerance in various parts of the world and desirable lines identified. In addition, more germplasm lines still need to be evaluated in order to identify new and better adapted sources of drought tolerance under various environmental conditions. The most common method of screening cowpea genotypes for drought tolerance has been the use of: visual symptoms of wilting or the plant death and recovery system as reported by Mai-Kodomi *et al.* (1999).

A decorative red border shaped like a scroll, with a vertical strip on the left and a horizontal strip on the right, both ending in small circular loops.

Material and Methods

III MATERIAL AND METHODS

Main aim of the study was to estimate the variability, heritability, genetic advance and gene action for the traits associated with seed yield and yield attributing traits in cowpea. The material used, methodologies followed for conducting the experiment and the methods adopted for statistical analysis of the data for experiment are presented in the following paragraphs.

3.1 Location of the experiment

The present experiment was carried out at Dry Land Agriculture Project, Gandhi Krishi Vignana Kendra, GKVK campus of the University of Agricultural Sciences, Bangalore which is situated at an altitude of 930 meters above mean sea level (MSL), 12 ° 15' north latitude and east longitude lying in the eastern dry zone. The soil type is red sandy loamy with pH of 5.2. The average annual rainfall is 851 mm.

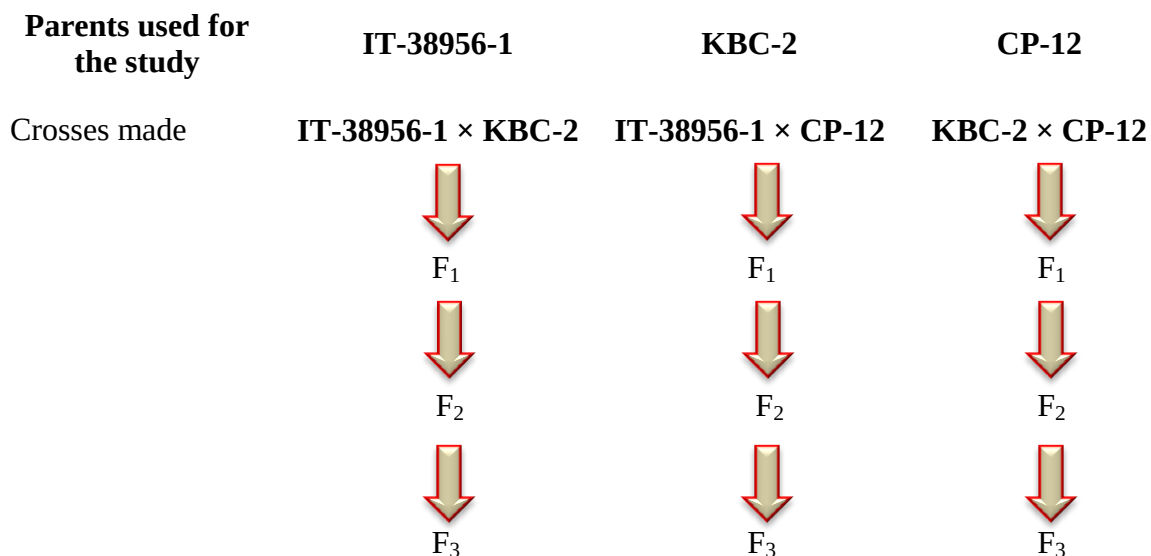
3.2 Generation of the experimental material

Based on the results of earlier studies, three diverse cowpea genotypes/varieties viz., IT-38956-1, KBC-2 and CP-12 were selected and used as parents for hybridization to produce three cross combinations.

The salient features of the parents used in the hybridization are shown in the Table 7.

Table 7: Salient features of parental lines used in the study

Parent	Pedigree or origin	Plant habitat	Year of release
IT-38956-1	Introduction from IITA, Nigeria	Semi determinant	2006
KBC-2	Selection from V-16 mutants	Semi determinant	1999
CP-12	Selection from germplasm line of AICRP on arid legumes	Determinate with high vegetative growth	-



The schematic drawing showing the details of parents and generations of F₁, F₂ and F₃ crosses using the selected parents.

Different generations of above crosses viz., F₁, F₂ and F₃ along with their respective parents formed the material for the present study.

3.2.1 Hybridization

Parents were grown during early summer-2008 to effect the hybridization. The crop was raised with the recommended package of practices and all necessary plant protection measures are followed to raise a good crop. For hybridization, flower buds which were about to open in the next morning were emasculated on the previous day evening by cutting keel petal and removing all the ten anthers with sterilized forceps. Next day morning, the receptive stigma was pollinated with pollen grains of male parents. Then the pollinated flower buds were bagged with butter paper cover to avoid contamination from foreign pollens. Five to ten per cent of successful pod setting was observed. The crossed pods were harvested separately after maturity. They were dried, threshed, stored with proper seed treatment and suitable labeling.



Plate 1: Field view of cowpea parent IT-38956-1



Plate 2: Field view of cowpea parent KBC-2



Plate 3: Field view of cowpea parent CP-12



Plate 4: Crossing block of cowpea



Plate 5: Crossed flowers of cowpea at initial stage



Plate 6: View of seeds of parents used for hybridization

3.2.2 Raising F₁ to get F₂ generation

By retaining sufficient F₁ seeds for the main experiment, the part of the seeds obtained from the four crosses were sown during *rabi* 2008. The F₁s were selfed and the F₂ seeds were harvested. After maturity the dried pods were harvested to get F₂ seeds. They were dried, threshed and preserved with proper care and labeling. By retaining sufficient F₂ seeds for the main experiment, part of the seeds from all the three crosses were sown during summer-2009 to raise F₃ seed.

3.2.3 Rising F₂ generation to get F₃ seeds by retaining sufficient seeds

The plant population in F₂ generation in all the three crosses ranged from 150 to 186. The crop was raised with all cultural practices recommended as per the standard package of practices for cowpea. The crop was kept weed free and plant protection measures were under taken to manage major pests and diseases.

3.2.4 Raising of F₃ families along with P₁, P₂, F₁, and F₂ for five generation mean analysis

Seeds of parents (P₁ and P₂), F₁, F₂ and F₃ generations for each of three crosses were sown during late *rabi* -2009, by following Randomized Complete Block Design with two replications. Separate blocks were assigned for all the crosses. Parent-1 (P₁), Parent-2 (P₂), F₁, F₂ and F₃ of each cross-formed three generations (Treatments) in each replication. Each replication consisted of four rows of each parent, three rows of F₁'s, one fifty to one eighty six (150-186) F₂ plants and 70 F₃ families of row length of three meters each, 70 randomly selected F₂ plants from previous generations were sown in 'Plant to Row Progeny' as F₃ families for the study of five generation mean analysis which were sown along with parents (P₁ and P₂), F₁, F₂ seeds simultaneously. The plant population from each of the F₃ families ranged from 10-25 plant. The crop was sown with a spacing of 45 cm between rows and 10 cm between plants. The crop was raised with protective irrigation, with all recommended package of practices and plant protection measures. Sufficient care was taken to maintain the minimum number of plants in all the treatments of all the crosses.

3.2.5 Recording of observations

In non-segregating generations which are replicated viz., parents and F_1 's, the data was recorded on ten randomly tagged plants in each replication, where as in case of segregating generations, the data were recorded on all 150-186 plants in F_2 generation and from 70 F_3 families. The observations on seed yield and its attributing characters were recorded on all selected plants as described as follows.

1. Days to first flowering

The days to first flowering was monitored and recorded as number of days taken from date of sowing to the day on which first flower opened was observed.

2. Days to maturity

Number of days taken from the date of sowing to 90 per cent physiological maturity i.e., when pods of the plants turned to yellow, with senescence of leaves was taken as days to maturity.

3. Plant height (cm)

The plant height was recorded in centimeter (cm) from ground level to the growing tip at the time of maturity.

4. Primary branches per plant

Number of primary branches were counted in each of selected plants and expressed as a number per plant.

5. Secondary branches per plant

Number of secondary branches were counted in selected tagged plants expressed as a number per plant.

6. Number of pods per plant

Number of pods per plant were counted in each of selected plants.

7. Pod length (cm)

From the selected plants, five dry pods were picked at random to record length of the pods in centimeter and average value was represented as pod length.

8. Seeds per pod

Five randomly selected pods were taken from each plant for counting number of seeds per pod. The seeds per pod from each of selected pods were counted and mean was calculated and expressed as number of seeds per pod.

9. Seed yield per plant (g)

Total seeds harvested from each selected plant were weighed using precession balance and expressed as grams/plant.

10. Hundred seed weight (g)

One hundred seeds were counted from each of the selected plants and weight was recorded in grams.

3.3 Study the extent of variability and character association of quantitative and physiological traits in F₃ generation of cowpea cross IT-38956-1 × KBC-2

3.3.1 Material for the study

For this study, the F₃ materials of the cross IT-38956-1 × KBC-2 were used for recording the observations and analysis.

3.3.2 Recording observations

The observations on only two physiological characters viz., specific leaf area and SCMR were recorded which are described below.

1. Specific leaf area(cm²/g)

The fully expanded, healthy leaf (avoiding the damaged leaf) from the apex of the main axis in each plant was collected in the early morning at 60 days after the sowing

(DAS) and leaf area has been measured using the leaf area meter, after that the leaf were oven dried at 80⁰c for at least 45 hours to determine the leaf dry weight. SLA was computed using the following formula.

$$SLA = \frac{\text{Leaf area (cm}^2\text{)}}{\text{Dry leaf weight (g)}}$$

2. SPAD chlorophyll meter reading

Among several leaf characters, leaf thickness and chlorophyll content determines the leaf transmittance. Leaf nitrogen content normally influences the leaf chlorophyll content. A device has been developed by MINOLTA company, New Jersey USA (SPAD-502) which measures the light attenuation at 430 nm (the peak wave length adsorption by chlorophyll a and chlorophyll b) and at 750 nm (near infrared) with no transmittance. The unit less value measured by the chlorophyll meter is termed as SPAD chlorophyll meter reading (SCMR) which indicate relative amount of leaf chlorophyll. The SPAD meter is a simple hand held instrument, which operates with DC power of three volts.

The full expanded second or third leaf of the secondary branches was used to record the observation. Selected leaf was clamped avoiding the mid rib and inserted in to the sensor head of SPAD meter. A gentle stroke was given to record the SPAD reading and the average of such four to five strokes was given to record the SPAD reading and the average of such five stokes per leaflet was considered. Since cowpea has trifoliate leaf, SCMR was recorded in all the four leaflets and average value was computed. SPAD chlorophyll meter readings were taken at 60 days after sowing in the early *rabi*-2009.

3.4 Study of genetic variability parameters in three F₂ populations of cowpea

For this study, F₂ generation of the three cowpea crosses viz., IT-38956-1 × KBC-2, IT-38956-1 × CP-12 and KBC-2 × CP-12 were used and the statistical methods used are described below.

3.4.1 Statistical Analysis

The mean and variance values of randomly selected plants in each entry were computed for all the quantitative traits mentioned above and were subjected to statistical analysis.

3.4.1.1 Descriptive Statistics: The following descriptive statistics were calculated as per Sundara Raj *et al.* (1972)

1. Mean

Mean is the sum of all the observations in a sample divided by the number of observations (n).

$$\text{Mean} = \Sigma x_i / n$$

where, x_i = i^{th} observation of a population

n = number of observations

2. Range

Range is the minimum and maximum values of the observations in a sample.

3. Standard Error

It is the measure of uncontrolled variation present in a sample. It is estimated by dividing the estimates of standard deviation by the square root of number of observations in the sample and is denoted by SE.

$$\text{Thus, SE} = \text{SD} / \sqrt{n}$$

where,

SD = Standard deviation and n = Number of observations

4. Variance

Variance is defined as the average of the squared deviations of individual observation from the mean or it is the square of the standard deviation. It is expressed as the sum of squares of the deviations of all observations of a sample from its mean and

divided by (n-1), where n is the number of observations. It is an effective measure of variability, which permits partition of variation into various components. It is estimated by the following formula,

$$\text{Variance} = \frac{\sum x_i^2 - (\sum x)^2/n}{N-1}$$

Where,

x_i = i^{th} observation of a population,

n=number of observations

5. Skewness and Kurtosis

Skewness, the third degree statistics and kurtosis, the fourth degree statistics were estimated as per Snedecor and Cochran (1967) to understand the nature of distribution of 10 quantitative traits in F_2 population of each cross. The mean values of 10 quantitative traits of each cross were used to estimate coefficients of skewness and kurtosis using 'SPSS' software program. Genetic expectations of skewness ($-3/2 d^2 h$) would reveal the nature of genetic control of the traits (Fisher *et al.*, 1932). The parameter 'd' represents additive gene effects and 'h' represents dominance gene effects. Kurtosis indicates the relative number of genes controlling the traits (Robson, 1956). Three types of kurtosis are recognized based on the kurtosis value which depends on distribution curve.

If kurtosis value = 3 = Normal curve = **Mesokurtic**

If kurtosis value > 3 = Leaping curve = **Leptokurtic**

If kurtosis value < 3 = Flat curve = **Platykurtic**

Similarly, the lack of symmetry *i.e.*, skewness was recognized based on the coefficient of skewness values which range from -3 to +3. The type of distribution based on the skewness values are as follows.

If skewness value is zero = **Symmetrical distribution**

If skewness value is negative = **Negatively skewed distribution**

If skewness value is positive = **Positively skewed distribution**

3.4.1.2 Estimation of variability parameters

The variability for traits related to yield per plant in cowpea were estimated in the two F₂ populations as detailed below.

1. Phenotypic and genotypic variance

Phenotypic and genotypic components of variance in F₂ population for each of the ten characters were computed as per the method suggested by Weber and Moorthy (1952).

i. Phenotypic variance (σ^2_p) = **Total observed variance (σ^2_{pF2})**

ii. Genotypic variance (σ^2_g) = $\sigma^2_{pF2} - \sigma^2_e$

Where,

$$\sigma^2_e = \text{Environmental variance} = (\sigma^2_{P1} + \sigma^2_{P2} + 2 \sigma^2_{F1}) / 4$$

Where,

σ^2_{P1} = Phenotypic variance of parent 1 of that particular cross.

σ^2_{P2} = Phenotypic variance of parent 2 of that particular cross

σ^2_{F1} = Phenotypic variance of F₁ of that particular cross.

2. Genotypic and phenotypic co-efficient of variation

Both phenotypic and genotypic co-efficient of variation for all the characters were estimated using the formulae of Burton and De Vane (1953).

i. **Genotypic Co-efficient of Variation (GCV):**

$$\text{GCV (\%)} = \frac{\sqrt{\text{Genotypic variance of } F_2}}{\text{Population Mean}} \times 100$$

ii. **Phenotypic Co-efficient of Variation (PCV):**

$$\text{PCV (\%)} = \frac{\sqrt{\text{Phenotypic variance of } F_2}}{\text{Population Mean}} \times 100$$

PCV and GCV were classified as shown below following the method suggested by Robinson *et al.* (1949).

0-10% - Low; 10 -20% - Moderate; >20% - High

3. Heritability in broad sense (h^2_{bs})

Heritability (broad sense) was estimated for all the characters as the ratio of genotypic variance to the total variance as suggested by Johnson *et al.* (1955).

$$h^2_{bs} = \frac{\text{Genotypic variance of } F_2 \text{ population}}{\text{Phenotypic variance of } F_2 \text{ population}} \times 100$$

The heritability was categorized as given below following the classification of Robinson *et al.* (1956).

5-10 % = Low; 10-30 % = Moderate; >30 % = High

4. Genetic Advance (GA)

The extent of genetic advance expected through selection for each character was estimated by using the following formula of Johnson *et al.* (1955)

$$GA = h^2 \times K \times \sigma_p$$

where,

h^2 = heritability estimate

K = selection differential which is equal to 2.06 at 5% intensity of selection

σ_p = phenotypic standard deviation

Further, the Genetic Advance as per cent of mean was computed by using the following formula,

$$\text{GA as per cent of mean} = \frac{\text{Genetic Advance}}{\text{Grand mean}} \times 100$$

Genetic advance as per cent of mean was categorized as given below following the method of Johnson *et al.* (1955).

0 - 10% = Low; 10 - 20% = Moderate; >20 % = High

3.4.1.3 Association analysis

To determine the degree of association of characters with seed yield per plant and among the yield components, the correlation coefficients were calculated as shown below using the formula given by Al-Jibouri *et al.* (1958)

$$r_p(xy) = \frac{\text{Cov}_p(xy)}{\sqrt{\sigma^2_p(x) \cdot \sigma^2_p(y)}}$$

Where,

$r_p(xy)$ = phenotypic correlation coefficient between 'x' and 'y' characters

$\text{Cov}_p(xy)$ = phenotypic covariance of 'x' and 'y' characters

$\sigma^2_p(x)$ = phenotypic variance of 'x' character

$\sigma^2_p(y)$ = phenotypic variance of 'y' character

The calculated value of 'r' was compared with table 'r' value with (n-2) degrees of freedom at 5% and 1% level of significance, where n refers to number of pairs of observations.

3.4.1.4 Path coefficient analysis

Path coefficient analysis was carried out using phenotypic correlation values of yield components on yield as suggested by Wright (1921) and illustrated by Dewey and Lu (1959). Standard path coefficients which are the standardized partial regression coefficients were obtained using statistical software package called INDOSTST. These values were obtained by solving the following set of 'P' simultaneous equations by using the above package.

$$r_{1y} = P_{1y} + r_{12}P_{2y} + r_{13}P_{3y} + \dots + r_{1n}P_{ny}$$

$$r_{2y} = r_{12}P_{1y} + P_{2y} + r_{23}P_{3y} + \dots + r_{2n}P_{ny}$$



$$r_{ny} = r_{1n}P_{1y} + r_{2n}P_{2y} + r_{3n}P_{3y} + \dots + P_{ny}$$

Where,

$P_{1y}, P_{2y}, \dots, P_{ny}$ are the direct effects of variables 1, 2, ..., n on the dependent variable y and $r_{12}, r_{13}, \dots, r_{1n}, \dots, r_{n(n-1)}$ are the possible correlation coefficients between various independent variables and $r_{1y}, r_{2y}, r_{3y}, \dots, r_{ny}$ are the correlations between dependent and independent variables.

The indirect effect of the i^{th} variable via j^{th} variable was obtained as $(r_{ij}P_{iy})$. The contribution of remaining unknown factor is measured as the residual factor (P_R), which is calculated and given below.

$$\text{Residual factor} = P_R = \sqrt{1 - \sum P_{iy} r_{iy}}$$

The direct and indirect effects are rated as given below following the method of Lenka and Mishra (1973).

0.00 – 0.09 = Negligible

0.10 – 0.19 = Low

0.20 – 0.29 = Moderate

0.30 – 1.00 = High

> 1.00 = Very High

3.5 Study of gene effects for seed yield and yield attributing traits through five generation mean analysis

For this experimental analysis means and variances of P_1, P_2, F_1, F_2 and F_3 populations of the three cowpea crosses (IT-38956 × KBC-2, IT-38956 × CP-12 and KBC-2 × CP-12) were used. The statistical procedures followed for this study are mentioned as below.

3.5.1 Biometrical analysis

3.5.1.1 Analysis of variance

The population means for each replication was calculated and these means were used for the analysis of variance. The total variance was portioned into that due to non-

segregating generations (Parents and F_1) and segregating generations (F_2 and F_3) and the interaction between segregating versus non-segregating generations. The model of Five generation mean analysis of ANOVA is given below.

Table 8: ANOVA table is given below

Source	d.f.	M.S.S.
Replication	(r-1)	Mr
Treatment	(t-1)	Mt
1. Nonsegregating (NS)	(NS-1)	Mns
a) Parents (P)	(P-1)	MP
b) F_1 's	(F_1 -1)	MF ₁
c) P Vs F_1 's	1	MpF ₁
2. Segregating (S)	(S-1)	Ms
a) F_2 's	(F_2 -1)	MF ₂
b) F_3 's	(F_3 -1)	MF ₃
c) F_2 's Vs F_3 's	1	MF ₂ F ₃
3. NS V s S	1	Mnss
Error	(r-1)(t-1)	Me

Where, r = number of replications (2)

F_1 = Number of F_1 's (3)

t = number of treatments (15)

F_2 = Number of F_2 's (3)

p = number of parents (3)

F_3 = Number of F_3 's (3)

3.5.1.2 The mean and variance

The mean and variance for the different quantitative attributes were calculated for each population. The standard error (S.E.) of population mean was worked out as:

$$S. E. = \sqrt{\frac{\text{Variance}}{\text{Total No. of plants}}}$$

3.5.1.3 Heterosis and Inbreeding depression

Heterosis was calculated as the percentage increase or decrease of mean F_1 performance by the methods of Turner (1953) and Hayes *et al.* (1955) as shown below.

$$\text{Heterosis over Mid parent} = \frac{\overline{F_1} - \overline{MP}}{\overline{MP}} \times 100$$

$$\text{Heterosis over Better parent} = \frac{\overline{F_1} - \overline{BP}}{\overline{BP}} \times 100$$

Mid parent Value (MP): For each character, the arithmetic average, value of the two parents involved in each cross was computed as given below:

$$MP = 1/2 (P_1 + P_2)$$

Better parent value (BP): For each character, the superior value among the parents in each cross was taken for computation of heterobeltiosis.

The ‘t’ tests suggested by Chaudhary and Khanna (1978) were employed to certain significance of heterosis and are as shown under.

$$t \text{ MP} = \frac{\overline{F_1} - \overline{MP}}{\sqrt{\frac{Me}{r} \times \frac{3}{2}}} \qquad t \text{ BP} = \frac{\overline{F_1} - \overline{MP}}{\sqrt{\frac{Me}{r} \times 2}}$$

Where, Me = Error variance, r = Number of replication.

3.5.1.4 Inbreeding depressions

Inbreeding depression was computed as the percentage decrease from F_1 to F_2 and from F_2 to F_3 generation considering the overall means of F_1 , F_2 and F_3 generations for the characters.

$$\text{Inbreeding depression from } F_1 \text{ to } F_2 = \frac{\overline{F_1} - \overline{F_2}}{\overline{F_1}} \times 100$$

$$\text{Inbreeding depression from } F_2 \text{ to } F_3 = \frac{\overline{F_2} - \overline{F_3}}{\overline{F_2}} \times 100$$

3.5.2 Estimation of gene effects

3.5.2.1 Joint scaling test

The parameters such as m , the means of all possible genotypes arising out of selfing of a cross, $[d]$ additive gene effects and $[h]$ dominance deviation effects were estimated from the observed means of five generations (P_1 , P_2 , F_1 , F_2 and F_3) using Joint scaling test (Cavalli, 1952) as described by Mather and Jinks (1983) was carried out to estimate gene effects and simultaneously the adequacy of additive-dominance (3 parameter viz., $[m]$, $[d]$ and $[h]$) model was determined. When variances among generations were not equal, the best estimate of gene effects were obtained if the generation means are weighted (Mather and Jinks, 1983). For this reason, weighted least square techniques were used to estimate the genetic parameters viz., $[m]$, $[d]$, $[h]$, $[i]$ and $[l]$. Each generation mean was weighted by the inverse of the variance of that generation mean. For instance weight for P_1 as $W(P_1)$ is calculated as $W(P_1) = 1/V(P_1)$, where P_1 is the mean of the better parent.

Three normal equations required to estimate three parameters viz., m , $[d]$ and $[h]$ were obtained by multiplying each element of the row in the table 9 by the product of weight and coefficient of m and adding over five generations. In a similar manner, each element of other rows were multiplied by the product of their respective weights and coefficient of m . In a similar fashion, other two normal equations were obtained by multiplying each element of each row by the product of coefficient $[d]$ and its weight and coefficient $[h]$ and its weight.

The three normal equations obtained were as follows:

$$a_{11}m + a_{12}d + a_{13}h = A_1$$

$$a_{21}m + a_{22}d + a_{23}h = A_2$$

$$a_{31}m + a_{32}d + a_{33}h = A_3$$

Table 9: Coefficients of gene effects in the analysis of means of five generations

Gene effects	Generations				
	Λ	Λ	Λ	Λ	Λ
	M	[d]	[h]	[i]	[l]
P ₁	1	1	0	1	0
P ₂	1	-1	0	1	0
F ₁	1	0	1	0	1
F ₂	1	0	1/2	0	1/4
F ₃	1	0	1/4	1/4	1/4

Where, $A_1 = \sum i=1$ (Weight $\times$ coefficient of m $\times$ mean)

$A_2 = \sum i=1$ (Weight $\times$ coefficient of [d] $\times$ mean)

and $A_3 = \sum i=1$ (Weight $\times$ coefficient of [h] $\times$ mean)

The three normal equations so derived were arranged in the following matrix form,

$$\begin{array}{c} \left(\begin{array}{ccc} a_{11} & a_{12} & a_{13} \\ a_{21} & a_{22} & a_{23} \\ a_{31} & a_{32} & a_{33} \end{array} \right) \\ [J] \end{array} \begin{array}{c} \left(\begin{array}{c} m \\ d \\ h \end{array} \right) \\ [M] \end{array} = \begin{array}{c} \left(\begin{array}{c} A_1 \\ A_2 \\ A_3 \end{array} \right) \\ [S] \end{array} \text{ and indicated as,}$$

The elements of the three normal equations were obtained from the coefficient matrix called as “information matrix” [J]. Parameters to be estimated viz., m, [d] and [h] were arranged in a column matrix of parameters [M]. Elements of normal equations obtained as a result of multiplication of observed values by coefficients and weights were arranged in a column matrix [S] called as “Score Matrix.”

Estimates of m, [d] and [h] were obtained as $M=S.J^{-1}$. Where, J^{-1} is the inverse of information matrix, which is a variance- covariance matrix in which principal diagonal elements represent variances of the estimates of the parameters, m, [d] and [h]. Estimates of m, [d] and [h] were then used to calculate expected means of five generations. The expected values of generation means were calculated using following formulae.

$$P_1 = m-[d]$$

$$P_2 = m+[d]$$

$$F_1 = m+[h]$$

$$F_2 = m+1/2 [h] \text{ and}$$

$$F_3 = m+ 1/4 [h]$$

Chi-square test was employed to test the adequacy of additive-dominance model. Chi-square statistic was computed using the formula.

$$\chi^2 = \frac{[(\text{Observed mean}) - (\text{Expected mean})]^2}{\text{Expected mean}} \times \text{weight}$$

The Chi-square value was compared with table χ^2 at (5-3) degrees of freedom. The non-significance of Chi-square value indicates the adequacy of additive-dominance model. Significance of Chi-square test was indicative of non-adequacy of additive-dominance model. For such traits for which additive-dominance model was inadequate to explain their inheritance, the di-genic interaction effects, viz., additive $\times$ additive and dominance $\times$ dominance were estimated employing five parameter model using perfect fit solution (Jinks and Jones, 1958).

3.5.2.2 Five generation mean analysis

The estimates of various main effects of gene and nonallelic interaction components based on generation means were estimated following perfect fit solution as suggested by Hayman (1958). The generation means were used to estimate five of the six gene effects and they are mentioned here under.

Sl. No.	Gene effects	Notations of Hayman (1958)
1	Mean	m
2	Additive	[d]
3	Dominance	[h]
4	Additive $\times$ additive	[i]
5	Dominance $\times$ dominance	[l]

Standard error of the estimates of five parameters were calculated as,

$$SE(m) = \sqrt{A_{11}}$$

$$SE(d) = \sqrt{A_{22}}$$

$$SE(h) = \sqrt{A_{33}}$$

$$SE(i) = \sqrt{A_{44}} \text{ and}$$

$$SE(l) = \sqrt{A_{55}}$$

where, A_{11} , A_{22} , A_{33} , A_{44} , and A_{55} are the diagonal elements of the matrix J^{-1} .

The 't' test was employed to test the significance of these estimates both at 0.01 and 0.05 probability level of significance and are given below.

$$tm = m/SE(m)$$

$$td = d/SE(d)$$

$$th = h/SE(h)$$

$$ti = i/SE(i)$$

$$tl = l/SE(l)$$

The calculated 't' values were compared with 1.96 and 2.575 which are the tabulated 't' values at 5 and 1 per cent level of significance, respectively.

3.5.2.3 Number of effective factors

The minimum number of effective factors differentiating the parent was worked out using the formula given by Wright (1968).

$$N = \frac{0.25 (0.75 - h + h^2) D^2}{\overline{VF_2} - \overline{VF_1}}$$

where, N = Estimated number of effective factors

$$h = \frac{\overline{F_1} - \overline{P_1}}{\overline{P_2} - \overline{P_1}}$$

$$D = \bar{P}_2 - \bar{P}_1$$

$\overline{VF_1}$ and $\overline{VF_2}$ = Variances of the F_1 and F_2 generations, respectively.

$\bar{P}_1$ and $\bar{P}_2$ = Means of the smaller and greater parent, respectively.

3.5.2.4 Potence Ratio (PR)

The Potence Ratio (PR) which indicates the degree of dominance was computed from generation means as per Peter and Frey (1966).

$$\text{In } F_1 \text{ generation, } h_1 = PR_1 = (F_1 - P) / (P_1 - P)$$

$$\text{In } F_2 \text{ generation, } h_2 = PR_2 = 2(F_2 - P) / (P_1 - P)$$

where, P = Average of two parents i.e., $(P_1 + P_2)/2$

P_1 = Mean of superior parent involved in the F_1

P_2 = Mean of inferior parents involved in the F_1

F_1 = Mean of F_1 population

F_2 = Mean of F_2 population

Based on the potence ratio, the degree of dominance in respect of different traits are classified as follows.

$PR > 0$ – No dominance, $PR > 1$ – Over dominance, $PR < 1$ – Partial dominance

$PR = 1$ – Complete dominance

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Experimental Results

IV EXPERIMENTAL RESULTS

The results obtained in the different experiments of the present study are presented in experiment wise as given bellow.

4.1 Study of genetic variability parameters in three F₂ populations of cowpea

4.1.1 Descriptive statistics of F₂ population of three crosses of cowpea

4.1.2 Genetic variability study in three crosses of cowpea

4.1.3 Character association

4.1.4 Path co-efficient analysis

4.1.5 Heterosis and inbreeding depression

4.2 Study of gene effects for yield and its attributing traits through generation mean analysis

4.2.1 Analysis of variances for segregating and non-segregating generations.

4.2.2 Means and variances for P₁, P₂, F₁, F₂ and F₃ populations

4.2.3 Estimation of gene effects

4.2.4 Scaling and joint scaling tests

4.2.5 Number of effective factors

4.2.6 Potence ratio

4.3 Estimating the relationship between physiological parameters with the seed yield of cowpea cross IT-38956-1 × KBC-2 in F₃ population

4.3.1 Descriptive statistics in the F₃ generation

4.3.2 Genetic variability parameters in F₃ generation

4.3.3 Correlation in F₃ generation

4.3.4 Path analysis in F₃ generation

4.4 Transgressive segregants

4.1 Study of genetic variability parameters in three F₂ populations of cowpea

4.1.1 Descriptive statistics in three F₂ population of cowpea crosses

The descriptive statistics viz., mean, range, variance, skewness (S) and kurtosis (K) with respect to all the ten quantitative characters in F₂ population of the three cowpea crosses are tabulated in Table 10 to Table 12 and briefly presented below.

4.1.1.1 Descriptive statistics in the F₂ population of cowpea cross IT- 38956-1 × KBC-2

The descriptive statistics for the F₂ population of the cowpea cross IT-38956-1 × KBC-2 are tabulated in the Table 10 and briefly outlined below.

1. Days to first flowering

Days to first flowering varied from 31 to 50 days with a mean of 33 days and variance of 32 days indicated high variation for this trait.

Platykurtic (K=-0.56) and positively skewed distribution (S=0.04) is an evidence of involvement of overall large number of genes with dominance and dominance based complementary interaction in the inheritance of days to first flowering (Fig. 1).

2. Days to maturity

Days to maturity ranged from 70 to 98 days with a mean value of 84 days and variance of 75 days indicating wide range of variability for the trait.

Platykurtic (K=-0.61) and negatively skewed (S=-0.29) distribution indicated the involvement of large number of dominant genes having increasing effects and duplicate type of gene interaction in the inheritance of days to maturity (Fig. 2).

3. Plant Height (cm)

Plant height varied from 10.20 to 42.70 cm with a mean value of 27.73 cm and variance of 81cm indicating high variability for the trait.

Table 10: Descriptive statistics for ten quantitative characters in F₂ generation of the cowpea cross IT-38956-1 × KBC-2

Sl. No.	Character	Mean	Range		Variance	Skewness	Kurtosis	Kurtosis type
			Minimum	Maximum				
1	Days to first flowering	33.68	31.00	50.00	33.68	0.04	-0.56	P
2	Days to maturity	84.39	70.00	98.00	75.08	-0.29	-0.61	P
3	Plant height(cm)	27.73	10.20	42.70	81.00	0.85	-0.61	P
4	Primary branches per plant	5.23	2.00	9.00	4.13	0.47	1.70	P
5	Secondary branches per plant	10.17	4.00	16.00	11.26	-0.37	-0.39	P
6	Pods per plant	14.65	9.00	20.00	9.03	-0.17	0.35	P
7	Pod length(cm)	16.69	9.10	26.00	16.64	0.02	0.34	P
8	Seeds per pod	13.30	6.00	20.00	10.95	0.33	-0.09	P
9	Seed yield per plant(g)	18.74	9.17	30.35	34.56	0.22	0.14	P
10	Hundred seed weight(g)	11.11	9.12	13.34	1.33	0.23	1.25	P

P: Platykurtic

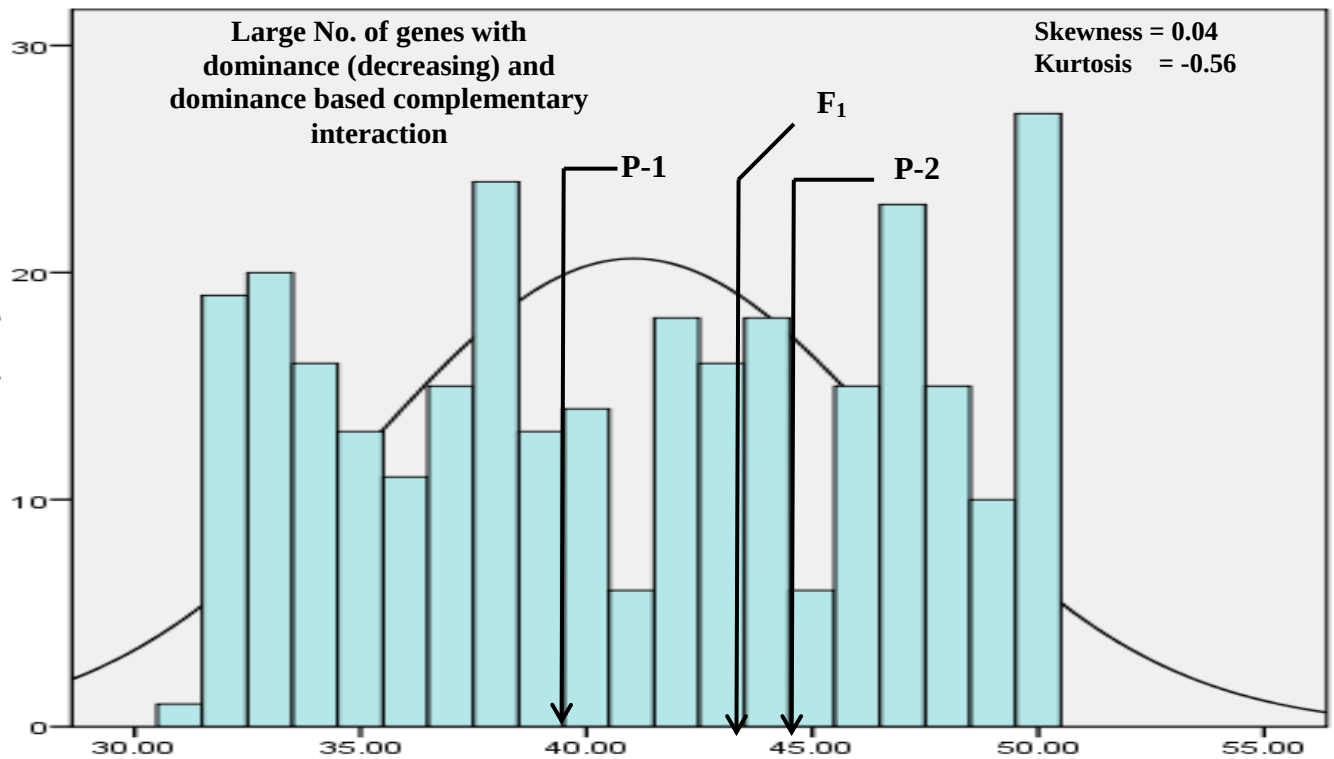


Figure 1: Platykurtic and positively skewed distribution of F₂ of IT-38956-1 × KBC-2 for days to first flowering

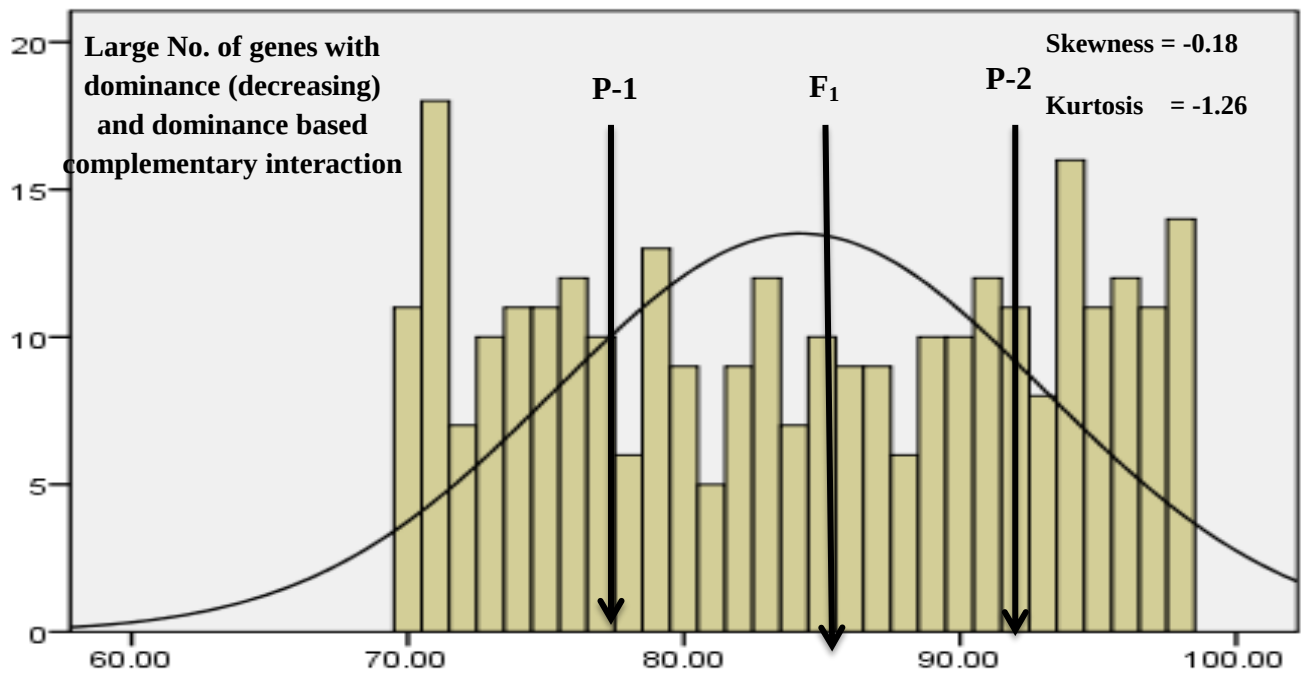


Figure 2: Platykurtic and negatively skewed distribution of F₂ of IT-38956-1 × KBC-2 for days to maturity

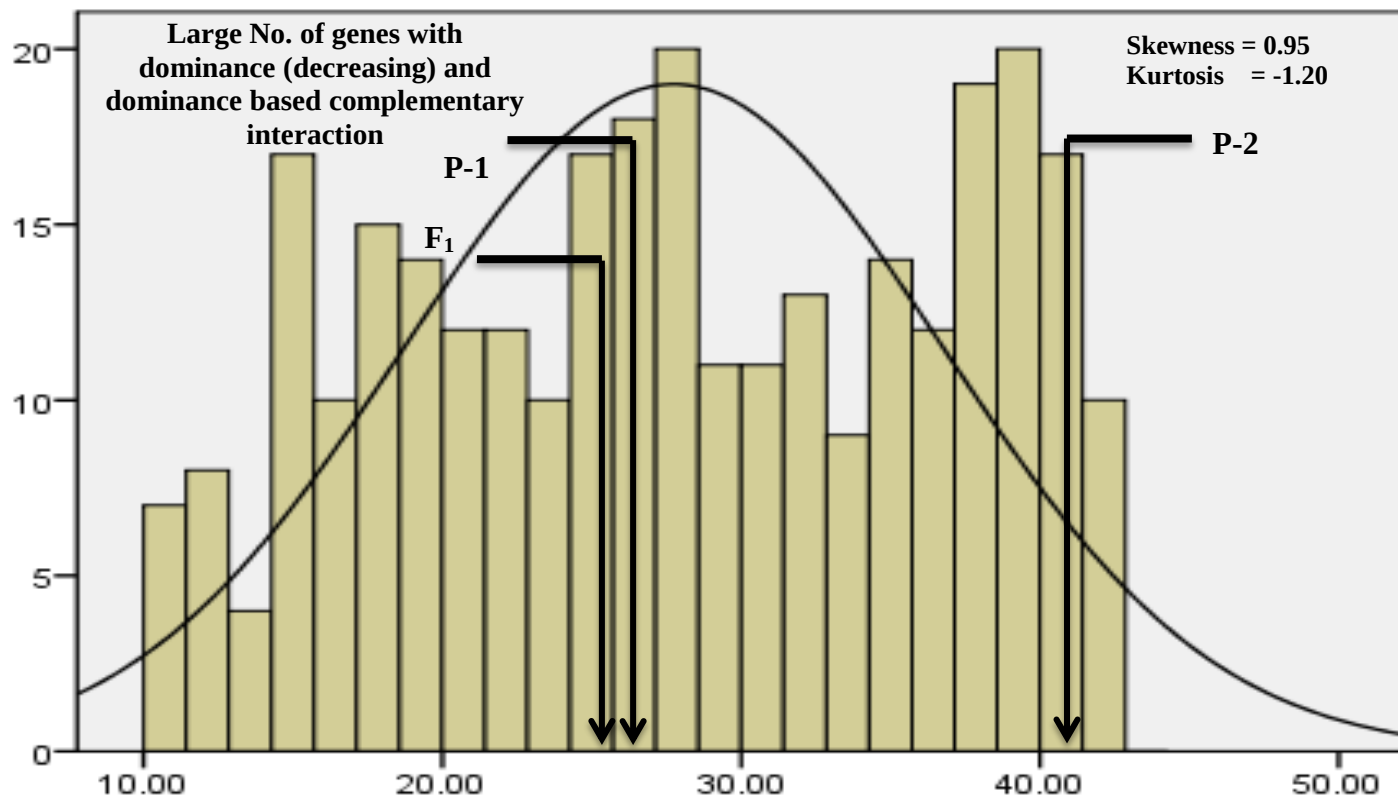


Figure 3: Platykurtic and positively skewed distribution of F₂ of IT-38956-1 × KBC-2 for plant height

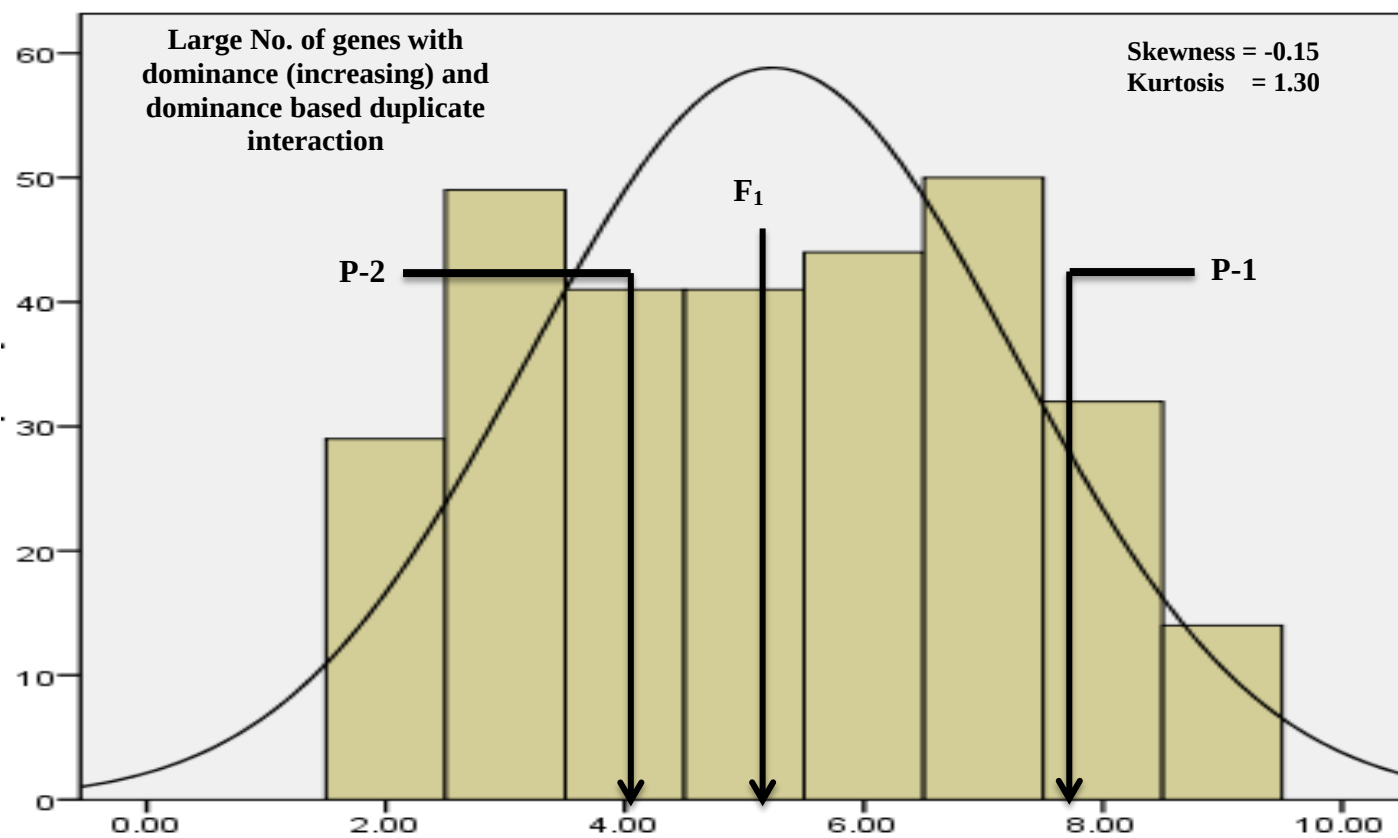


Figure 4: Platykurtic and negatively skewed distribution of F₂ of IT-38956-1 × KBC-2 for primary braches per plant

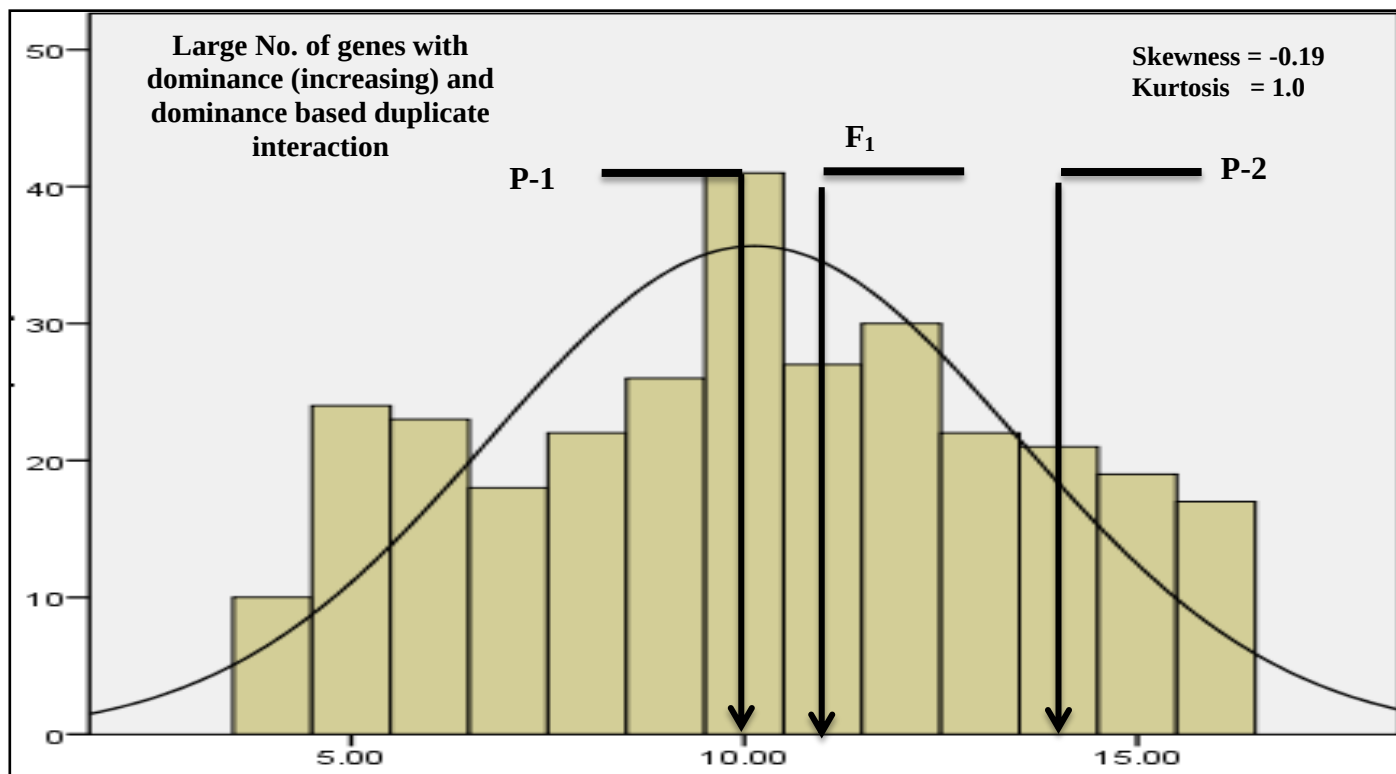


Figure 5: Platykurtic and negatively skewed distribution of F₂ of IT-38956-1 × KBC-2 for secondary braches per plant

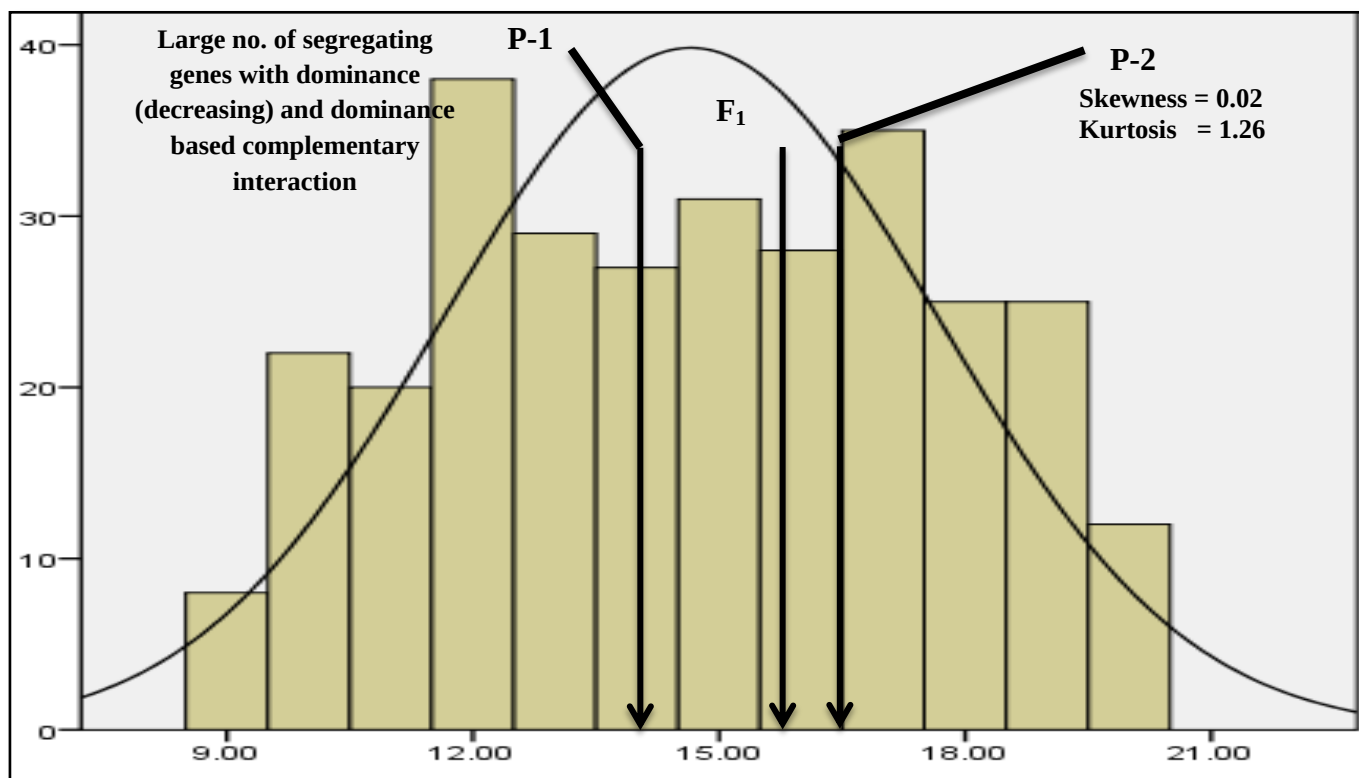


Figure 6: Platykurtic and positively skewed distribution of F₂ of IT-38956-1 × KBC-2 for pods per Plant.

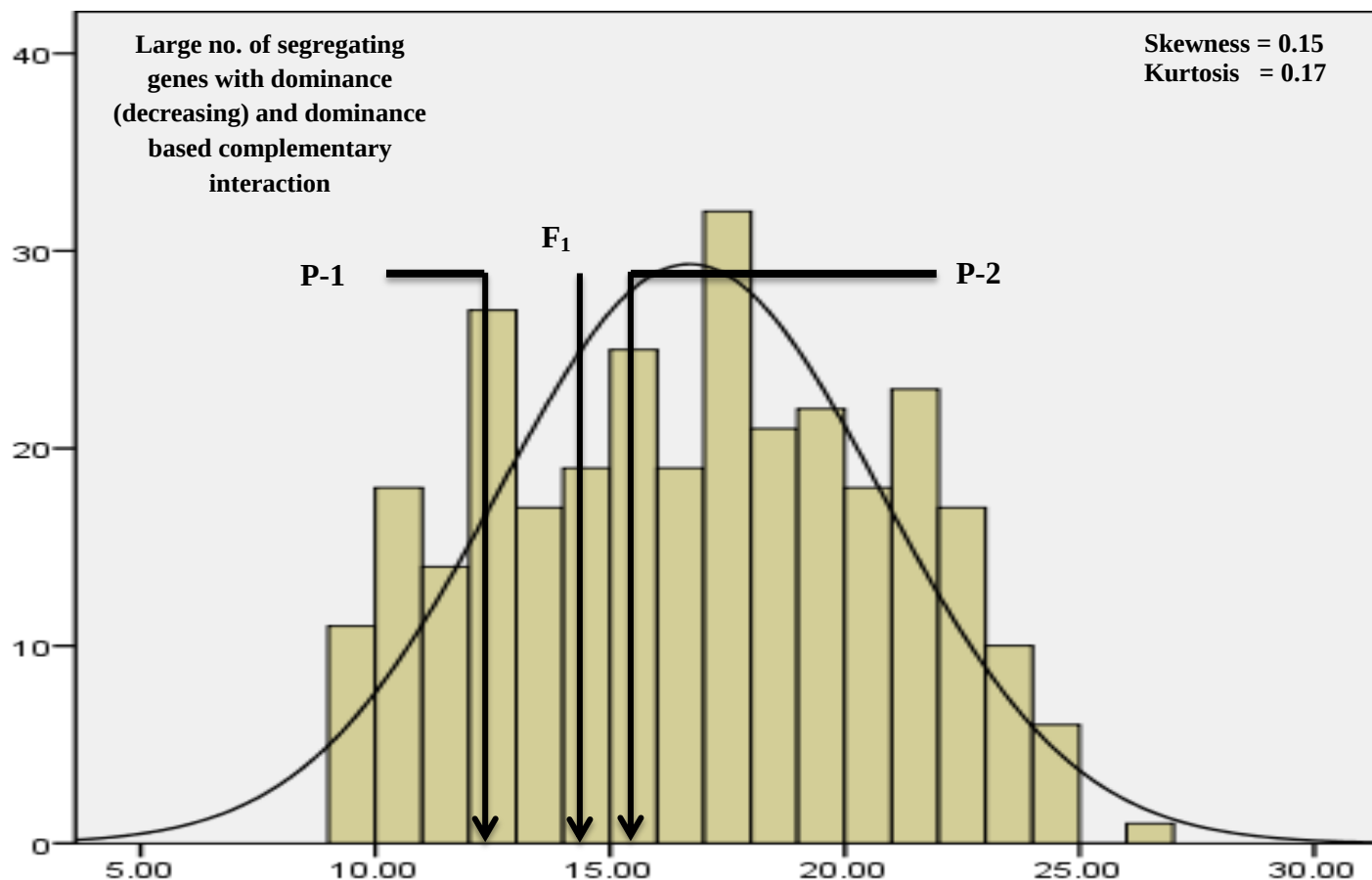


Figure 7: Platykurtic and positively skewed distribution of F₂ of IT-38956-1 × KBC-2 for pod Length.

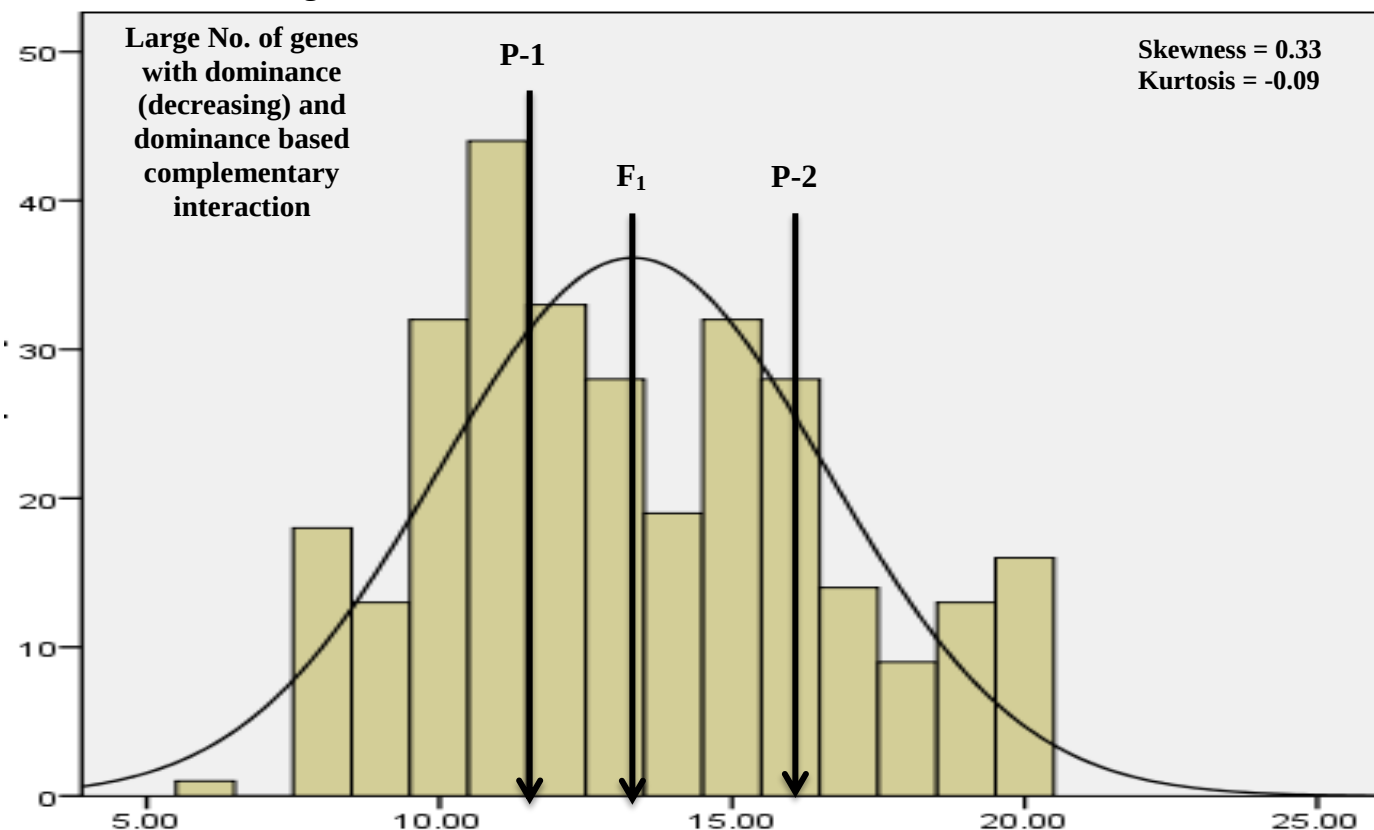


Figure 8: Platykurtic and positively skewed distribution of F₂ of IT-38956-1 × KBC-2 for seeds per pod.

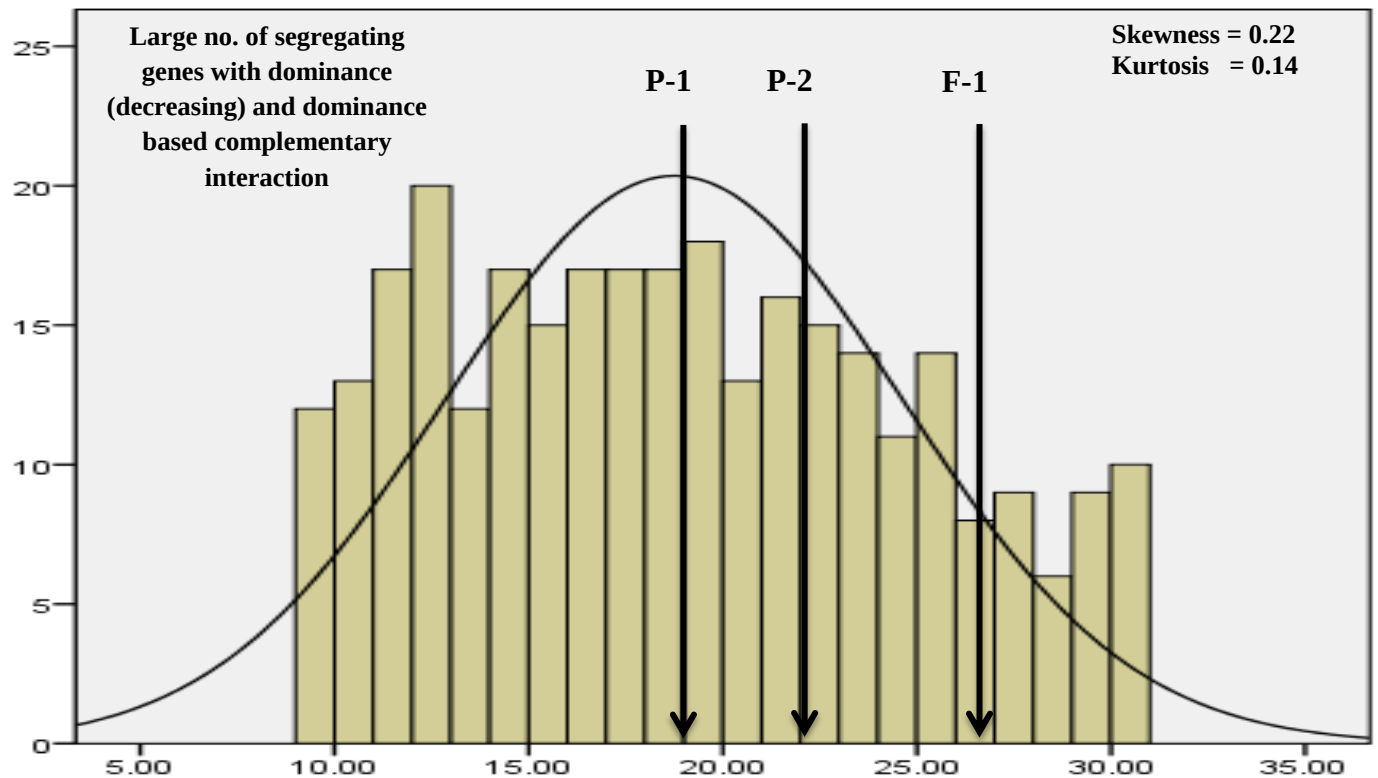


Figure 9: Platykurtic and positively skewed distribution of F_2 of IT-38956-1 $\times$ KBC-2 for seed yield per plant.

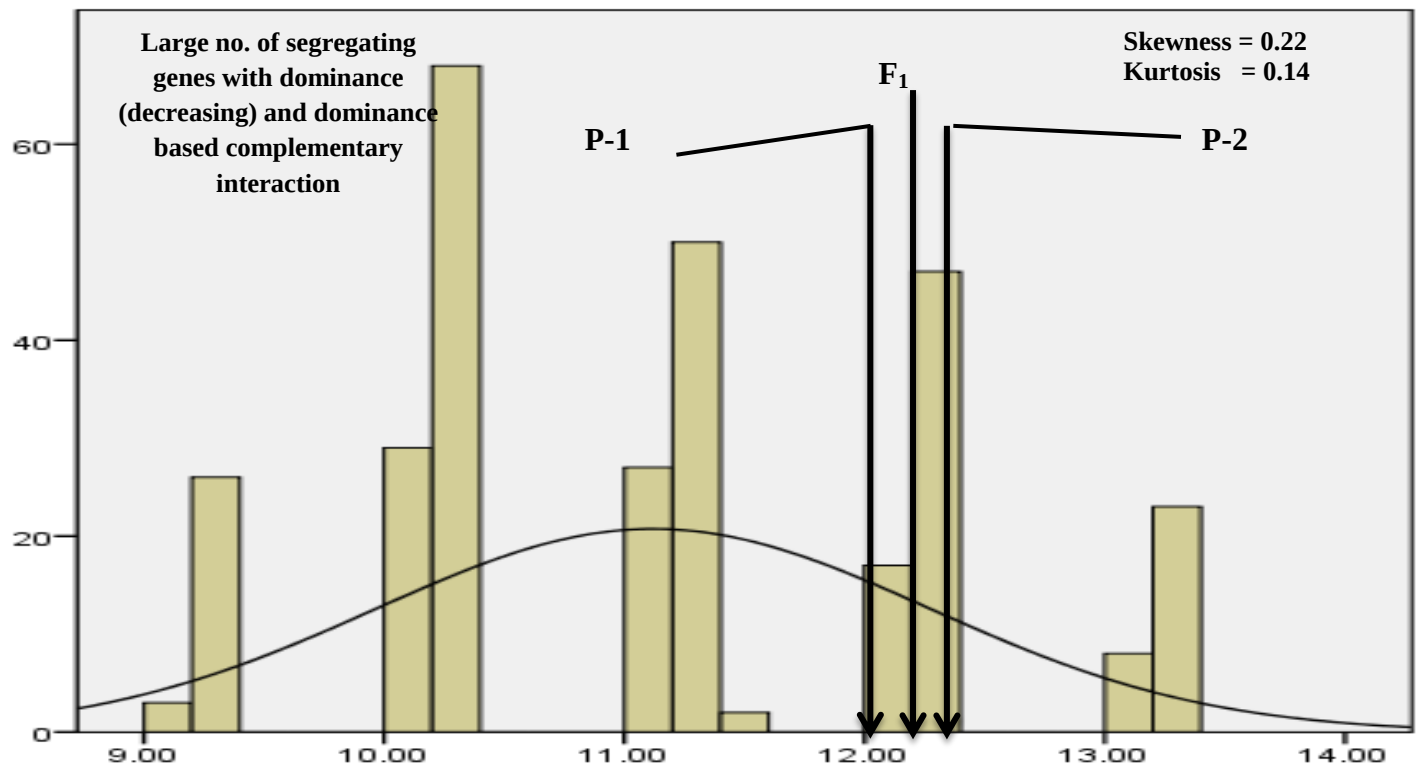


Figure 10: Platykurtic and positively skewed distribution of F_2 of IT-38956-1 $\times$ KBC-2 for hundred seed weight

The platykurtic ($K=-0.61$) and positively skewed distribution ($S=0.85$) suggested involvement of relatively larger number of genes with majority of them having decreasing effects and dominance based complementary type of interaction in the inheritance of plant height (Fig. 3).

4. Primary branches per plant

Primary braches per plant ranged between 2.0 to 9.0 with a mean value of 5.23 and variance of 4.13, indicating the presence of low variability for this trait.

The inheritance of this trait was under the control of dominance based complementary interaction as suggested by platykurtic ($K=1.70$) and positively skewed ($S=0.47$) distribution, an indicative involvement of larger number of genes having decreasing effects (Fig. 4).

5. Secondary branches per plant

Secondary branches varied between 4.0 to 16.0 per plant with a mean value of 10.17 and variance of 11.26 indicating low variability of the trait.

Negatively skewed ($S=-0.37$) and platykurtic ($K=-0.39$) distribution is an evidence for involvement of a large number of dominant genes with majority of them having increasing effects and duplicate type of epistasis in the inheritance of secondary branches per plant (Fig. 5).

6. Pods per plant

Pods per plant ranged from 9.0 to 20.0 with a mean value of 14.65 and variance of 9.03 suggesting presence of moderate variability for the trait.

Negatively skewed ($S=-0.17$) and platykurtic ($K=0.35$) distribution is an evidence for involvement of a large number of dominant genes with majority of them having increasing effects and duplicate type of epistasis in the inheritance of pods per plant (Fig. 6).

7. Pod length (cm)

Pod length varied between 9.0 to 20.0 cm per plant with a mean value of 16.69 cm and variance of 16.64 cm indicating presence of narrow variability for the trait.

The expression of this trait appears to be controlled by larger number of genes having decreasing effects and involvement of dominance based complementary interaction as evidenced by platykurtic ($K=0.34$) and positively skewed ($S=0.02$) distribution (Fig.7).

8. Seeds per pod

The seeds per pod varied between 6.0 to 20.0 with a mean value of 13.30 and variance of 10.95 indicating presence of considerable amount of variability.

Platykurtic ($K=-0.09$) and positively skewed ($S=0.33$) distribution indicated involvement of relatively larger number of genes with decreasing effects and dominance based complementary type of interaction in the inheritance of seeds per pod (Fig. 8).

9. Seed yield per plant (g)

Seed yield per plant varied between 9.17 to 30.35 g per plant with a mean value of 18.74 g and variance of 34.26 g indicating presence of high amount of variability for the trait.

The involvement of large number of dominant genes having decreasing effects and dominance based complementary interaction in the inheritance of seed yield per plant as evidenced by platykurtic ($K=0.14$) and positively skewed ($S=0.22$) distribution (Fig. 9).

10. Seed yield per plant (g)

Seed yield per plant varied between 9.12 to 13.34 g per plant with a mean value of 11.11 g and variance of 1.33 g indicating presence of low variability for the trait.

The involvement of large number of dominant genes having decreasing effects and dominance based complementary interaction in the inheritance of seed yield per plant as evidenced by platykurtic ($K=1.25$) and positively skewed ($S=0.23$) distribution (Fig. 10).

4.1.1.2 Descriptive statistics in F_2 population of cowpea cross IT- 38956-1 $\times$ CP-12

The descriptive statistics for the F_2 population of the cowpea cross IT-38956-1 $\times$ CP-12 are presented in the Table 11 and briefly outlined below.

1. Days to first flowering

The number of days to first flowering varied from 31 to 56 days with a mean value of 40 days and variance of 28 days indicating moderate variability for this trait.

The days to first flowering appeared to be controlled by dominance based complementary gene interaction involving presence of large number of genes having decreasing effects as indicated by platykurtic ($K=0.11$) and positively skewed ($S= 0.37$) distribution (Fig. 11).

2. Days to maturity

Days to maturity ranged between 70 to 99 days with a mean value of 85 days and variance of 71 days indicating presence of wide range of variability for the trait.

The trait was controlled by dominance based complementary interaction involving large number of dominant genes having decreasing effects as evidenced by positively skewed ($S= 0.07$) and platykurtic ($K=-0.32$) distribution (Fig.12).

3. Plant height (cm)

Plant height ranged from 20.30 cm to 46.80 cm with an average of 32.87 cm and variance of 43.03 cm indicating presence of considerable amount of variability for the trait.

Table 11: Descriptive statistics for 10 quantitative characters in F₂ generation cowpea cross IT-38956-1 × CP-12

Sl. No.	Character	Mean	Range		Variance	Skewness	Kurtosis	Kurtosis type
			Minimum	Maximum				
1	Days to first flowering	40.25	31.00	56.00	28.03	0.37	0.11	P
2	Days to maturity	85.11	70.00	99.00	71.63	0.07	-0.32	P
3	Plant height(cm)	32.87	20.30	46.80	43.03	0.78	-0.26	P
4	Primary branches per plant	4.94	2.00	8.00	4.20	0.12	-0.06	P
5	Secondary branches per plant	6.87	5.00	10.00	12.09	0.22	2.25	P
6	Pods per plant	12.09	6.00	19.00	16.32	0.15	0.66	P
7	Pod length(cm)	11.59	4.35	18.75	13.69	0.22	5.09	L
8	Seeds per pod	10.20	3.00	17.00	11.39	0.20	0.26	P
9	Seed yield per plant(g)	17.43	8.16	25.36	23.98	-0.68	0.86	P
10	Hundred seed weight(g)	10.85	9.10	11.30	13.65	-0.38	9.03	L

P: Platykurtic, L: Leptokurtic

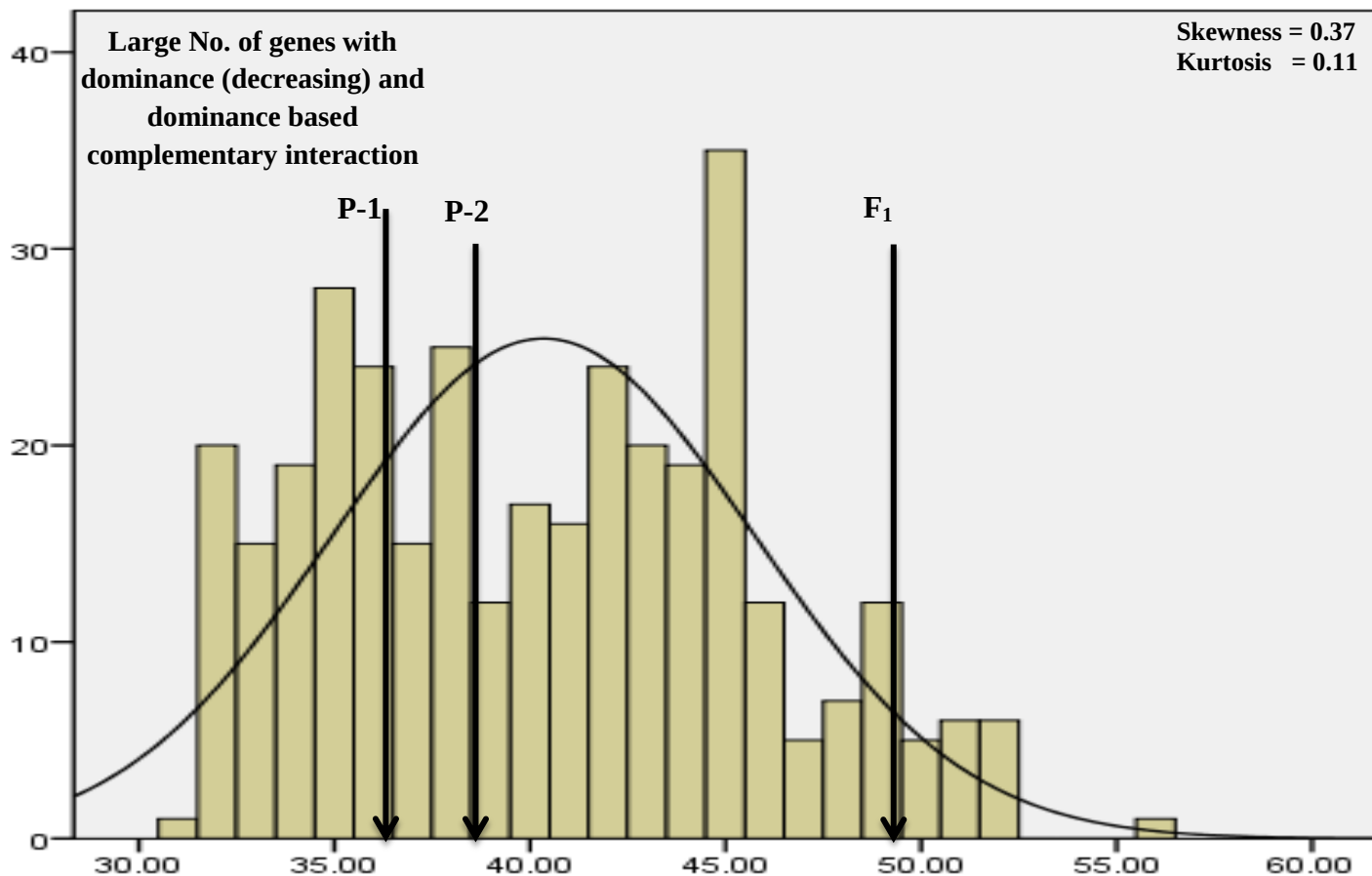


Figure 11: Platykurtic and positively skewed distribution of F₂ of IT-38956-1 × CP-12 for Days to first flowering

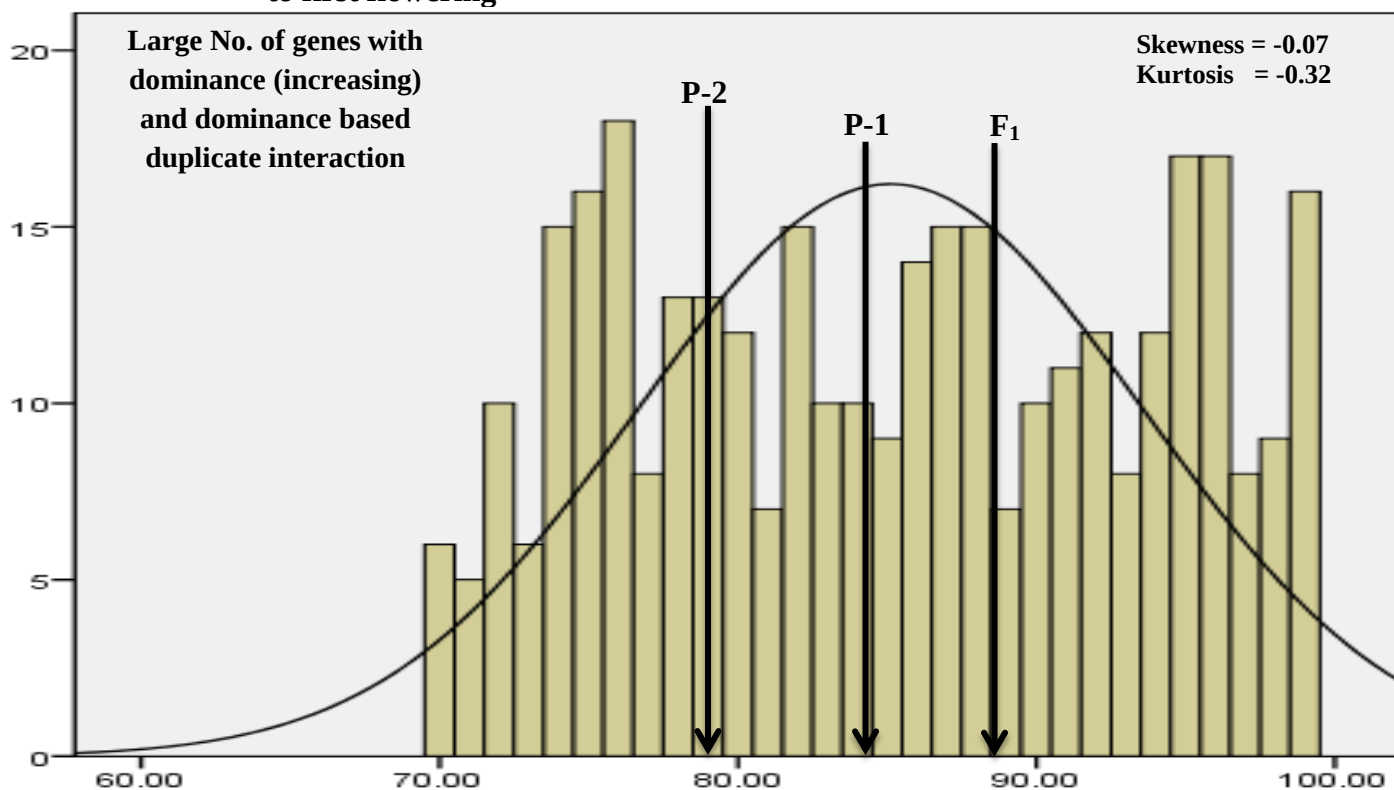


Figure 12: Platykurtic and negatively skewed distribution of F₂ of IT-38956-1 × CP-12 for Days to maturity

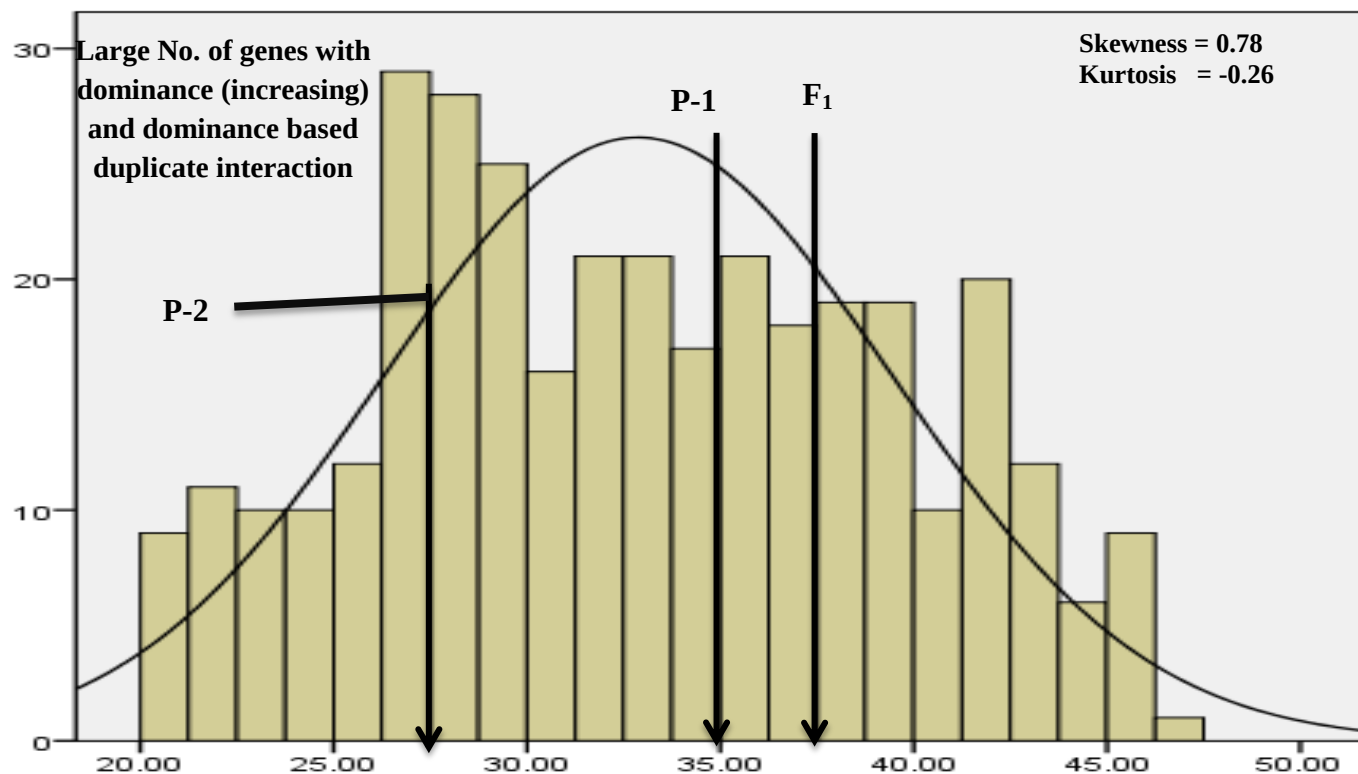


Figure 13: Platykurtic and positively skewed distribution of F₂ of IT-38956-1 × CP-12 for plant height

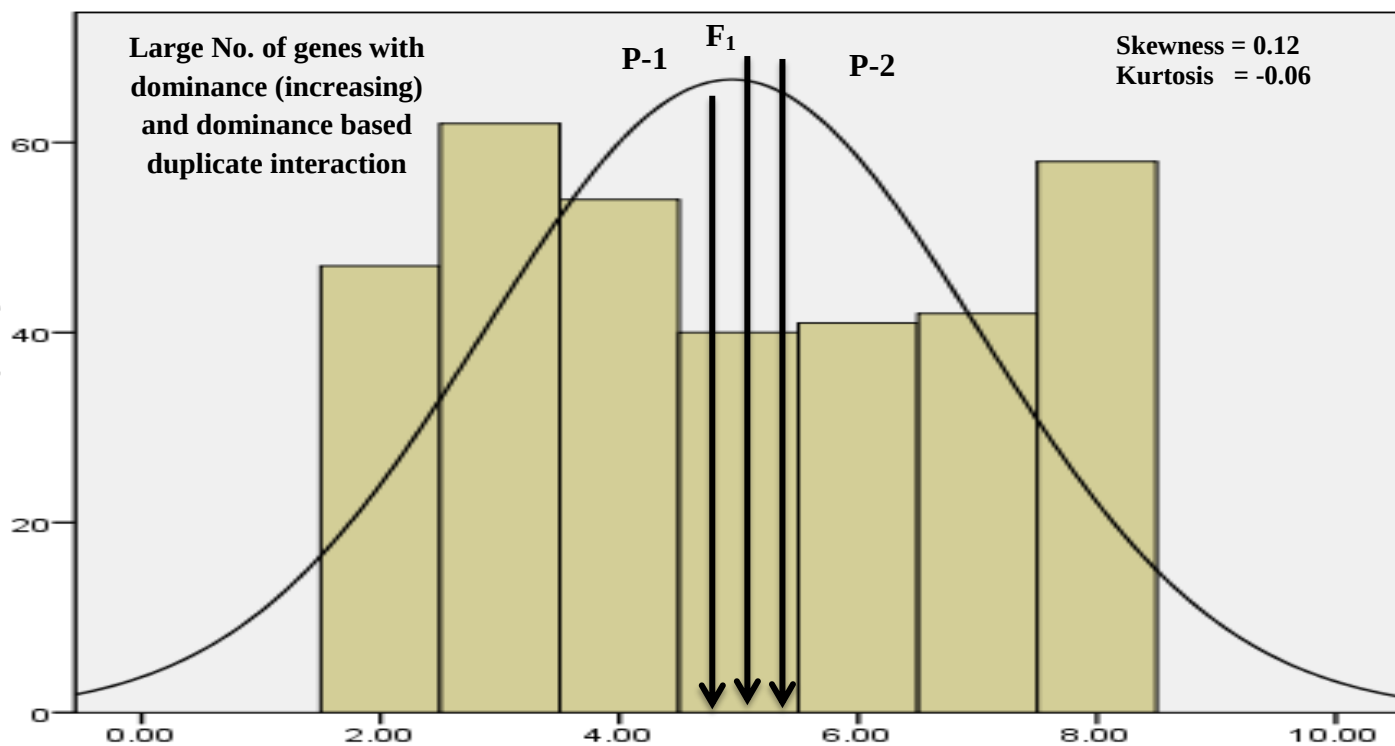


Figure 14: Platykurtic and positively skewed distribution of F₂ of IT-38956-1 × CP-12 for primary braches per plant

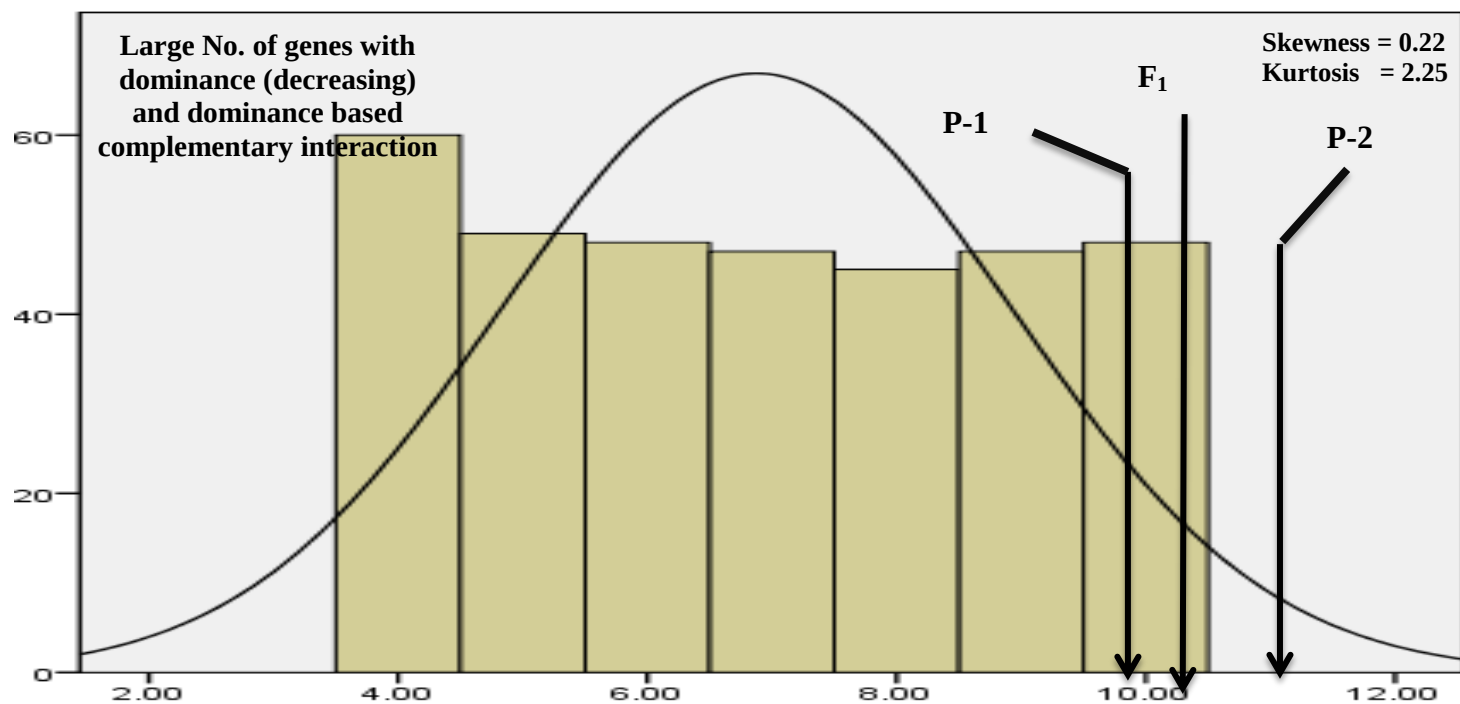


Figure 15: Platykurtic and positively skewed distribution of F₂ of IT-38956-1 × CP-12 for secondary braches per plant

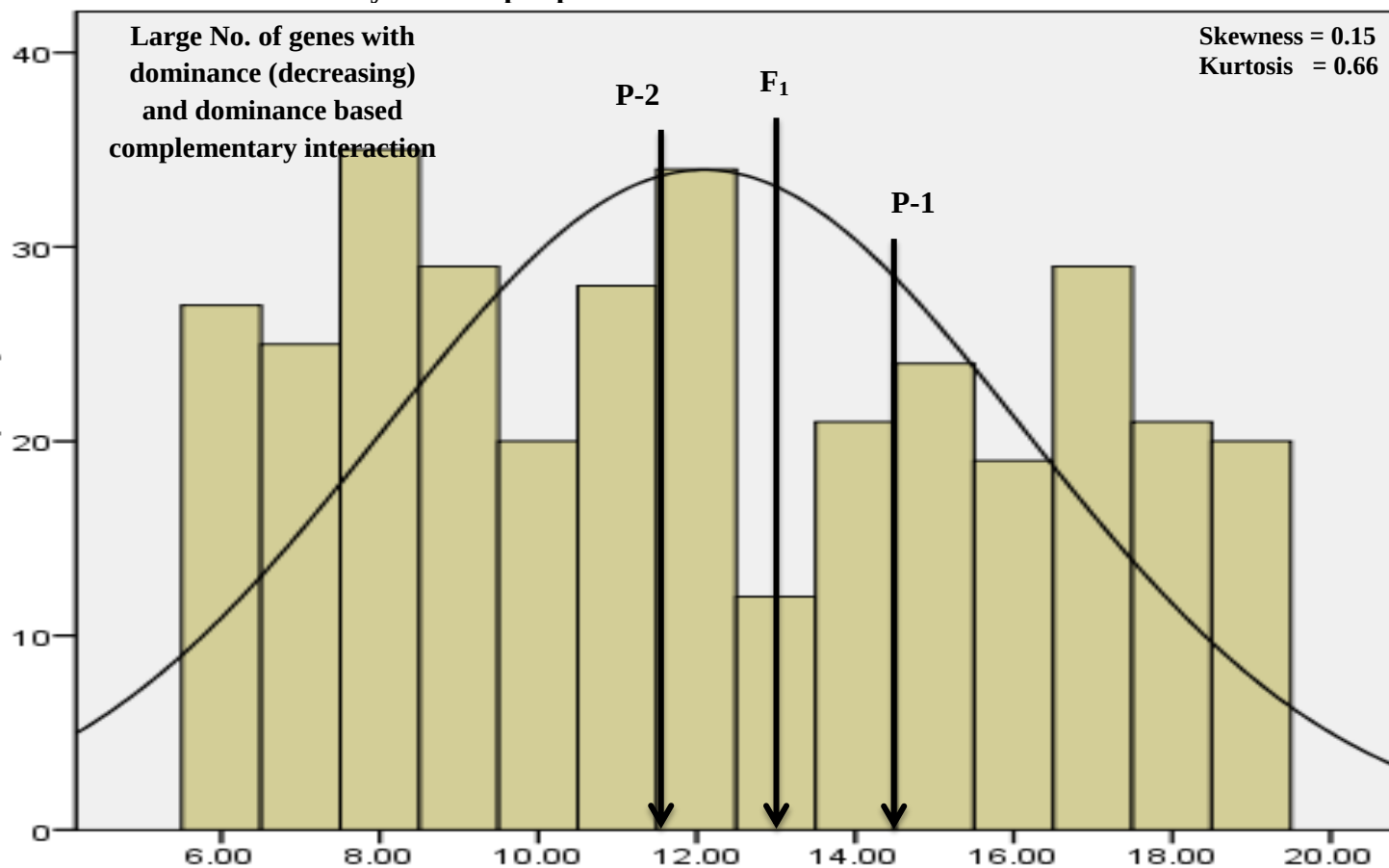


Figure 16: Platykurtic and positively skewed distribution of F₂ of IT-38956-1 × CP-12 for pods per plant.

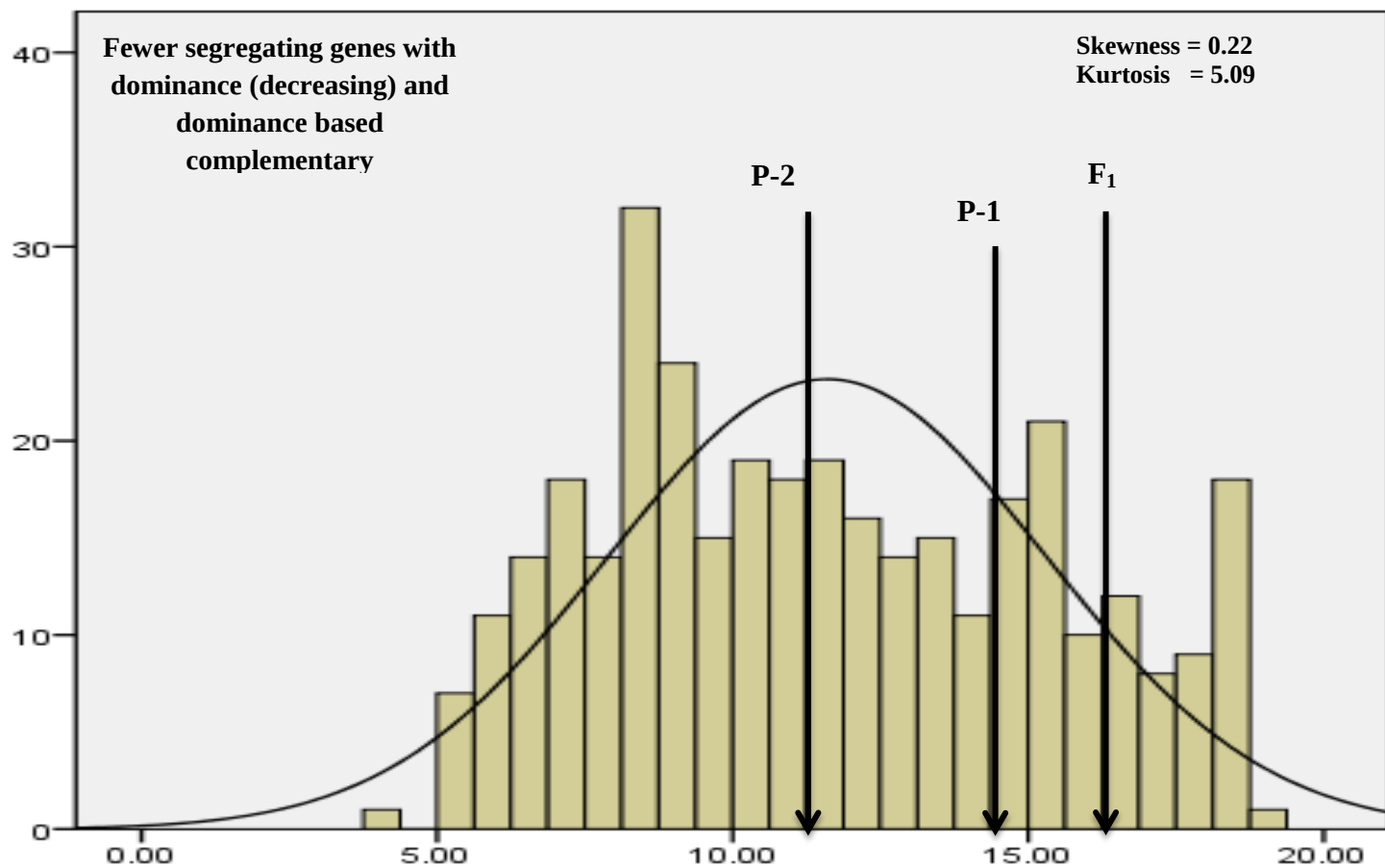


Figure 17: Leptokurtic and positively skewed distribution of F₂ of IT-38956-1 × CP-12 for pods length

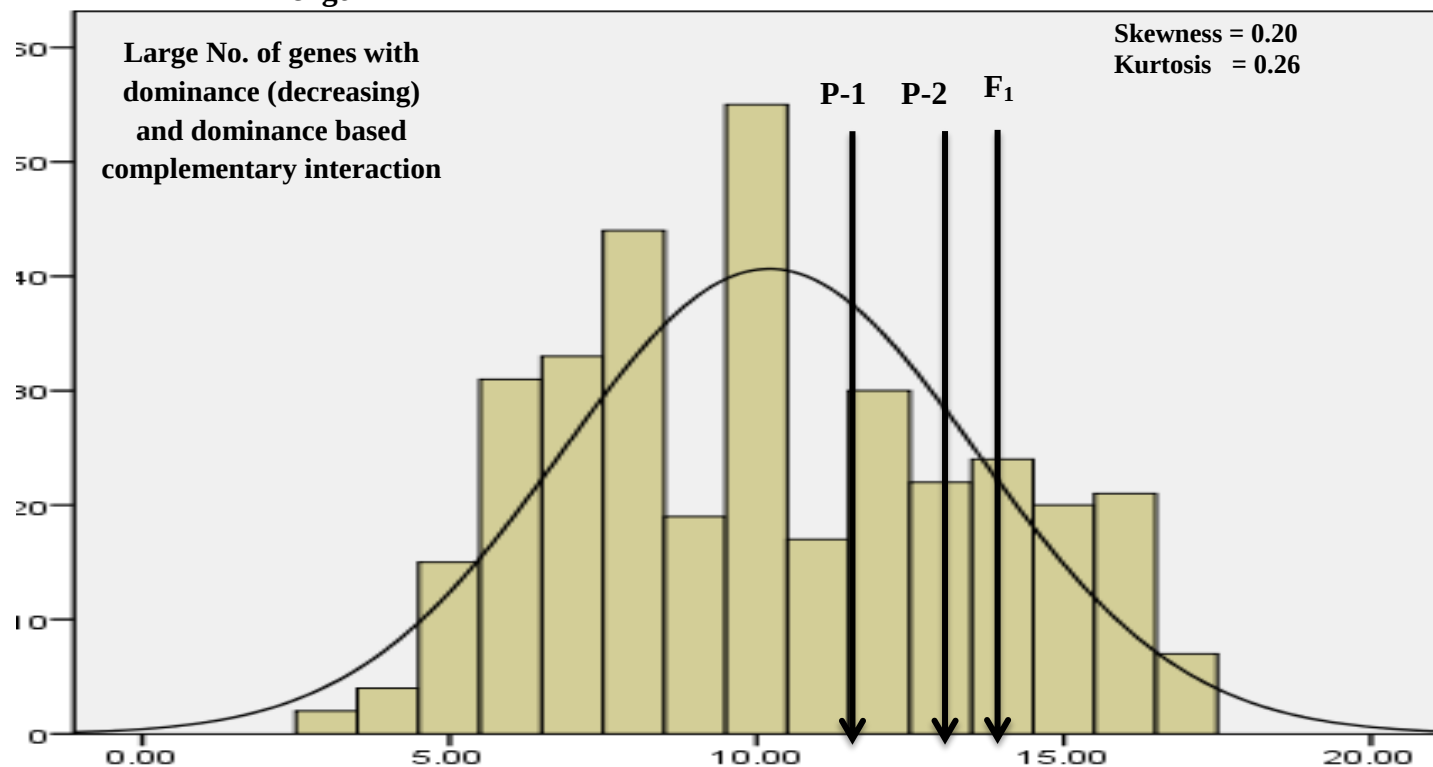


Figure 18: Platykurtic and positively skewed distribution of F₂ of IT-38956-1 × CP-12 for seeds per pod

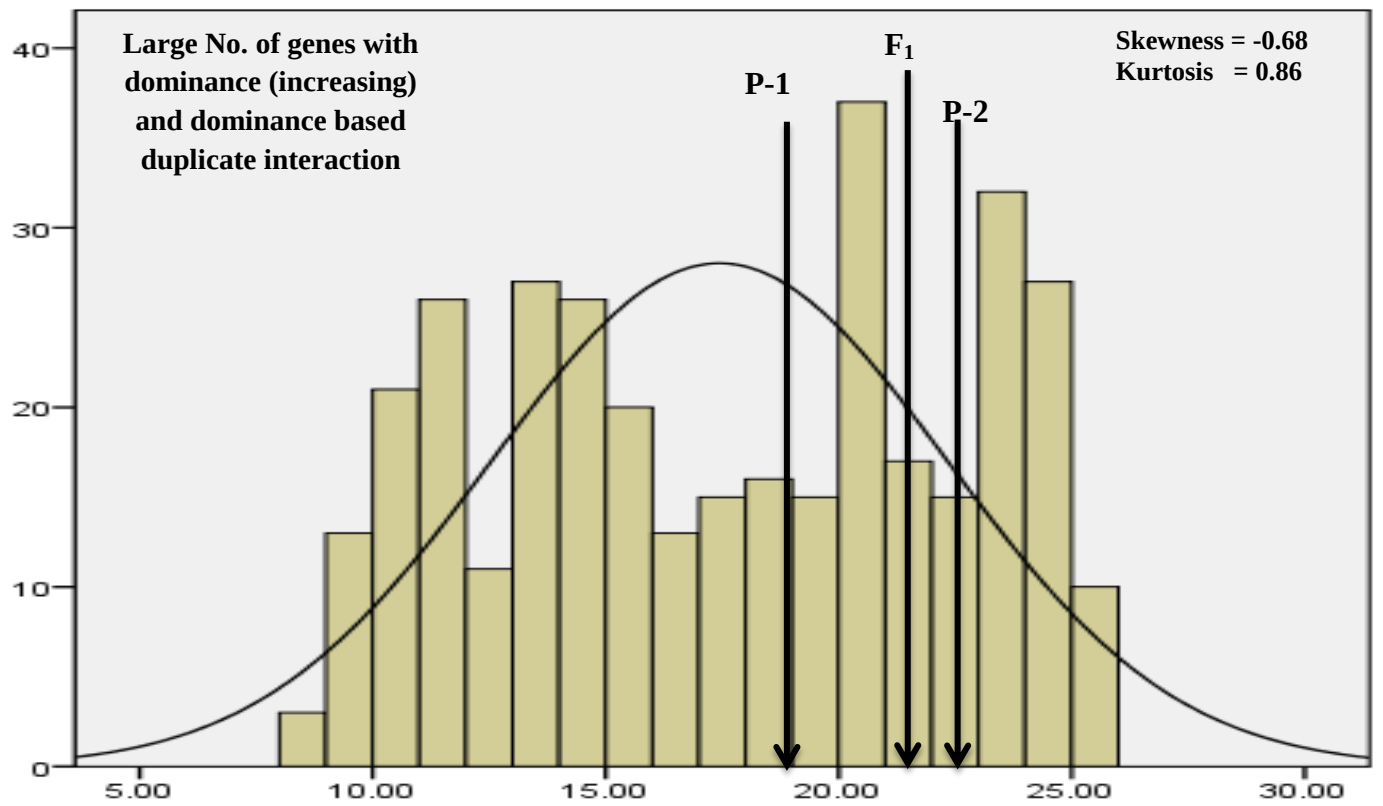


Figure 19: Platykurtic and negatively skewed distribution of F₂ of IT-38956-1 × CP-12 for seed yield per plant

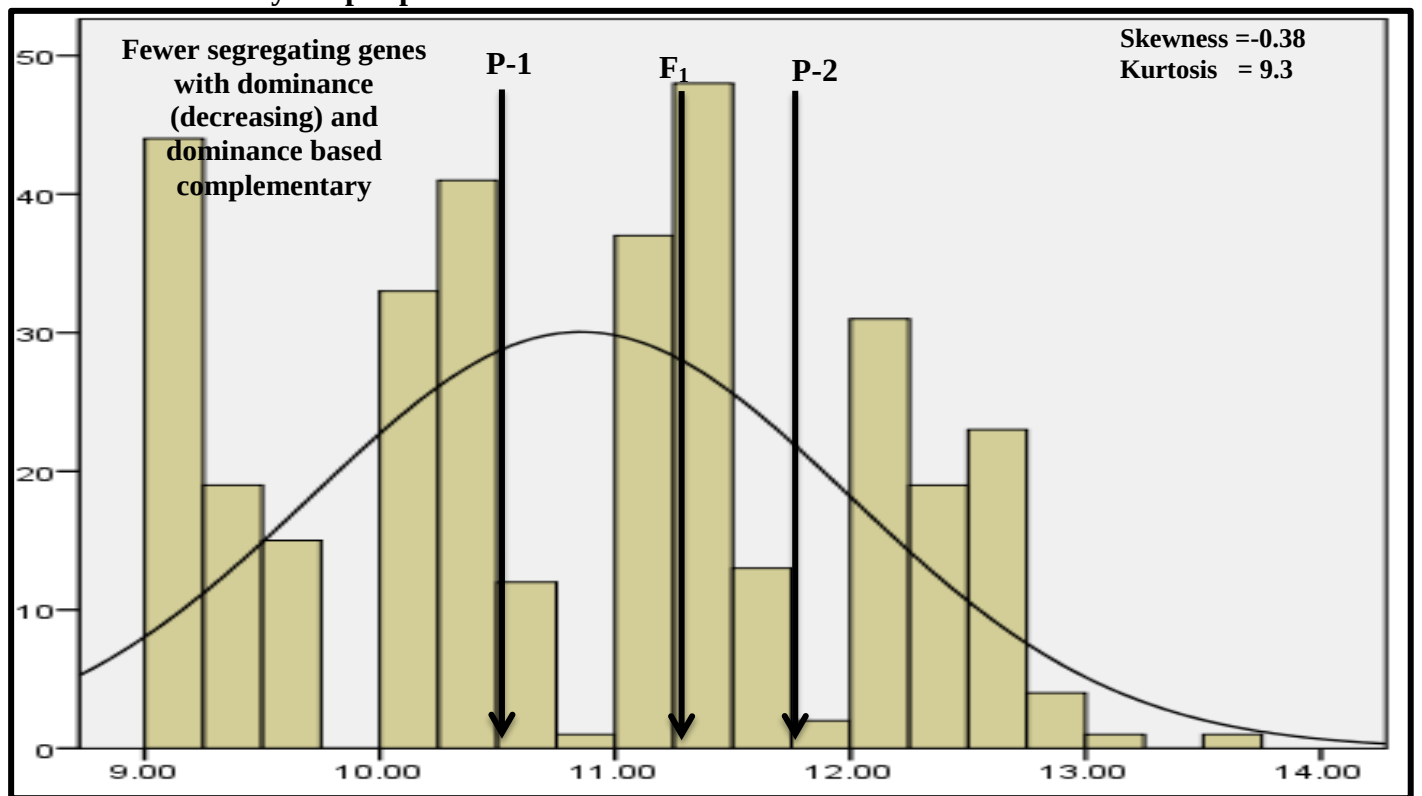


Figure 20: Leptokurtic and negatively skewed distribution of F₂ of IT-38956-1 × CP-12 for pods length.

The trait was controlled by dominance based complementary interaction involving large number of dominant genes having decreasing effects as evidenced by positively skewed ($S=0.78$) and platykurtic ($K=-0.26$) distribution (Fig.13).

4. Primary branches per plant

Primary branches per plant varied from 2 to 8 with a mean value of 4.94 and variance of 4.2 indicating the presence of low variability for this trait.

The trait was controlled by dominance based complementary interaction involving large number of dominant genes having decreasing effects as evidenced by positively skewed ($S=0.12$) and platykurtic ($K=-0.06$) distribution (Fig. 14).

5. Secondary branches per plant

Secondary branches per plant ranged from 5 to 10, with an average of 6.87 and variance of 12.09 indicating the presence of medium variability.

The secondary branches per plant appeared to be controlled by dominance based complementary gene interaction involving presence of large number of genes having decreasing effects as indicated by platykurtic ($K=2.25$) and positively skewed ($S= 0.22$) distribution (Fig. 15).

6. Pods per plant

Pods per plant varied from 6.0 and 19.0 with a mean value of 12.09 with a variance of 16.32 indicating moderate variability for the trait.

The pods per plant appeared to be controlled by dominance based complementary gene interaction involving presence of large number of genes having decreasing effects as indicated by platykurtic ($K=0.66$) and positively skewed ($S= 0.15$) distribution (Fig.16).

7. Pod length (cm)

Pod length varied from 4.35 to 18.75 cm with a mean value of 11.59 cm and variance of 13.69 cm suggesting presence of medium amount of variability for the trait.

Leptokurtic ($K=5.09$) and positively skewed distribution ($S=0.22$) suggested the involvement of relatively fewer number of segregating genes with majority of them having decreasing effects and dominance based complementary type of interaction in the inheritance of pod length (Fig.17).

8. Seeds per pod

Seeds per pod ranged from 3 to 17 with a mean value of 10.20 and variance of 11.39 shows the presence of considerable amount of variability.

Platykurtic ($K=0.26$) and positively skewed ($S=0.20$) distribution suggested the involvement of overall excess dominant genes with majority of them having decreasing effects and dominance based complementary type of interaction in the genetic control of seeds per pod trait (Fig.18).

9. Seed yield per plant (g)

Seed yield per plant ranged from 8.16 g to 25.36 g with a mean value of 17.43 g and variance of 23.98 g indicating presence of considerable amount of variability for this trait.

Negatively skewed ($S=-0.68$) and platykurtic ($K=0.86$) distribution is an evidence for involvement of a large number of dominant genes with majority of them having increasing effects and duplicate type of epistasis in the inheritance of seed yield per plant (Fig.19).

10. Hundred seed weight (g)

Hundred seed weight ranged from 9.10 g to 11.30 g with a mean value of 10.85 g and variance of 13.65 g indicated the presence of medium amount of variability for the trait.

The involvement of relatively fewer number of genes with majority of them having decreasing effects and dominance based complementary type of interaction in the genetic control of the trait was indicated by leptokurtic ($K=9.03$) and negatively skewed ($S=-0.38$) distribution of hundred seed weight (Fig. 20).

4.1.1.3 Descriptive statistics in F₂ generation of cowpea cross KBC-2 × CP-12

The descriptive statistics for the F₂ population of the cowpea cross KBC-2 × CP-12 are presented in the Table 12 and briefly outlined below.

1. Days to first flowering

The number of days to first flowering varied from 35 to 54 days with a mean value of 44 days and variance of 30 days indicating high variability for this trait.

Negatively skewed ($S=-0.09$) and platykurtic ($K=1.64$) distribution is an evidence for involvement of a large number of dominant genes with majority of them having increasing effects and duplicate type of epistasis in the inheritance of days to first flowering trait (Fig. 21).

2. Days to maturity

Days to maturity ranged between 65 to 86 days with a mean value of 75.45 days and variance of 41.27 days indicated the presence of wide range of variability for the trait.

The days to maturity appeared to be controlled by dominance based complementary gene interaction involving presence of large number of genes having decreasing effects as indicated by platykurtic ($K=0.13$) and positively skewed ($S=0.55$) distribution (Fig. 22).

3. Plant height (cm)

Plant height ranged from 18 to 48.90 cm with an average of 33.49 cm and variance of 84.03 cm indicating presence of high variability for the trait.

The plant height appeared to be controlled by dominance based complementary gene interaction involving presence of large number of genes having decreasing effects as indicated by platykurtic ($K=2.5$) and positively skewed ($S=0.35$) distribution (Fig. 23).

Table 12: Descriptive statistics for 10 quantitative characters in F₂ generation of cowpea cross KBC-2 × CP-12

Sl. No.	Character	Mean	Range		Variance	Skewness	Kurtosis	Kurtosis type
			Minimum	Maximum				
1	Days to first flowering	44.66	35.0	54.00	30.09	-0.09	1.64	P
2	Days to maturity	75.45	65.0	86.00	41.27	0.55	0.13	P
3	Plant height(cm)	33.49	18.0	48.90	84.03	0.35	2.5	P
4	Primary branches per plant	10.86	4.0	12.00	20.85	0.12	0.32	P
5	Secondary branches per plant	14.53	8.10	20.90	14.25	0.21	0.66	P
6	Pods per plant	8.78	5.0	13.00	6.66	0.44	0.86	P
7	Pod length(cm)	12.53	3.0	19.0	13.69	0.04	9.12	P
8	Seeds per pod	7.72	7.72	12.00	6.88	0.12	0.24	P
9	Seed yield per plant(g)	15.55	10.12	23.34	14.53	0.20	0.28	P
10	Hundred seed weight(g)	11.29	10.13	12.65	0.68	-0.47	0.84	P

P: Platykurtic

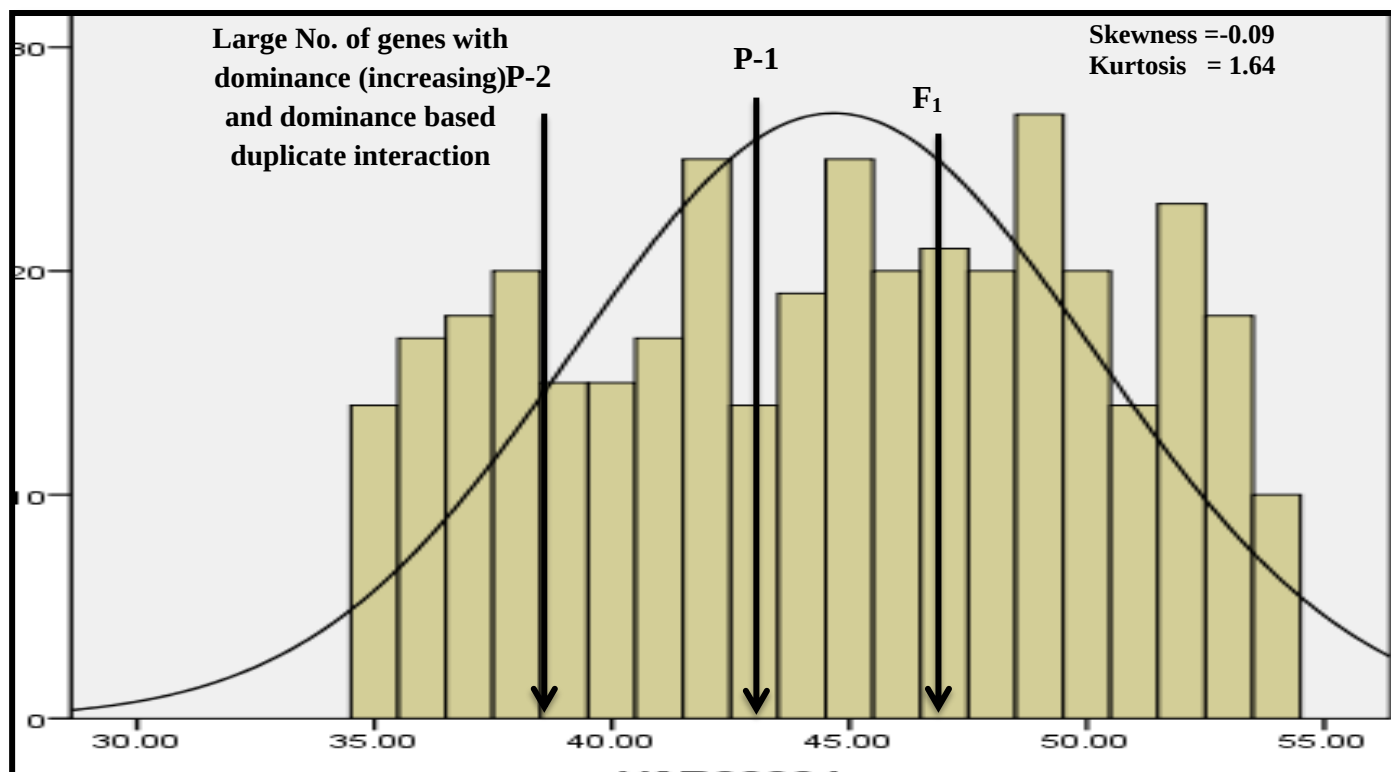


Figure 21: Platykurtic and negatively skewed distribution of F₂ of KBC-2 × CP-12 for days to first flowering

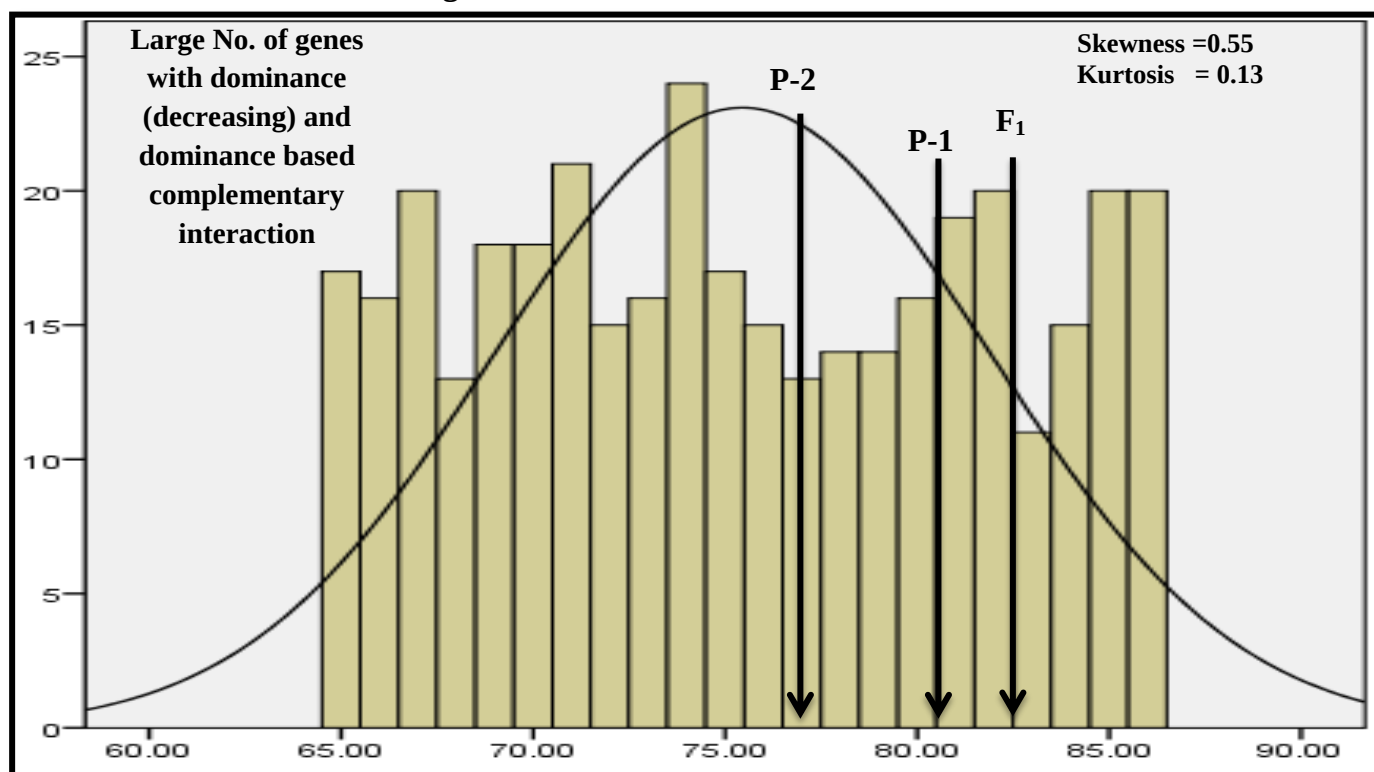


Figure 22: Platykurtic and positively skewed distribution of F₂ of KBC-2 × CP-12 for days maturity

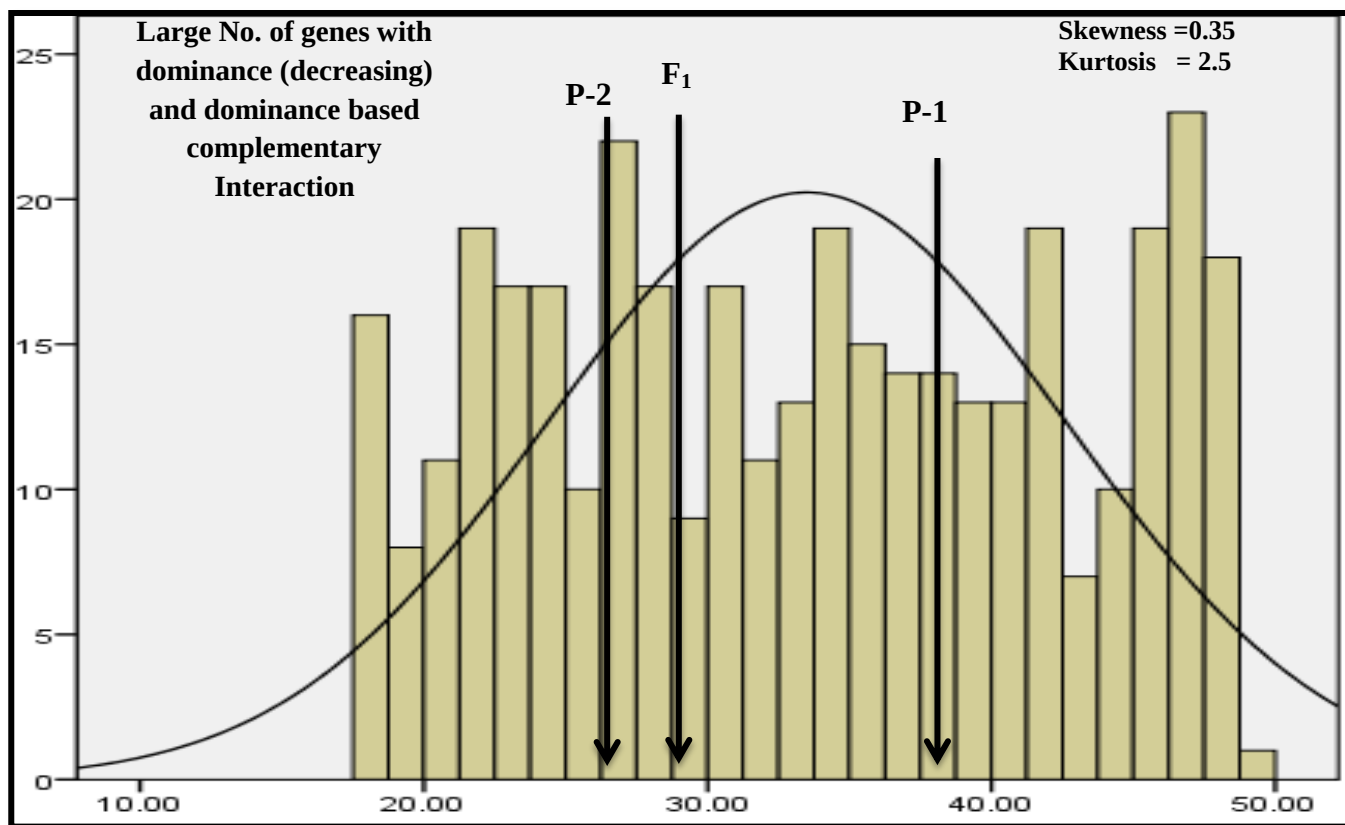


Figure 23: Platykurtic and positively skewed distribution of F₂ of KBC-2 × CP-12 Plant height

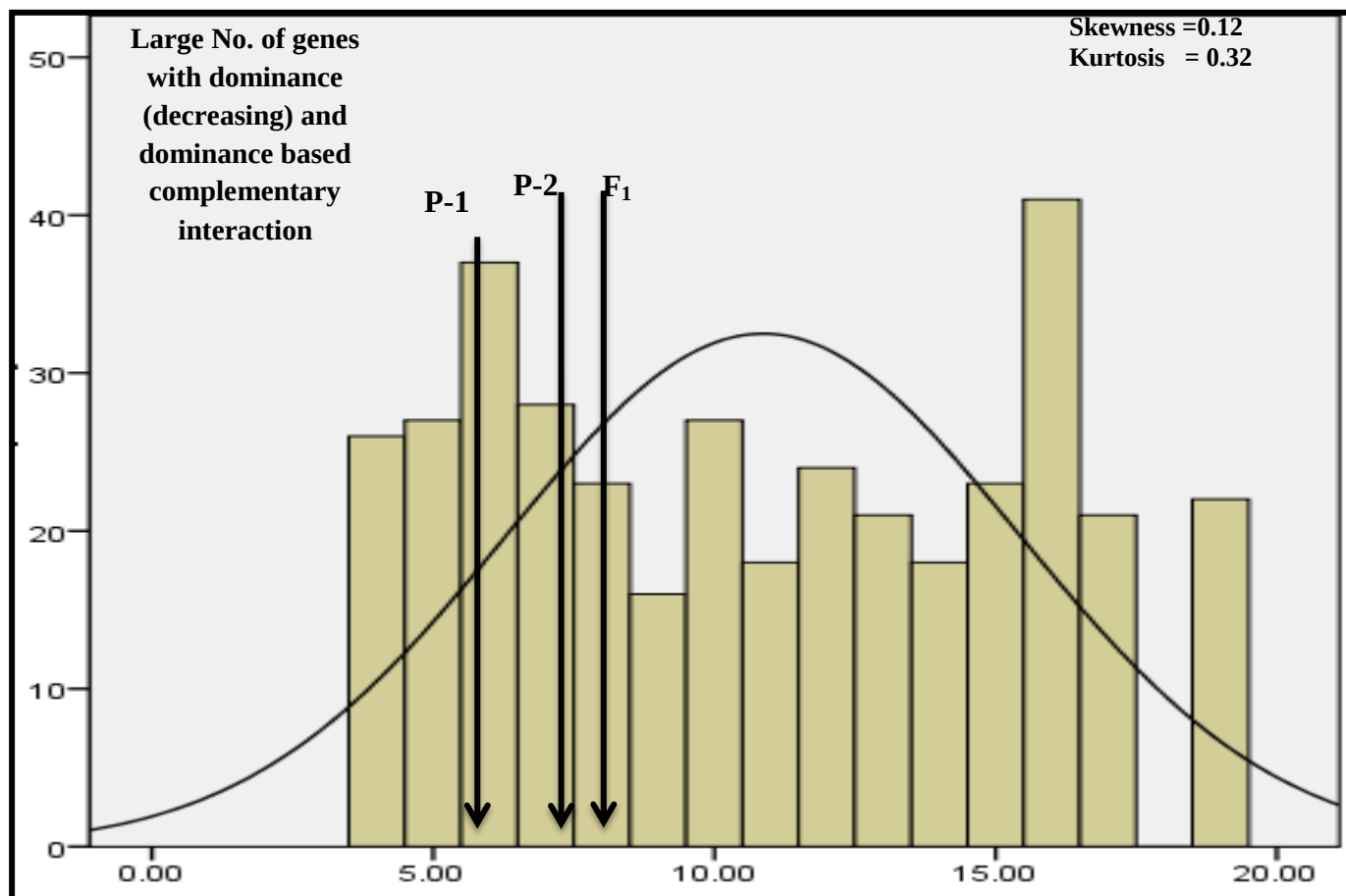


Figure 24: Platykurtic and positively skewed distribution of F₂ of KBC-2 × CP-12 primary braches per plant

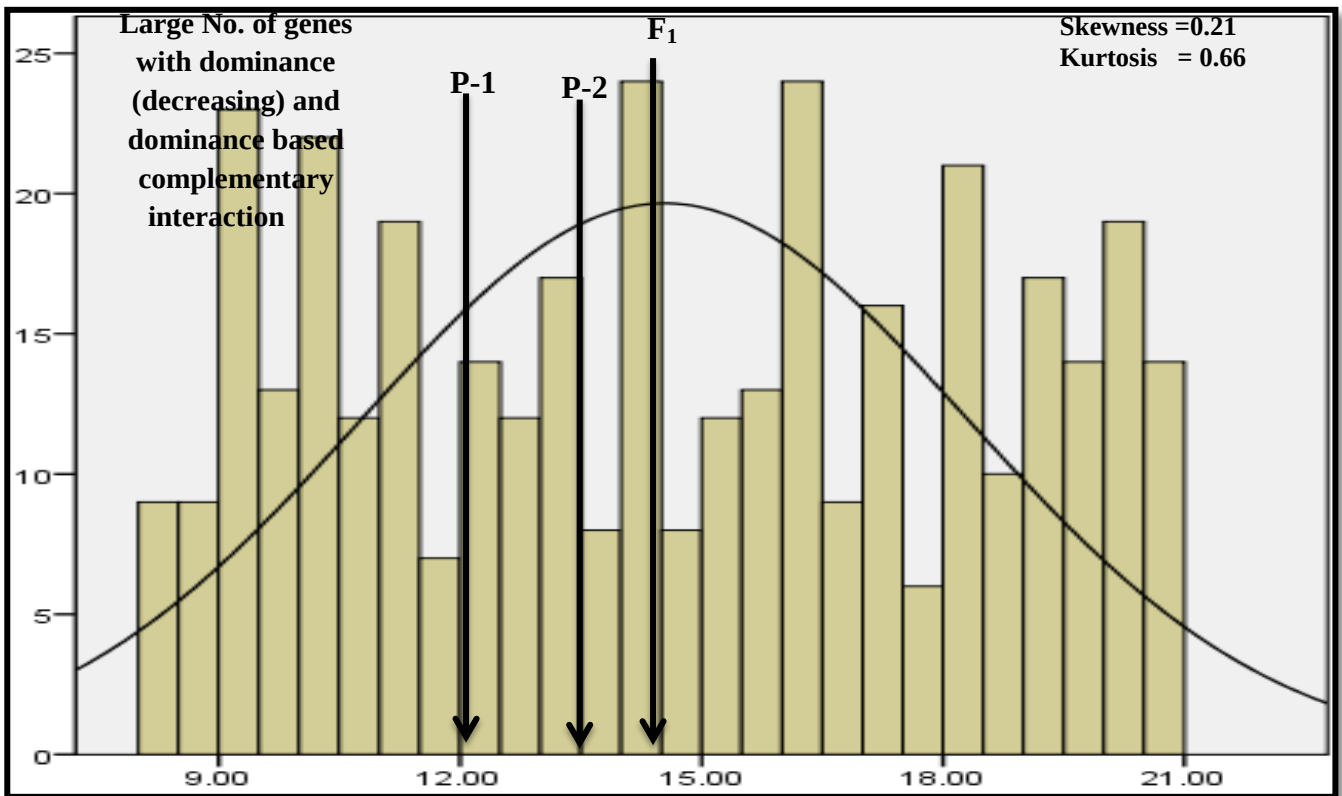


Figure 25: Platykurtic and positively skewed distribution of F₂ of KBC-2 × CP-12 secondary braches per plant

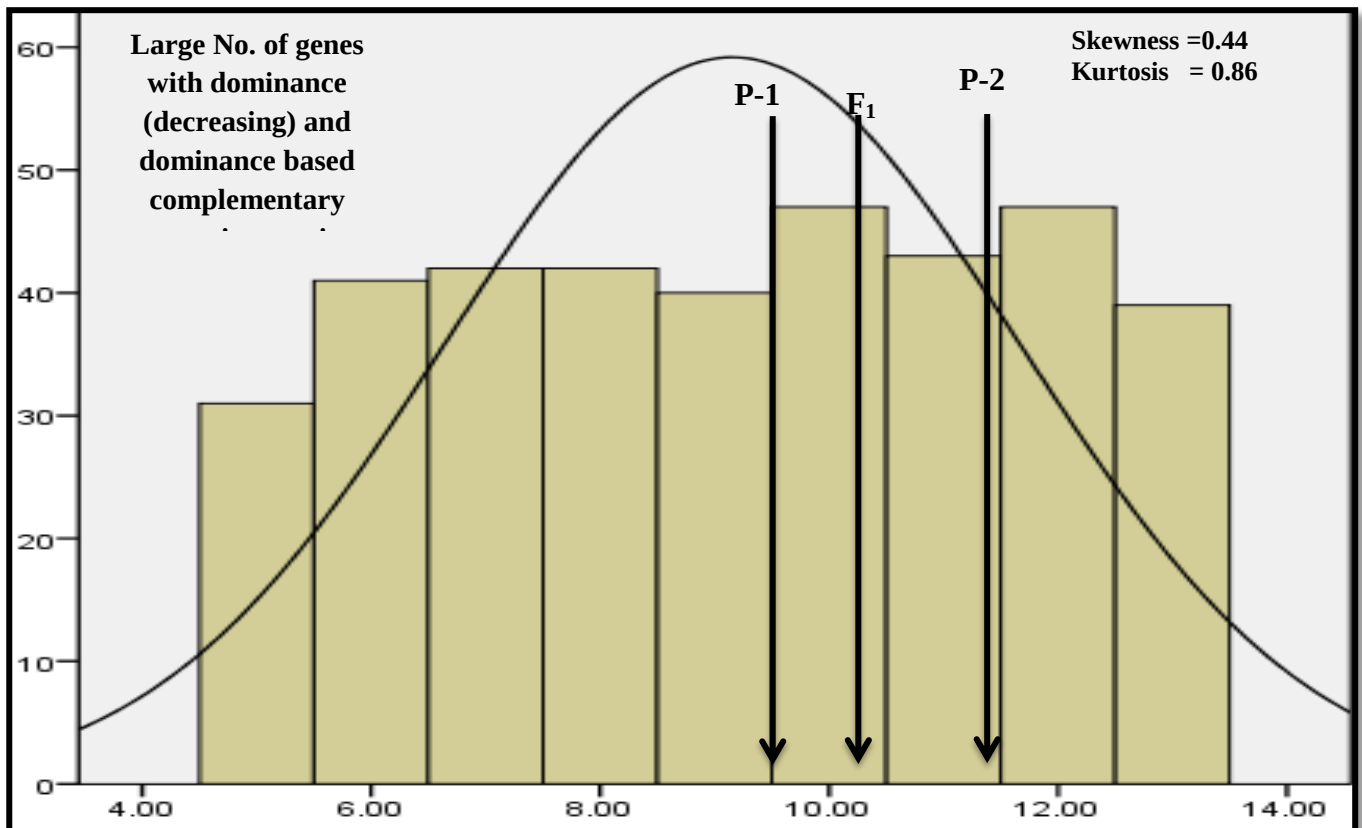


Figure 26: Platykurtic and positively skewed distribution of F₂ of KBC-2 × CP-12 pods per plant.

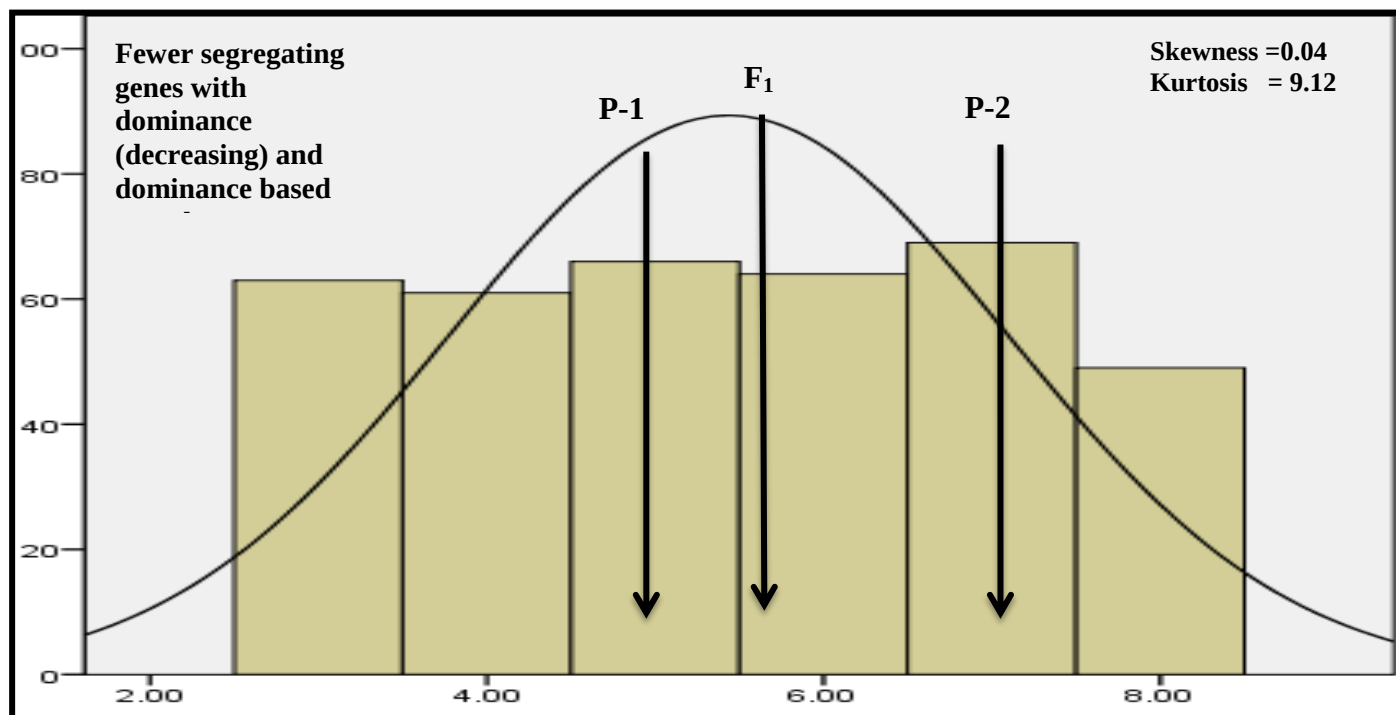


Figure 27: Leptokurtic and positively skewed distribution of F_2 of KBC-2 $\times$ CP-12 pod length

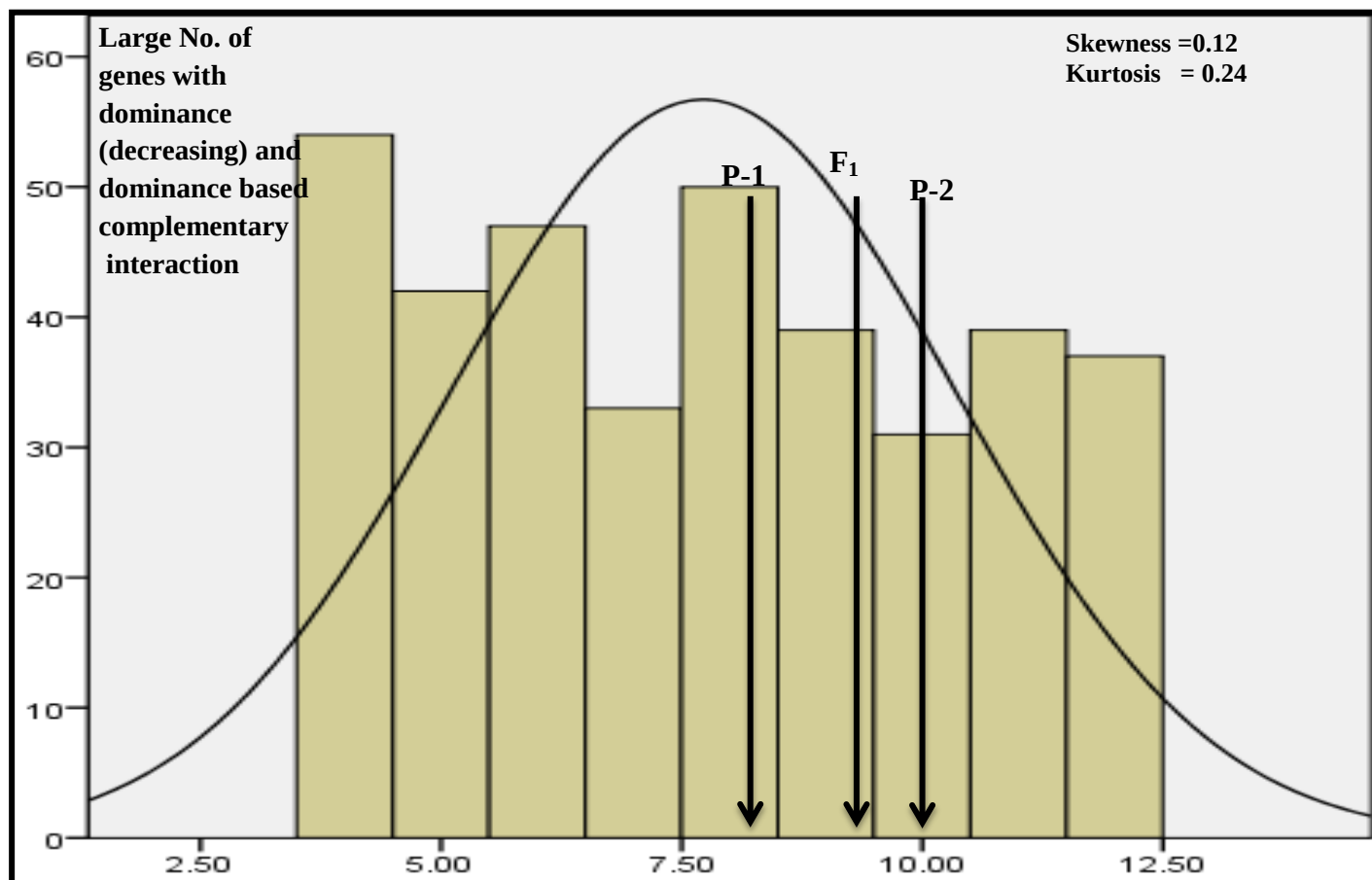


Figure 28: Platykurtic and positively skewed distribution of F_2 of KBC-2 $\times$ CP-12 seeds per pod

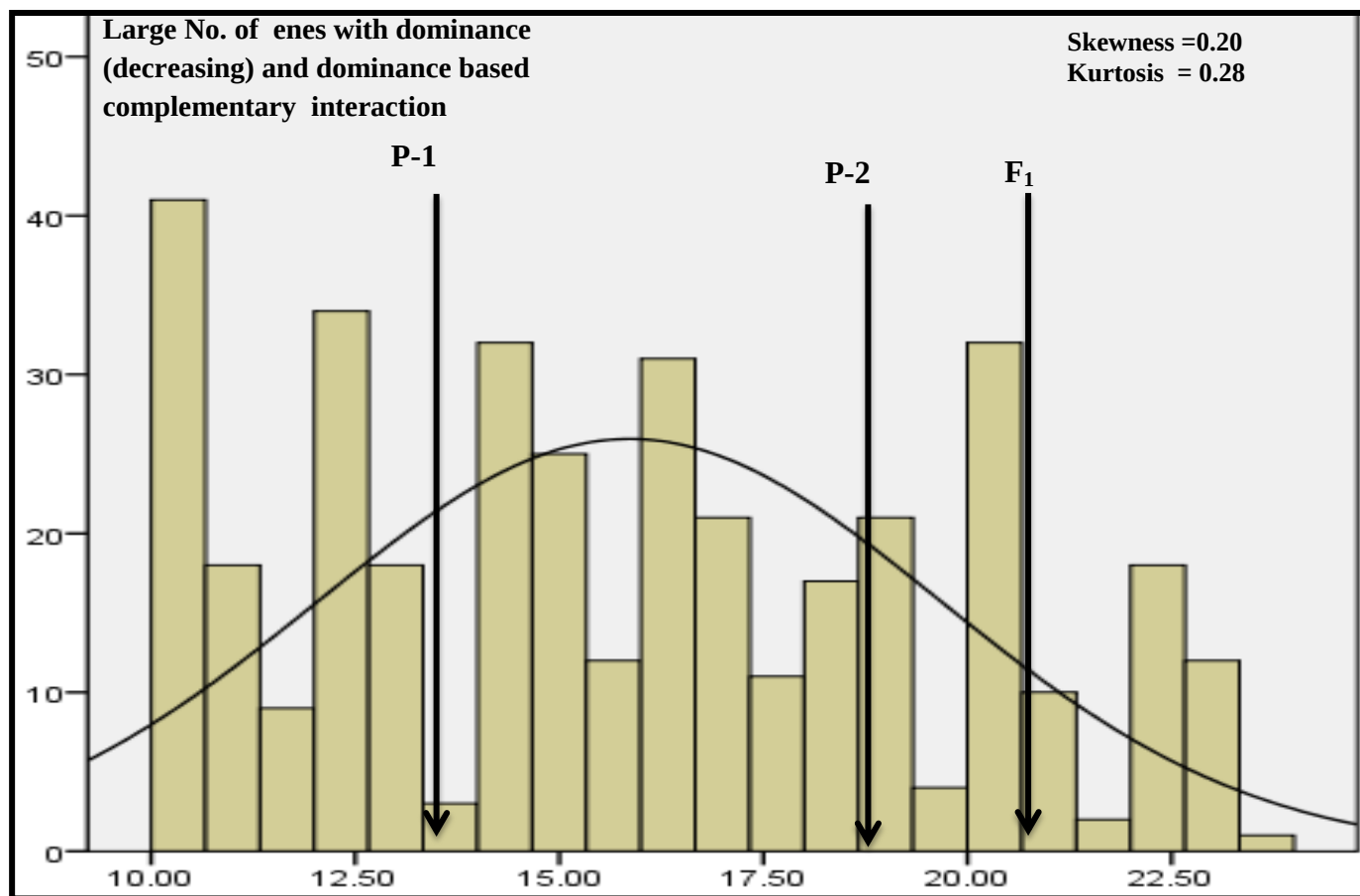


Figure 29: Platykurtic and positively skewed distribution of F₂ of KBC-2 × CP-12 seed yield per plant

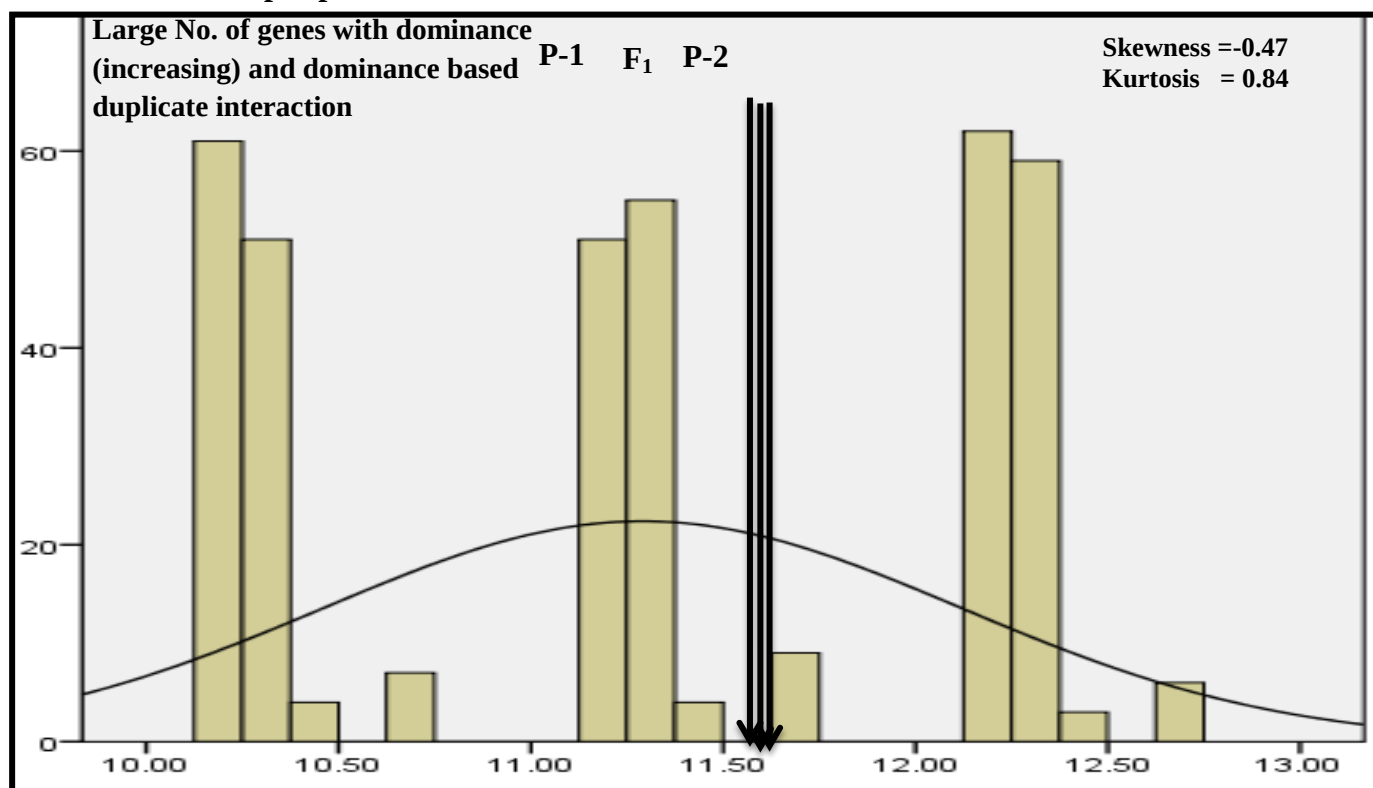


Figure 30: Platykurtic and negatively skewed distribution of F₂ of KBC-2 × CP-12 hundred seed weight.

4. Primary branches per plant

Primary branches per plant varied from 4 to 12 with a mean value of 10.86 and variance of 20.85 indicating the presence of high variability for this trait.

The primary branches per plant appeared to be controlled by dominance based complementary gene interaction involving presence of large number of genes having decreasing effects as indicated by platykurtic ($K=0.32$) and positively skewed ($S=0.12$) distribution (Fig. 24).

5. Secondary branches per plant

Secondary branches per plant ranged from 8.10 to 20.90 with an average of 14.53 and variance of 14.25 indicating the presence of medium variability.

The secondary branches per plant appeared to be controlled by dominance based complementary gene interaction involving presence of large number of genes having decreasing effects as indicated by platykurtic ($K=0.66$) and positively skewed ($S=0.21$) distribution (Fig. 25).

6. Pods per plant

Pods per plant varied from 5 to 13.00 with a mean value of 8.78 and variance of 6.66 indicating low variability for the trait.

The pods per plant appeared to be controlled by dominance based complementary gene interaction involving presence of large number of genes having decreasing effects as indicated by platykurtic ($K=0.86$) and positively skewed ($S=0.44$) distribution (Fig. 26).

7. Pod length (cm)

Pod length varied from 3 to 19.0 cm with a mean value of 12.53 cm and variance of 13.69 cm suggesting presence of medium amount of variability for the trait.

Leptokurtic ($K=9.12$) and positively skewed distribution ($S=0.04$) suggested the involvement of relatively fewer number of segregating genes with majority of them

having decreasing effects and dominance based complementary type of interaction in the inheritance of pod length (Fig. 27).

8. Seeds per pod

Seed per pod ranged from 7.72 to 12.0 with a mean value of 7.72 and variance of 6.88 suggesting presence of considerable amount of variability for this trait.

Platykurtic ($K=0.24$) and positively skewed ($S=0.12$) distribution suggested the involvement of overall excess dominant genes with majority of them having decreasing effects and dominance based complementary type of interaction in the genetic control of seed per plant trait (Fig. 28).

9. Seed yield per plant (g)

Seed yield per plant ranged from 10.12 g to 23.34 g with a mean value of 15.55 g and variance of 14.53 g indicating the presence of considerable amount of variability for this trait.

Platykurtic ($K=0.28$) and positively skewed ($S=0.20$) distribution suggested the involvement of overall excess dominant genes with majority of them having decreasing effects and dominance based complementary type of interaction in the genetic control of seed yield per plant trait (Fig. 29).

10. Hundred seed weight (g)

Hundred seed weight ranged from 10.13 g to 12.65 g with a mean value of 11.29 g and variance of 0.68 g indicating the presence of low variability for the trait.

Negatively skewed ($S=-0.47$) and platykurtic ($K=0.84$) distribution is an evidence for involvement of a large number of dominant genes with majority of them having increasing effects and duplicate type of epistasis in the inheritance of hundred seed weight trait (Fig. 30).

4.1.2 Genetic variability studies in three cowpea crosses

Genetic variability parameters viz., phenotypic co-efficient of variation (PCV), genotypic co-efficient variation (GCV), broad sense heritability (h^2) and genetic advance as per cent of population mean (GAM) in respect of seed yield and yield attributing characters in three cowpea crosses are tabulated in Table 13 to Table 15 and briefly outlined below.

The PCV values are relatively higher than GCV values in respect of all the traits. However the difference between PCV and GCV values were low in respect of all the traits indicating the less environmental influence on all the characters.

The present analysis has been carried out on the F_2 populations of cowpea cross viz., IT-38956-1 $\times$ KBC-2, IT-38956-1 $\times$ CP-12 and KBC-2 $\times$ CP-12. The results obtained in this experiment are tabulated in Table 13 to Table 15 and briefly out lined bellow.

4.1.2.1 Genetic variability parameters in the cross IT-38956-1 $\times$ KBC-2

The genetic variability parameters in F_2 population of cowpea cross IT-38956-1 $\times$ KBC-2 are presented in the Table 13 and briefly outlined below.

1. Days to first flowering

The PCV (10.28 %) and GCV (2.86 %) values were recorded for the days to first flowering, while high heritability (79.79 %) and moderate genetic advance as per cent of mean(11.66 %) indicating the major role of non additive gene action in respect of this trait.

2. Days to maturity

The PCV (7.12 %) and GCV (1.81 %) values were low for days to maturity with high (64.3 %) heritability and low genetic advance as per cent of mean(22.65 %) revealing non additive gene action in the control of this trait.

Table 13: Genetic variability parameters for yield and yield attributing traits in cowpea cross IT-38956-1 × KBC-2

Genetic parameters	Days to first flowering	Days to maturity	Plant height (cm)	Primary branches/plant	Secondary branches /plant	Pods per plant	Pod length (cm)	Seeds per pod	Seed yield per plant (g)	Hundred seed weight (g)
Mean	41.03	84.44	27.73	5.23	10.12	14.65	16.69	13.30	18.74	11.11
PCV (%)	10.28	7.12	23.13	25.54	13.71	13.64	18.44	19.78	22.81	7.24
GCV (%)	2.86	1.81	3.75	14.14	5.52	7.09	9.0	12.85	7.91	1.72
Heritability (%)	79.7	64.3	36.3	16.13	16.23	11.27	23.0	42.2	12.05	6.25
GA as % Mean	11.66	22.65	1.25	3.06	4.58	7.6	16.69	13.30	18.74	11.11

3. Plant height (cm)

Moderate values of PCV (23.13 %) and GCV (3.75 %) were registered for the plant height. However the moderate genetic advance (36.3 %) and low genetic advance as per cent of mean (1.39 %) indication the major role of non additive gene action in control of this trait.

4. Primary branches per plant

Primary braches per plant registered the moderate values for PCV (25.54 %) and GCV (14.14 %). While, high heritability (16.13 %) and low genetic advance as per cent of mean (3.94 %) revealing the traits are under the control of non additive gene action.

5. Secondary braches per plant

The PCV (13.71 %) and GCV (5.52 %) value were moderate for secondary braches per plant. However, estimate of broad sense high heritability (16.23 %) and moderate genetic advance as per cent of mean (4.58 %) revealing the major role of non additive gene action controlling of secondary braches per plant.

6. Pods per plant

PCV and GCV registered higher values (13.64 and 7.09 % respectively) for pods per plant. However, estimate of broad sense heritability was moderate (11.27 %) and low genetic advance as per cent of mean (7.6 %) revealing the non additive gene action in the control of this trait.

7. Pod length (cm)

PCV and GCV registered moderate values (18.44 % and 9 % respectively) for pod length. However, estimate of broad sense heritability was high (23 %) and moderate genetic advance as per cent of mean (16.69 %) revealing the additive gene action in the control if this trait.

8. Seeds per pod

PCV and GCV registered higher values (19.78 % and 12.85 % respectively) for seeds per plant. However, estimate of broad sense heritability was high (42.2 %) and genetic advance as per cent of mean (13.30 %) revealing the additive gene action in the control of this trait.

9. Seed yield per plant (g)

Seed yield per plant registered moderate values for PCV (22.81 %) and GCV (7.91 %) coupled with broad sense heritability moderate (12.05 %) and moderate genetic advance as per cent of mean (18.74 %) revealing the additive gene action controlling this trait.

10. Hundred seed weight (g)

PCV (7.24 %) and GCV (1.72 %) recorded low values. However, low heritability (6.25 %) and genetic advance as per cent of mean (11.11 %) indicating the major role of non additive gene action in the control of hundred seed weight.

4.1.2.2 Genetic variability parameters in cowpea cross IT-38956-1 × CP-12

Genetic variability parameters for the cross IT-38956-1 × CP-12 has been tabulated in Table 14 and briefly outline below.

1. Days to first flowering

The PCV (10.47 %) and GCV (5.20 %) values were recorded for the days to first flowering, while high heritability (24.7 %) and moderate genetic advance as per cent of mean (6.82 %) indicating the major role of non additive gene action in respect of this trait.

2. Days to maturity

The PCV (7.13 %) and GCV (1.70 %) values are low for days to maturity with high (75.7 %) heritability and low genetic advance as per cent of mean (11.07 %) revealing non additive gene action in the control of this trait.

Table 14: Genetic variability parameters for yield and yield attributing traits in cowpea cross IT-38956-1 × CP-12

Genetic parameters	Days to first flowering	Days to maturity	Plant height (cm)	Primary branches/plant	Secondary branches/plant	Pods per plant
Mean	39.93	85.11	32.87	4.94	6.87	12.09
PCV (%)	10.47	7.13	14.60	27.97	20.93	24.57
GCV (%)	5.20	1.70	5.21	13.15	3.83	10.22
Heritability (%)	24.7	75.7	12.8	22.1	23.4	17.3
GA as % Mean	6.82	11.07	23.91	16.33	1.85	11.22

Genetic parameters	Pod length (cm)	Seeds per pod	Seed yield per plant (g)	Hundred seed weight (g)
Mean	11.59	10.20	17.43	10.85
PCV (%)	23.93	24.84	20.98	7.97
GCV (%)	11.27	21.77	9.52	4.07
Heritability (%)	22.2	32.5	20.6	11.26
GA as % Mean	14.01	14.72	11.41	5.48

3. Plant height (cm)

Moderate values of PCV (14.60 %) and GCV (5.21 %) were registered for the plant height. However the moderate heritability (12.8 %) and moderate genetic advance as per cent of mean (23.91 %) indicated the major role of non additive gene action in control of this trait.

4. Primary branches per plant

Primary braches per plant registered the moderate values for PCV (27.97 %) and GCV (13.15 %). While, high heritability (22.1 %) and moderate genetic advance as per cent of mean (16.33 %) revealing the traits are under the control of non additive gene action.

5. Secondary braches per plant

The PCV (20.93 %) and GCV (3.83 %) value were moderate for secondary braches per plant. However, estimate of broad sense moderate heritability (23.4 %) and low genetic advance as per cent of mean (1.85 %) revealing the non additive gene action controlling this trait.

6. Pods per plant

PCV and GCV registered higher values (24.57 % and 10.22 % respectively) for pods per plant. However, estimate of broad sense heritability was moderate (17.30 %) and low genetic advance as per cent of mean (11.22 %) revealing the non additive gene action in the control of this trait.

7. Pod length (cm)

PCV and GCV registered moderate values (23.93 % and 11.27 % respectively) for pod length. However, estimate of broad sense heritability was high (22.2 %) and moderate genetic advance as per cent of mean (14.01 %) revealing the additive gene action in the control if this trait.

8. Seeds per pod

PCV and GCV registered higher values (24.84 % and 21.77 % respectively) for seeds per plant. However, estimate of broad sense heritability was high (32.5 %) and genetic advance as per cent of mean (14.72 %) revealing the additive gene action in the control of this trait.

9. Seed yield per plant (g)

Seed yield per plant registered moderate values for PCV (20.98 %) and GCV (9.52 %) coupled with moderate broad sense heritability (20.6 %) and moderate genetic advance as per cent of mean (11.41 %) revealing the additive gene action controlling this trait.

10. Hundred seed weight (g)

PCV (7.97 %) and GCV (4.07 %) recorded low values. However, low heritability (11.26 %) and genetic advance as per cent of mean (5.48 %) indicating the major role of non additive gene action in the control of this trait.

4.1.2.3 Genetic variability parameters in cowpea cross KBC-2 × CP-12

Genetic variability parameters for the cross KBC-2 × CP-12 are tabulated in the Table 15 and briefly outlined below

1. Days to first flowering

The PCV (8.59 %) and GCV (1.57 %) values were estimated for days to first flowering, while high heritability (34.0 %) and moderate genetic advance as per cent of mean (17.6 %) indicating the major role of non additive gene action in respect of this trait.

2. Days to maturity

The PCV (6.28 %) and GCV (2.50 %) values are low for days to maturity with moderate (15.9 %) heritability and low genetic advance as per cent of mean (12.64 %) revealing non additive gene action in the control of this trait.

Table 15: Genetic variability parameters for seed yield and yield attributing traits in cowpea cross KBC-2 × CP-12

	Days to first flowering	Days to maturity	Plant height (cm)	Primary branches/ plant	Secondary branches/ plant	Pods per plant	Pod length (cm)	Seeds per pod	Seed yield per plant (g)	Hundred seed weight (g)
Mean	41.66	75.45	33.49	5.40	7.72	10.86	14.53	9.03	15.85	11.29
PCV (%)	8.59	6.28	19.09	21.71	24.73	30.04	18.55	20.74	17.71	5.14
GCV (%)	1.57	2.50	4.52	3.74	8.85	5.99	3.5	8.64	7.42	1.00
Heritability (%)	34.0	15.9	25.6	43.0	12.8	34.0	24.5	17.4	17.5	23.8
GA as % Mean	17.6	12.64	12.82	23.70	8.36	10.86	14.53	9.03	15.85	11.29

3. Plant height (cm)

Moderate values of PCV (19.09 %) and GCV (4.52 %) were registered for the plant height. However the high heritability (25.6 %) and moderate genetic advance as per cent of mean (12.82 %) indication the major role of non additive gene action in control of this trait.

4. Primary branches per plant

Primary braches per plant registered the moderate values for PCV (21.71 %) and GCV (3.74 %). While, high heritability (43.0 %) and moderate genetic advance as per cent of mean (23.70 %) revealing the traits are under the control of non additive gene action.

5. Secondary braches per plant

The PCV (24.73 %) and GCV (8.85 %) value were moderate for secondary braches per plant. However, estimate of broad sense moderate heritability (12.8 %) and low genetic advance as per cent of mean (8.36 %) revealing the additive gene action controlling this trait.

6. Pods per plant

PCV and GCV registered higher values (30.04 % and 5.99 % respectively) for pods per plant. However, estimate of broad sense heritability was moderate (34.0 %) and low genetic advance as per cent of mean (10.86 %) revealing the non additive gene action in the control if this trait.

7. Pod length (cm)

PCV and GCV registered moderate values (18.55 % and 3.5 % respectively) for pod length. However, estimate of broad sense heritability was high (24.5 %) and moderate genetic advance as per cent of mean (14.53 %) revealing the non additive gene action in the control of this trait.

8. Seeds per pod

PCV and GCV registered higher values (20.74 % and 8.64 % respectively) for seeds per plant. However, estimate of broad sense heritability was high (17.4 %) and genetic advance as per cent of mean (9.03 %) revealing the non additive gene action in the control of this trait.

9. Seed yield per plant (g)

Seed yield per plant registered moderate values for PCV (17.71 %) and GCV (7.42 %) coupled with moderate broad sense heritability (17.5 %) and moderate genetic advance as per cent of mean (15.85 %) revealing the non additive gene action controlling this trait.

10. Hundred seed weight (g)

PCV (5.14 %) and GCV (1.0 %) recorded low values. However, low heritability (23.8 %) and genetic advance as per cent of mean (11.29 %) indicting the major role of non additive gene action in the control of this trait.

4.1.3 Character Association

The correlation co-efficient among all the characters related to seed yield in F_2 population of three crosses were estimated and results are presented in Table 16 to Table 18.

4.1.3.1 Correlation in F_2 generation of cowpea cross IT- 38956-1 $\times$ KBC-2

The correlation studies in F_2 population of cowpea cross IT-38956-1 $\times$ KBC-2 are tabulated in the Table 16 and briefly outlined below.

4.1.3.1.1 Association between seed yield per plant with its component characters

Seed yield per plant was significant and positively correlated with pod length (0.846), days to maturity (0.645), plant height (0.626), primary braches per plant (0.556), secondary braches per plant (0.400), pods per plant (0.236) and seeds per pod (0.235).

Table 16: Correlation co-efficients among seed yield per plant and its attributing traits in F₂ generation of cowpea cross IT-38956-1 × KBC-2

Character	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀
X ₁	1.000	0.951**	0.950**	-0.045	0.582**	0.572**	0.506**	0.489**	0.283**	0.397**
X ₂		1.000	0.996**	0.002	0.681**	0.517**	0.639**	0.605**	0.250**	0.645**
X ₃			1.000	-0.030	0.676**	0.527**	0.620**	0.578**	0.260**	0.626**
X ₄				1.000	0.387**	-0.483**	0.529**	0.599**	0.141	0.556**
X ₅					1.000	-0.259**	0.751**	0.744**	0.293**	0.400**
X ₆						1.000	0.241**	0.478**	0.158**	0.236**
X ₇							1.000	0.924**	0.211**	0.846**
X ₈								1.000	0.221**	0.115
X ₉									1.000	0.235**
X ₁₀										1.000

* Significant at P = 0.05, **Significant at P = 0.01

X₁: Days to first flowering

X₂: Days to maturity

X₃: Plant height (cm)

X₄: Primary branches per plant

X₅: Secondary branches per plant

X₆: Pods per plant

X₇: Pod length (cm)

X₈: Seeds per pod

X₉: Hundred seed weight (g)

X₁₀: Yield per plant (g)

4.1.3.1.2 Association among seed per plant and attributing characters

Among the seed yield per plant and attributing characters, positive and significant association of days to first flowering with days to maturity (0.951), plant height (0.950), secondary branches per plant (0.582), pods per plant (0.572), pod length (0.506), seeds per pod (0.489) and hundred seed weight (0.283); days to maturity with plant height (0.996), secondary branches (0.681), pod length (0.639), seed per pod (0.605), pods per plant (0.517) and hundred seed weight (0.250); plant height with secondary branches per plant (0.676), pod length (0.620), seeds per pod (0.578), pods per plant (0.527) and hundred seed weight (0.260); primary branches per plant with seeds per pod (0.599), pod length (0.529), secondary branches per plant (0.387), hundred seed weight (0.141) and pods per plant exhibited negative significant association (-0.483) with primary branches per plant; secondary branches per plant with pod length (0.751), seeds per pod (0.744), hundred seed weight (0.293) and on other hand pods per plant exhibited negative association (-0.259); pods per plant with seeds per pod (0.478), pod length (0.241) and hundred seed weight (0.158); pod length with seeds per pod (0.924) and hundred seed weight (0.211); Seeds per pod with hundred seed weight (0.221) was observed.

4.1.3.2 Correlation in F₂ generation of cowpea cross IT- 38956-1 × CP-12

The correlation studies in F₂ population of cowpea cross IT-38956-1 × CP-12 are tabulated in the Table 17 and briefly outlined below.

4.1.3.2.1 Association between seed yield per plant and its component characters

Seed yield per plant exhibited significant and positive correlation with pod length (0.855), seeds per pod (0.791), pods per plant (0.362), days to first flowering (0.275) and primary braches per plant (0.225) and having significant negative association with plant height (-0.609) and days to maturity (-0.308).

4.1.3.2.2 Association among seed yield per plant and its attributing characters

Among the seed yield per plant and attributing characters, positive and significant association of days to first flowering with plant height (0.910), days to maturity (0.488),

Table 17: Correlation co-efficients for seed yield per plant and yield attributing characters in F₂ generation of cowpea cross IT-38956-1 × CP-12

	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀
X ₁	1.000	0.488**	0.910**	0.416**	0.456**	0.231*	0.291*	0.402**	-0.171*	0.275**
X ₂		1.000	0.467**	0.333**	-0.016	0.155	0.332**	0.406**	-0.042	-0.308**
X ₃			1.000	-0.566**	-0.367**	-0.056	-0.538**	-0.540**	-0.317**	-0.609**
X ₄				1.000	0.604**	0.272*	0.287*	0.222*	-0.176	0.225**
X ₅					1.000	-0.198	0.784**	0.453**	-0.8220	0.188*
X ₆						1.000	-0.761**	-0.511**	-0.355**	0.362**
X ₇							1.000	0.985**	0.117	0.855**
X ₈								1.000	0.070	0.791**
X ₉									1.000	0.103
X ₁₀										1.000

*- Significance at 0.05 **- Significance at 0.01

X₁: Days to first flowering

X₂: Days to maturity

X₃: Plant height (cm)

X₄: Primary branches per plant

X₅: Secondary branches per plant

X₆: Pods per plant

X₇: Pod length (cm)

X₈: Seeds per pod

X₉: Hundred seed weight (g)

X₁₀: Yield per plant (g)

secondary branches per plant (0.456), primary branches per plant (0.416), seeds per pod (0.402), pod length (0.291), pods per plant (0.231) and negative association with hundred seed weight (-0.171); days to maturity with plant height (0.476), seeds per pod (0.406), primary branches per plant (0.333) and pod length (0.332); plant height having negative significant association with primary branches per plant (-0.566), pods per plant (-0.540), pod length (-0.538), secondary branches per plant (-0.367) and hundred seed weight (-0.317); primary branches per plant with secondary branches per plant (0.604), pod length (0.287), pods per plant (0.272) and seeds per plant (0.222); secondary branches per plant with pod length (0.784), seeds per pod (0.453), hundred seed weight is having the negative association for the secondary branches per plant (-0.822); pods per plant is having the significant negative association between pod length (-0.761), seeds per pod (-0.511) and hundred seed weight (-0.355); pod length with seeds per pod (0.988) and non-significant association between hundred seed weight (0.117); seeds per pod having non-significant association with test weight (0.070).

4.1.3.3 Correlation in F₂ generation of cowpea cross KBC-2 × CP-12

The correlation studies in F₂ population of cowpea cross IT-38956-1 × CP-12 are tabulated in the Table 18 and briefly outlined below.

4.1.3.3.1 Association between seed yield per plant and its component characters

Seed yield per plant exhibited significant and positive correlation with pod length (0.970), days to maturity (0.915), primary braches per plant (0.706), secondary branches per plant (0.679), days to maturity (0.662), hundred seed weight (0.611), plant height (0.533) and seeds per pod (0.397).

4.1.3.3.2 Association among seed yield per plant and its attributing characters

Among the seed yield per plant and attributing characters, positive and significant association of days to first flowering with plant height (0.527), secondary branches per plant (0.385), hundred seed weight (0.326) and days to maturity (0.206); days to maturity having at 1% significance with pods per plant (0.820) and hundred seed weight (0.327) and significant positive association with primary branches per plant (-0.217); primary

Table 18: Correlation coefficients for seed yield per plant and yield attributing characters in F₂ generation of cowpea cross KBC-2 × CP-12

	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀
X ₁	1.000	0.206**	0.527**	-0.347**	0.385**	-0.269*	-0.269**	-0.150*	0.326**	0.915**
X ₂		1.000	0.110	-0.217**	0.135	0.820**	-0.074	-0.141	0.372**	0.662**
X ₃			1.000	-0.499**	-0.079	-0.396**	0.032	-0.432**	0.894**	0.533**
X ₄				1.000	0.239**	0.366**	0.097	0.204**	-0.357**	0.706**
X ₅					1.000	0.954**	-0.233*	-0.283**	-0.071	0.679**
X ₆						1.000	-0.071	-0.366**	0.177*	0.264**
X ₇							1.000	0.097	0.530**	0.970**
X ₈								1.000	-0.800**	0.397**
X ₉									1.000	0.611**
X ₁₀										1.000

* Significant at P = 0.05

**Significant at P = 0.01

X₁: Days to first flowering

X₂: Days to maturity

X₃: Plant height (cm)

X₄: Primary branches per plant

X₅: Secondary branches per plant

X₆: Pods per plant

X₇: Pod length (cm)

X₈: Seeds per pod

X₉: Hundred seed weight (g)

X₁₀: Yield per plant (g)

branches per plant is having the positive significant with pods per plant (0.366), secondary branches per plant (0.239) and seeds per pod (0.204) with negative association with hundred seeds weight (-0.357); secondary branches per plant with pods per plant (0.954) and negative with seeds per pod (-0.283), pod length (-0.233); pods per plant with seeds per pod (-0.366), positive significance at one percent with hundred seed weight (0.177); pod length with hundred seed weight (0.530) and non-significant association with seeds per pod (0.097); seeds per pod with negative association with the hundred weight (-0.800).

4.1.4 Path analysis in F₂ generation

4.1.4.1 Direct and Indirect effects of component characters on seed yield per plant in cowpea cross IT-38956-1 × KBC-2

The direct and indirect effect of seed yield by component characters are tabulated in Table 19 and briefly outlined below.

1. Days to first flowering on seed yield

The direct effect of this trait was negative and low (-0.1364). However, its positive indirect effect through the pod length (0.3972) and primary braches per plant (0.2879) negative indirect effect through days to maturity (-0.1653) and other parameters are having the negligible positive effect on seed yield.

2. Days to maturity on seed yield

Plant height exhibited high negative direct effect (-0.4895) on seed yield per plant; whereas, high correlation of this trait with plant height was due to high indirect contribution *via.*, primary braches per plant (0.2066) as well as pod length (0.7543). and secondary braches per plant (0.1334).

3. Plant height on seed yield

Direct contribution of plant height to seed yield per plant was highest and positive (0.4081), whereas, it's indirect effect through other traits were medium except pod length

Table 19: Direct and indirect effects of component characters on seed yield per plant in F₂ generation of cowpea cross IT-38956-1 × KBC-2

Character	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	‘r’ Seed yield per plant
X ₁	-0.1364	-0.1653	0.2879	0.0041	0.0286	0.0336	0.3972	-0.0406	-0.0118	0.397**
X ₂	-0.1297	-0.4895	0.2066	-0.0002	0.1334	0.0303	0.7543	0.1503	-0.0104	0.645**
X ₃	-0.1297	-0.4876	0.4081	0.0027	0.0332	0.0309	0.7314	0.0481	-0.0108	0.626**
X ₄	0.0061	-0.001	-0.0121	-0.0903	0.1129	-0.0284	0.6246	-0.0498	-0.0059	0.556**
X ₅	-0.0793	-0.3334	0.2759	-0.0349	0.4912	-0.0152	0.8287	-0.0618	-0.0122	0.400**
X ₆	-0.0781	-0.1553	0.2151	0.0436	-0.0127	0.1587	-0.0488	0.1028	0.0105	0.236**
X ₇	-0.1697	-0.3127	0.1528	-0.0477	0.1369	-0.2024	1.1206	0.2768	-0.1088	0.846**
X ₈	-0.0667	-0.2961	0.2361	-0.0541	0.1365	-0.0056	0.0914	0.0831	-0.0092	0.115
X ₉	-0.0386	-0.1225	0.1062	-0.0128	0.1144	-0.0007	0.2491	-0.0184	-0.0416	0.235**

Residual effect= 0.072

* Significant at P = 0.05

**Significant at P = 0.01

X₁: Days to first flowering

X₅: Secondary branches per plant

X₉: Hundred seed weight (g)

X₂: Days to maturity

X₆: Pods per plant

X₃: Plant height (cm)

X₇: Pod length (cm)

X₄: Primary branches per plant

X₈: Seeds per pod

(0.7314) which has very high and positive indirect effects. The days to maturity (-0.4876) shows the negative indirect high effect.

4. Primary braches per plant on seed yield

This trait registered high negative negligible direct effect (-0.0903) on seed yield per plant, but highest indirect positive effect viz., pod length (0.6246), secondary branches per plant (0.1129). The indirect negative effect was observed in plant height (-0.0121), days to maturity (-0.0010), pods per plant (-0.0284), seeds per pod (-0.0498) and hundred seed weight (-0.0059) were found to be negligible contribution towards the seed yield per plant.

5. Secondary branches per plant on seed yield

Secondary braches per plant recorded a highest direct association (0.4912) with seed yield per plant. However, the highest positive indirect correlation through pod length (0.8287) along with plant height (0.2759).The trait days to maturity shows highest negative indirect effect (-0.3334) and all other characters shows the negligible indirect effect on seed yield.

6. Pods per plant on seed yield

Pods per plant exhibited negligible direct effect (0.1587) on seed yield per plant. However, positive indirect effect on seed yield per plant viz., plant height (0.2151), seeds per pod (0.1028) followed by and primary branches per plant (0.0436). The trait days to maturity (-0.1553) shows the indirect negative effect on the seed yield.

7. Pod length on seed yield

Pod length exhibited highest positive direct effect (1.1206) on seed yield per plant. However, its indirect contribution through seeds per pod (0.2768), plant height (0.1528) along with secondary branches per plant (0.1369). The trait days to maturity (-0.3127) showed the high negative indirect effect on the seed yield.

8. Number of seeds per pod on seed yield

Number of seeds per pod exhibited low positive direct effect (0.0831) on seed yield per plant which is negligible. However, its indirect contribution through plant height (0.2361), secondary branches per plant (0.1365) and pod length (0.0914) on seed yield per plant.

9. Hundred seed weight on seed yield

Hundred seed weight exhibited the negative negligible direct effect (-0.0416). However, its indirect effect contributions through pod length (0.2491) along with plant height (0.1062) and secondary branches per plant (0.1144) and other characters shows the negligible effect on seed yield.

4.1.4.2 Direct and Indirect effects of component characters on seed yield per plant in cowpea cross IT-38956-1 × CP-12

The direct and indirect effect of component character on seed yield of cowpea cross IT-38956-1 × CP-12 are tabulated in the Table 20 and briefly outlined below.

1. Days to flowering on seed yield

The direct effect of this trait was positive (0.2331). However, the positive indirect effect of this trait with plant height (0.2166), pod length (0.0572) and all other traits exhibited the negligible contribution for the association of days to first flowering on seed yield.

2. Days to maturity on seed yield

Plant height exhibited negative high direct effect (-0.3046) on seed yield per plant; whereas, its positive indirect effect for the trait through secondary branches per plant (0.0024), seeds per pod (0.0503), pod length (0.0443) and pods per plant (0.0303) was found to be negligible contribution for the seed yield through the days to maturity.

Table 20: Direct and indirect effects of component characters on seed yield/plant in F₂ generation of cowpea cross IT-38956-1 × CP-12

Character	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	‘r’ Seed yield per plant
X ₁	0.2331	-0.225	0.2166	0.0002	0.0215	0.0236	0.0572	-0.0406	-0.0108	0.275**
X ₂	-0.1267	-0.3046	0.0066	-0.0002	0.0024	0.0303	0.0443	0.0503	-0.0104	-0.308**
X ₃	-0.1297	-0.3877	-0.2084	0.0031	0.0132	0.0309	0.0314	0.0481	-0.0108	-0.609**
X ₄	0.0061	-0.0001	-0.0121	0.0703	0.0198	-0.0284	0.0246	0.1498	-0.0049	0.225**
X ₅	-0.0793	-0.0304	0.0059	-0.0024	0.0412	-0.0152	0.0087	0.2618	-0.0022	0.188*
X ₆	-0.0681	-0.1561	0.5151	0.0271	-0.0127	0.1051	-0.0488	0.0008	0.0005	0.362**
X ₇	-0.0671	-0.3127	0.1528	-0.0587	0.1369	-0.0024	0.9012	0.1146	-0.0088	0.855**
X ₈	-0.1467	-0.3006	0.2006	-0.0841	0.1365	-0.0256	0.0012	1.0151	-0.0052	0.791**
X ₉	-0.0346	-0.0021	0.1003	-0.0031	0.0144	-0.0007	0.0346	-0.0184	0.0127	0.103

Residual effect= 0.071 * Significant at P = 0.05 **Significant at P = 0.01

X₁: Days to first flowering

X₅: Secondary branches per plant

X₉: Hundred seed weight (g)

X₂: Days to maturity

X₆: Pods per plant

X₃: Plant height (cm)

X₇: Pod length (cm)

X₄: Primary branches per plant

X₈: Seeds per pod

3. Plant height on seed yield

Direct contribution of plant height with seed yield per plant was high and negative (-0.2084), whereas, it's indirect effect through the traits pod length (0.0314) and seeds per pod (0.0481) and all other characters were found to be negligible contribution for the seed yield per plant.

4. Primary braches per plant on seed yield

This trait registered a positive direct effect to seed yield per plant (0.0703) where it is negligible, whereas its indirect effect was found positive and negligible with days to first flowering (0.0061), secondary branches plant (0.0198) and pod length (0.0246) was made strong correlation of this trait with the seed yield per plant except seeds per pod (0.1498) is having low positive indirect effect.

5. Secondary branches per plant on seed yield

Secondary braches per plant recorded a negligible direct effect (0.0412) with seed yield per plant. However, high positive indirect effect with the trait seeds per pod (0.2618), medium effect with the trait pod length (0.0087) and negligible effect with plant height.

6. Pods per plant on seed yield

Pods per plant exhibited high direct effect (0.1051) on seed yield per plant. However, indirect positive effect with the plant height (0.5151) along with low negligible indirect effect with the traits through primary branches per plant (0.0271), seeds per pod (0.0080) and negative contribution through the days to maturity (-0.1561), secondary braches per plant (-0.0127), days to first flowering (-0.0681) and pod length (-0.0488) was found to be negligible effect on seed yield.

7. Pod length on seed yield

Pod length exhibited highest positive direct effect (0.9012) on seed yield per plant. Whereas, it's indirect contribution through plant height (0.1528), secondary branches per plant (0.1369), seed per pod (0.1146) and its negative indirect effect through

the days to maturity (-0.3127) was found to be high, days to first flowering (-0.0671), primary braches per plant (-0.0587), pods per plant (-0.0024) and hundred seed weight (-0.0088) was found to be negligible contribution for the seed yield.

8. Number of seeds per pod on seed yield

Number of seeds per pod exhibited positive high direct effect (1.0151) on seed yield per plant. However, it's indirect positive contribution through plant height (0.2006), and secondary branches per plant (0.1365). The days to maturity showed the highest (-0.3006) negative indirect effect on seed yield.

9. Hundred seed weight on seed yield

Hundred seed weight exhibited the negligible direct effect (0.0127). However its positive indirect effect through plant height (0.1003), secondary branches per plant (0.0144), pod length (0.0346) and indirect negative effect through days to first flowering (-0.0346), seeds per pod (-0.0184), primary braches per plant (-0.0031) and plant height (-0.0021) was found to be negligible effect on seed yield per plant.

4.1.4.3 Direct and Indirect effects of component characters on seed yield per plant in cowpea cross KBC-2 × CP-12

The direct and indirect effect of component character on seed yield of cowpea cross IT-38956-1 × CP-12 are tabulated in the Table 21 and briefly out lined below.

1. Days to first flowering on seed yield

The direct effect of this trait was highly positive (0.3740). However, the positive indirect effect of this trait through seeds per pod (0.2560), secondary branches per plant (0.2028), pod length (0.1216), pods per plant (0.1415) and hundred seed weight (0.1251) exhibited the high indirect effect. Its, indirect negative effect through the primary braches per plant (-0.2034) and days to maturity (-0.1985) was found to the associated with the seed yield.

Table 21: Direct and indirect effects of component characters on seed yield/plant in F₂ generation of cowpea cross KBC-2 × CP-12

Character	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	‘r’ Seed yield per plant
X ₁	0.374	-0.1985	0.0954	-0.2034	0.2028	0.1415	0.1216	0.256	0.1251	0.915**
X ₂	-0.3556	0.1046	0.079	0.0002	0.1605	0.1244	0.235	0.1471	0.1671	0.662**
X ₃	-0.3555	-0.1043	0.0793	-0.0026	0.1578	0.1338	0.416	0.1541	0.054	0.533**
X ₄	0.0168	-0.0002	-0.0023	0.0891	0.2048	-0.2099	0.4208	-0.127	0.3142	0.706**
X ₅	-0.2135	-0.0713	0.0536	0.0345	0.3293	-0.1124	0.1151	0.1783	0.3651	0.679**
X ₆	-0.2111	-0.0541	0.0418	-0.0431	-0.1372	0.4342	-0.0691	0.1574	0.1454	0.264**
X ₇	-0.1838	-0.0623	0.0429	0.0534	0.1937	-0.0417	0.7193	0.1462	0.1026	0.970**
X ₈	-0.1242	0.0122	0.0146	0.0243	-0.0125	-0.1462	0.012	0.4642	0.1523	0.397**
X ₉	0.4117	0.0461	0.0264	0.002	-0.0146	0.2461	0.238	0.0021	-0.347	0.611**

Residual effect = 0.036

* Significant at P = 0.05

**Significant at P = 0.01(R value=0.190)

X₁: Days to first flowering

X₅: Secondary branches per plant

X₉: Hundred seed weight (g)

X₂: Days to maturity

X₆: Pods per plant

X₃: Plant height (cm)

X₇: Pod length (cm)

X₄: Primary branches per plant

X₈: Seeds per pod

2. Days to maturity on seed yield

Plant height exhibited low positive direct effect (0.1046) on seed yield per plant; whereas, highest indirect effects through pod length (0.2350), secondary branches per plant (0.1605), hundred seed weight (0.1671) and seeds per pod (0.1471). Days to first flower (-0.3556) shows the indirect highest negative effect of days to maturity with the seed yield per plant.

3. Plant height on seed yield

Direct contribution of plant height to seed yield per plant positive and negligible (0.0793), whereas, its indirect effect through other traits such as pod length (0.4162) which has very high and positive indirect effects along with secondary branches per plant (0.1578), pods per plant (0.1338) and seeds per pod (0.1541). Days to first flower (-0.3553) shows the indirect highest negative effect on days to maturity.

4. Primary braches per plant on seed yield

This trait registered a positive direct effect with seed yield per plant (0.0891), whereas its indirect effect was found to be highest with hundred seed weight (0.3142), pods length (0.4208) and secondary branches per plant (0.2048). The trait pods per plant showed the negative indirect effect.

5. Secondary branches per plant on seed yield

Secondary braches per plant recorded a high direct effect (0. 3293) with seed yield per plant. However, high positive indirect effect with hundred seed weight (0.3651), seeds per pod (0.1783), pod length (0.1151) and negligible indirect effect with plant height (-0.0713) along with primary branches per plant (0.0345).

6. Pods per plant on seed yield

Pods per plant exhibited high direct effect (0.4342) on seed yield per plant. However, positive indirect effect through seeds per pod (0.1574) and hundred seed weight (0.1454), negligible indirect effect through plant height (0.0418) was found for this trait.

7. Pod length on seed yield

Pod length exhibited highest positive direct effect (0.7193) on seed yield per plant. Whereas, it's indirect contribution through secondary branches per plant (0.1937), seeds per pod (0.1462), hundred seed weight (0.1026) and primary branches per plant (0.0534).

8. Number of pods per plant on seed yield

Number of pods per seed exhibited high positive direct effect (0.4642) on seed yield per plant. However, its highest indirect contributions *via* hundred seed weight (0.1523) along with negligible indirect effect through primary braches per plant (0.0243), plant height (0.0146) and days to maturity (0.0146).

9. Hundred seed weight on seed yield

Hundred seed weight exhibited the negative direct effect (-0.3471). However its high indirect effect contribution through pods per plant (0.2461) and pod length (0.2381) and days to maturity (0.4117) showed the highest indirect effect.

4.1.5 Heterosis and inbreeding depression

Heterosis of the F_1 over the mid parent and better parent, inbreeding depression from F_1 to F_2 and F_2 to F_3 are presented character wise for three cowpea crosses viz., IT-38956-1 $\times$ KBC-2, IT-38956-1 $\times$ CP-12 and KBC-2 $\times$ CP-12 has been tabulated in Table 22 and these are briefly outlined below.

4.1.5.1 Days to first flower

Significant positive heterosis over mid parent and better parent was observed for Days to first flower in cross I and cross III. But the cross II recorded significant negative heterosis for both mid parent and better parent.

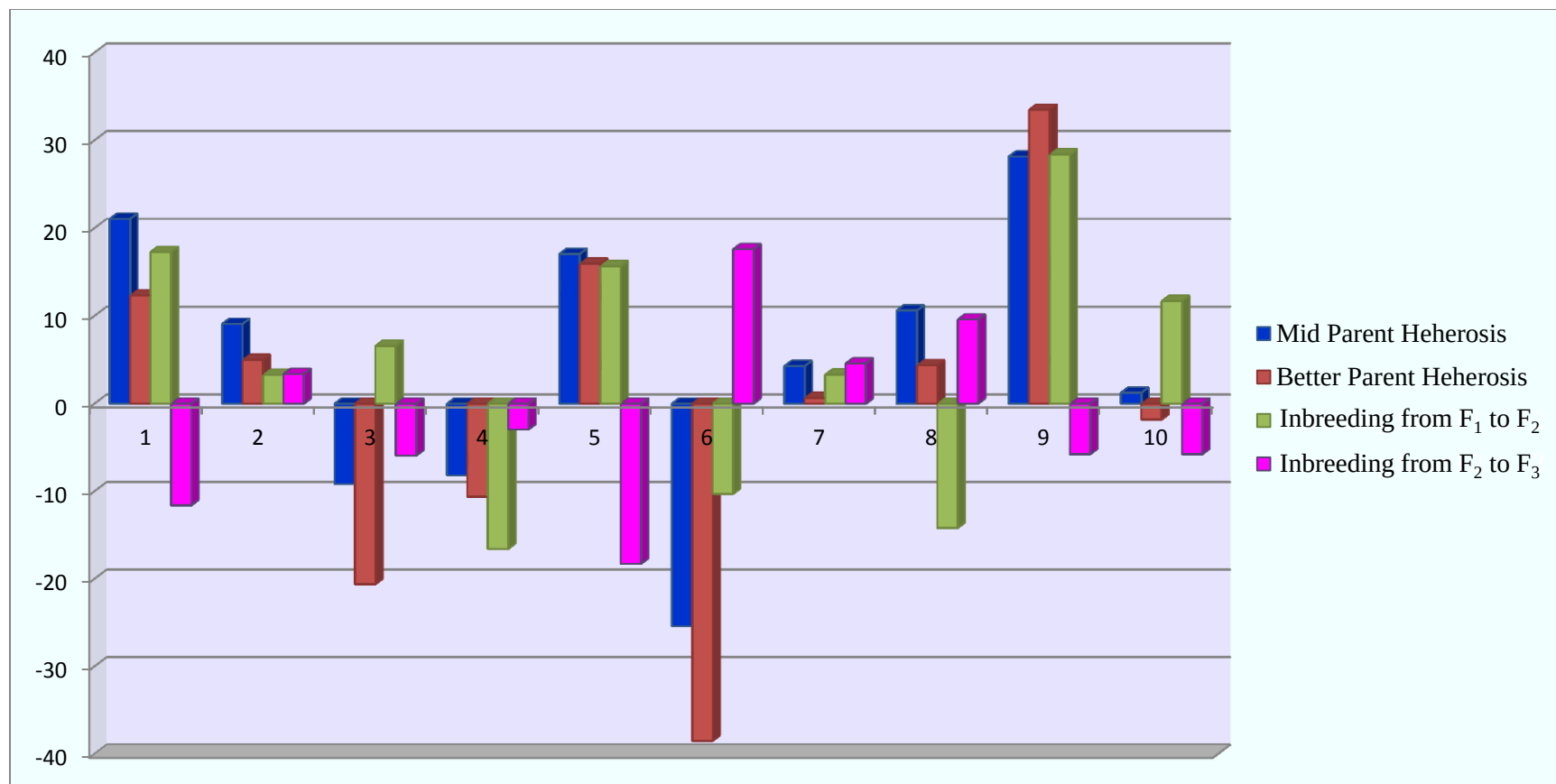
Significant positive inbreeding depression from F_1 to F_2 was observed in Cross I & cross III, but negative inbreeding depression was recorded in cross-II.

Table 22: Estimates of heterosis and inbreeding depression in three cowpea crosses

Sl. No.	Characters	Crosses	Heterosis (%)		Inbreeding depression	
			Mid parent	Better parent	F ₁ -F ₂	F ₂ -F ₃
1.	Days to first flower initiation					
		Cross 1	21.05**	12.34**	17.28**	-11.60**
		Cross 2	-5.80**	-8.51**	-9.33**	-4.55**
		Cross 3	18.10**	7.50**	6.96**	-15.47**
2.	Days to maturity					
		Cross 1	9.09**	4.99**	3.28	3.38
		Cross 2	1.95	1.54	-3.23	-1.03
		Cross 3	8.87**	5.68**	11.65**	-22.25**
3.	Plant height (cm)					
		Cross 1	-9.17**	-20.61**	6.58**	-5.93**
		Cross 2	1.15	-0.98	7.47**	0.28
		Cross 3	10.55**	6.80**	1.82	-6.30**
4.	Primary branches per plant					
		Cross 1	-8.17**	-10.61**	-16.58**	-2.93**
		Cross 2	3.95**	4.4**	54.43**	38.64**
		Cross 3	16.43**	10.21**	8.44**	-2.34
5.	Secondary branches per plant					
		Cross 1	17.07**	15.94**	15.67**	-18.28**
		Cross 2	12.00**	12.30**	6.00**	3.41**
		Cross 3	25.65**	17.48**	37.51**	2.88
6.	Pods per plant					
		Cross 1	-25.39**	-38.50	-10.30**	17.60**
		Cross 2	15.18**	8.20**	12.71**	0.48
		Cross 3	14.98**	6.10**	40.84**	-19.30**
7.	Pod length(cm)					
		Cross 1	4.28**	0.66	3.30	4.57**
		Cross 2	-11.06**	-12.62**	14.97**	-3.88**
		Cross 3	-15.10**	-30.41**	-16.41**	31.32**
8.	Seeds per pod					
		Cross 1	10.61**	4.37**	-14.19**	9.59**
		Cross 2	6.80**	-0.38	21.24**	-27.94**
		Cross 3	11.31**	0.32	29.94**	-16.02**
9.	Seed yield (g)					
		Cross 1	28.16**	33.48**	28.39**	-5.76**
		Cross 2	7.15**	-2.09	31.0**	-4.88**
		Cross 3	17.59**	16.45**	35.83**	-18.42**
10.	Hundred seed weight (g)					
		Cross 1	1.25	-1.80	11.69**	-5.76*
		Cross 2	4.1**	-8.63**	13.20**	-8.39**
		Cross 3	-1.99	-4.19**	0.53	-4.52**

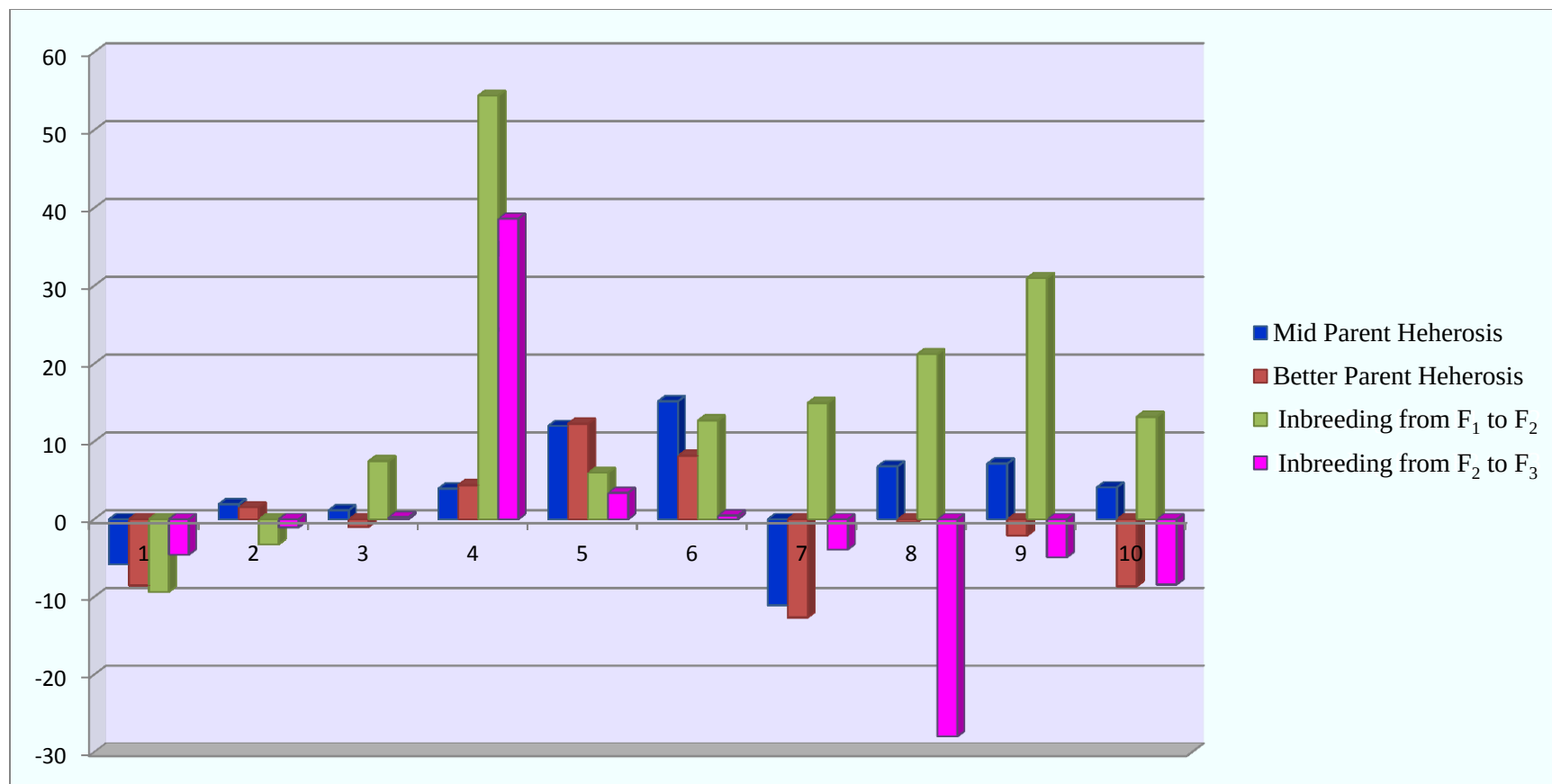
*- Significance at 0.05 probability level, **- Significance at 0.01 probability level

Cross 1- IT-38956-1 × KBC-2, Cross 2 – IT-38956-1 × CP-12, Cross 3 – BC-2 × CP-12



1. Days to first flowering
 2. Days to maturity
 3. Plant height (cm)
 4. Primary braches per plant
 5. Secondary branches per plant
 6. Pods per plant
 7. Pod length (cm)
 8. Seeds per pod
 9. Seed yield per plant (g)
 10. Hundred seed weight (g)

Figure 33: Histogram showing the nature and magnitude of heterosis and inbreeding depression for ten characters in IT-38956 × KBC-2

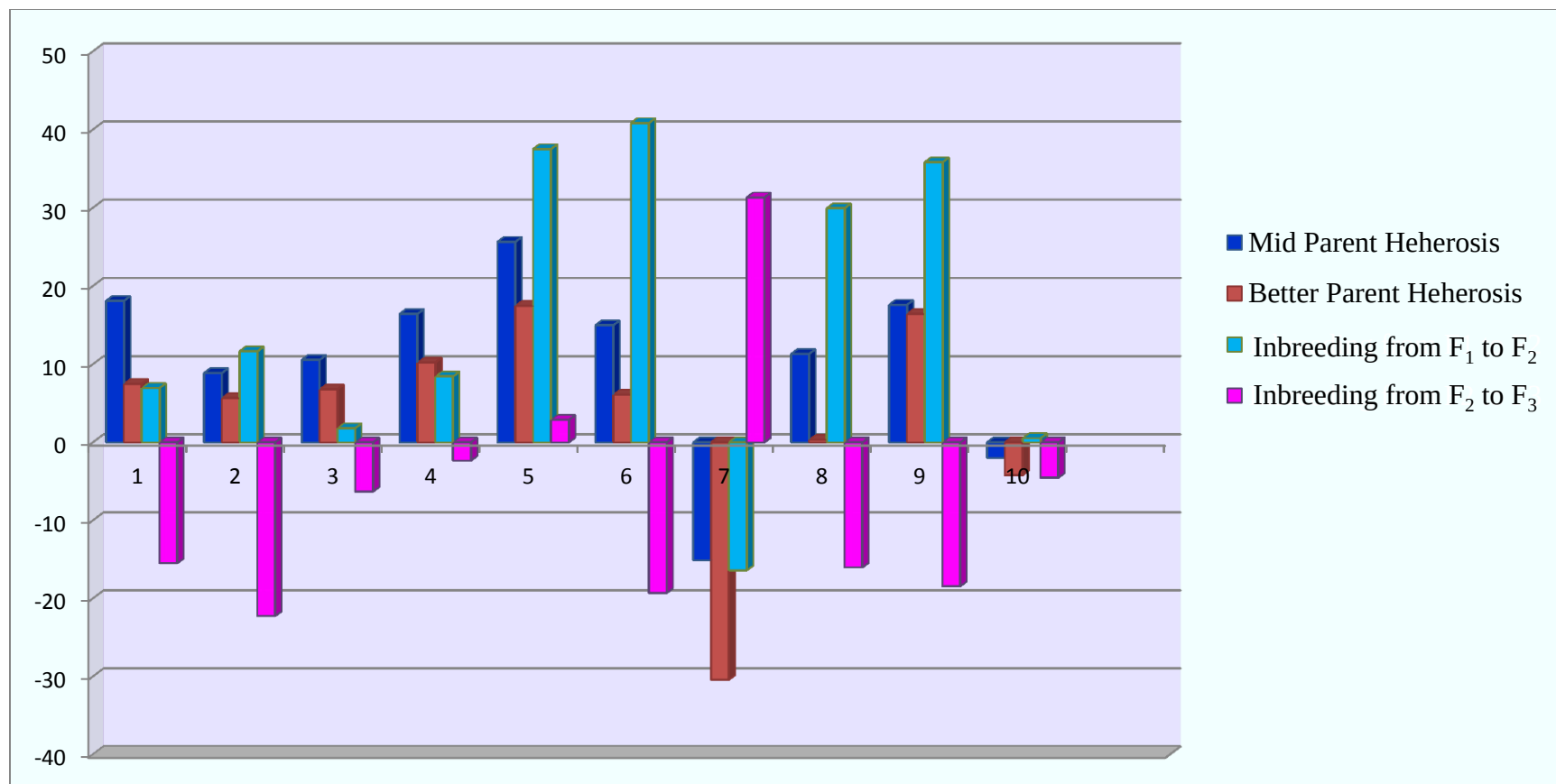


1. Days to first flowering
 2. Days to maturity
 3. Plant height (cm)
 4. Primary braches per plant

5. Secondary branches per plant
 6. Pods per plant
 7. Pod length (cm)
 8. Seeds per pod

9. Seed yield per plant (g)
 10. Hundred seed weight (g)

Figure 34: Histogram showing the nature and magnitude of heterosis and inbreeding depression for ten characters in IT-38956 × CP-12



1. Days to first flowering
 2. Days to maturity
 3. Plant height (cm)
 4. Primary braches per plant

5. Secondary branches per plant
 6. Pods per plant
 7. Pod length (cm)
 8. Seeds per pod

9. Seed yield per plant (g)
 10. Hundred seed weight (g)

Figure 35: Histogram showing the nature and magnitude of heterosis and inbreeding depression for ten characters in KBC-2 × CP-12.

4.1.5.2 Days to maturity

Cross I and cross III showed positive significant heterosis over mid parent and better parent, cross-II showed positive heterosis but non significant. Inbreeding depression from F_1 to F_2 significantly positive for cross-III, inbreeding depression from F_2 to F_3 was found negatively significant for the cross-III. Inbreeding depression from F_1 to F_2 and F_2 to F_3 for cross-I found positive and non significant. Inbreeding depression from F_1 to F_2 and F_2 to F_3 for cross-II found negative and non significant.

4.1.5.3 Plant height (cm)

Crosse I showed significant heterosis for plant height but in negative direction, Cross- II showed positive heterosis over mid parent but non significant and recorded negative non significant heterosis over better parent. Cross III recorded positive significant heterosis over mid parent and better parent.

Inbreeding depression from F_1 to F_2 was found positive for all three crosses but significant for cross-I and cross-II and non significant for cross-III. Inbreeding depression from F_2 to F_3 was found negatively non significant for the cross-I and cross-III but cross-II recorded positive non significant inbreeding depression.

4.1.5.4 Primary branches per plant

Significant negative heterobeltosis was found for primary branches per plant for the cross-I, for the cross-II mid parent and better parent heterosis was found positive and significant, for cross-III it found positive significant Heterosis for both mid parent and better parent.

Inbreeding depression from F_1 to F_2 was found positive and significant for cross II for cross-III and cross-I it found negatively significant. Inbreeding depression from F_2 to F_3 was found negative for the cross-I and Cross-III but found non significant, but cross-II recorded positive significant inbreeding depression.

4.1.5.5 Secondary branches per plant

All the crosses found to be significantly positive heterosis over mid parent and better parent. Inbreeding depression from F_1 to F_2 was found positive and significant for all the three crosses. Inbreeding depression from F_2 to F_3 was found negatively significant for cross-I positive significant inbreeding depression was recorded for cross-II and Cross-III.

4.1.5.6 Number of pods per plant

Negative significant heterobeltosis observed in cross-I, positive significant heterosis over mid parent and better parent for the cross II and III. Significant negative inbreeding depression was observed in cross- I in F_1 to F_2 , positive significant inbreeding depression was observed in cross II and III for F_1 to F_2 . Inbreeding depression Significant negative was found for the cross-III from F_2 to F_3 and significant positive inbreeding depression was found in cross-I.

4.1.5.7 Number of seeds per pod

All the crosses found to be significantly positive for the heterosis over mid parent and better parent for cross-I showed positive significant heterosis but cross-II and III recorded significant heterosis. Inbreeding depression from F_1 to F_2 for the cross- II and III was found positive and significant. But cross-I recorded negative significant inbreeding depression. Inbreeding depression from F_2 to F_3 was found negatively significant for cross-II & cross-III, positive significant inbreeding depression was recorded for cross-I.

4.1.5.8 Pod length (cm)

The heterosis over mid parent for pod length ranged from 4.28 % for cross-I to -15.10 % for cross-II and better parent heterosis ranged from -11.06 (cross-II) to -15.70 (cross-III). Significant inbreeding depression was found for the cross-II for F_1 to F_2 and for cross-III if found negatively significant. Significant inbreeding depression was found in cross I and cross-III for F_2 to F_3 . For the cross-III if found negatively significant for F_2 to F_3 on other two crosses found positively significant.

4.1.5.9 Seed yield per plant (g)

Significant positive for the heterosis over mid parent has been observed in all the three crosses. Significant positive heterosis was observed in cross-I and cross-III and in cross-II showed negative but non significant heterosis.

Inbreeding depression from F_1 to F_2 recorded positive and significant in all the crosses. Inbreeding depression for F_2 to F_3 recorded negative and significant for all the crosses.

4.1.5.10 Hundred seed weight (g)

Mid parent heterosis was significant and positive in cross-II and in cross-I is positive but non significant where as cross-III recorded negative and non significant mid parent heterosis. Negative and significant better parent heterosis was found in cross-II & III and in cross-I it is negative and non significant.

Inbreeding depression from F_1 to F_2 shows positive direction for all the crosses and cross-III found non significant. All the three crosses found to be in negative direction and significant from F_2 to F_3 inbreeding depression.

4.2 Study of gene action for yield and its attributing traits through generation mean analysis

4.2.1 Analysis of variances for segregating and non-segregating generations

Analysis of variance of the means from three parents, three F_1 's, F_2 's and F_3 's for ten characters are given in Table 23.

There were significant differences among the means for all the characters as evidenced by the significance of mean sum of square due to non-segregating and segregating generations. Among non-segregating generations, the differences in parents were also highly significant for all characters except pods per plant. When F_1 's and Parents versus F_1 's were considered separately, all the characters except primary branches per plant differed significantly. When we consider segregating generations, F_2 's

Table 23: Analysis of variances for ten quantitative characters in five generations mean analysis of cowpea

Source of variation	Df	Days to first flowering	Days to maturity	Plant height (cm)	Primary branches/ plant	Secondary branches/ plant	Pods/ plant	Pod length (cm)	Number of seeds /pod	Seed yield (g)	Hundred seed weight (g)
		Mean sum of squares									
Replications	1	3.17	2.39	2.10	1.73	0.68	1.00	0.50	1.85	0.91	0.09
Treatments	14	52.02**	41.20**	72.65**	4.88**	10.28**	8.97**	8.51**	7.02**	8.77**	3.38**
1. Non segregating (NS)	11	57.35**	40.83**	424.60**	4.10**	7.41**	7.06**	10.58**	9.56**	7.66**	5.05**
a. Parents (P)	2	56.16**	48.94**	42.78**	5.87**	6.73**	1.27	13.65**	9.93**	6.13**	4.48**
b. F₁'s	2	57.13**	15.29**	83.44**	0.92	7.19**	10.85**	4.88**	9.35**	4.23**	3.18**
c. P Vs F₁'s	1	66.34**	60.68**	80.82**	1.25	12.83**	36.22**	6.19**	7.60**	28.66**	14.65**
2. Segregating (S)	7	48.94**	50.07**	58.62**	1.78	3.75**	1.26	2.69*	3.98**	7.52**	0.86
a. F₂'s	2	77.70**	58.98**	60.01**	2.00	4.28*	1.39	5.48**	8.16**	9.70**	0.43
b. F₃'s	2	1.26	2.16	1.45	2.07	4.48**	1.42	0.48	0.86	5.73**	1.13
c. F₂'s Vs F₃'s	1	0.33**	0.80	1.62	0.25	0.27	0.39	0.95**	0.80	6.35**	1.34
3. NS Vs S	1	25.07**	31.63**	24..99**	0.25	15.56**	21.35**	26.48**	0.36	29.73**	26.50**
Error	14	1.15	1.56	2.05	0.59	0.63	0.92	0.43	0.38	0.34	0.05
S. Em ±	-	0.87	1.02	1.17	0.63	0.65	0.78	0.54	0.51	0.47	0.19
CD at 5%	-	1.66	1.99	2.29	1.23	1.27	1.52	1.06	0.99	0.92	0.37
CV (%)	-	1.76	1.38	5.08	13.50	7.70	6.16	4.29	4.81	4.49	2.35

*- Significance level at 5% , **- Significance level at 1%

separately, there were significant differences among themselves for all the characters except primary branches per plant, pods per plant and test weight. For two characters in F_3 's generations showed the significant differences whereas other characters were differed non-significantly.

When we considered the interaction between F_2 's Vs F_3 's there was no significant differences among all the other characters, except Days to first flower, pod length and seed yield. When segregating populations and non-segregating populations were compared each other, there was significant differences for all the characters except primary branches per plant and number of seeds per pod.

4.2.2 Means and variances for P_1 , P_2 , F_1 , F_2 and F_3 populations

Means and standard error of the means and variances of parents and five generations of three cowpea crosses for 10 different quantitative characters are presented in Table 24 to Table 26.

4.2.2.1 Means and variances of quantitative characters in cowpea cross IT- 38956-1 × KBC-2

Means and variances of quantitative characters in cowpea cross IT-38956-1 × KBC-2 has been tabulated in Table 24 and these are briefly outlined below

1. Days to first flower

IT- 38956-1 was found to be earliest in flower initiation than KBC-2 by 7 days, F_3 took 45 Days to first flower whereas F_2 took only 41 Days to first flower. Among the segregating population F_2 showed very high variance.

2. Days to maturity

IT- 38956-1 was early mature than KBC-2 by 7 days, however F_2 took 84 days which is more than both the parents with high variance, F_3 took 81 days to maturity which is earlier than KBC-2. Mean days to maturity of F_1 87 days which is higher than the both the parents.

Table 24: Means, standard errors and variances ten quantitative characters in cowpea cross IT-38956-1 × KBC-2

Generations	Days to first flowering		Days to maturity		Plant height (cm)		Primary branches per plant	
	Mean ± SE	Variance	Mean ± SE	Variance	Mean ± SE	Variance	Mean ± SE	Variance
P ₁	37.8±0.59	7.01	76.90±0.87	16.20	26.51±0.16	8.25	6.55±0.32	2.15
P ₂	44.15±0.34	1034	83.15±0.82	10.34	40.88±0.13	6.10	4.90±0.11	1.60
F ₁	42.6±0.45	0.21	87.3±0.89	3.90	25.14±0.13	7.3	5.20±0.15	1.95
F ₂	41.03.17±0.47	34.25	84.44±0.55	45.69	27.73±0.02	41.66	5.23±0.05	5.62
F ₃	45.79±0.34	10.25	81.59±0.24	17.37	22.85±0.24	19.40	5.54±0.08	3.58
Generations	Secondary branches per plant		Pods / plant		Pod length (cm)		Seeds / pod	
	Mean ± SE	Variance	Mean ± SE	Variance	Mean ± SE	Variance	Mean ± SE	Variance
P ₁	10.15±0.30	2.09	13.75±0.36	2.61	12.58±0.32	2.17	13.35±0.29	1.73
P ₂	10.35±0.34	1.18	15.25±0.42	2.30	14.18±0.26	1.42	15.25±0.24	2.30
F ₁	12.0±0.26	6.95	15.15±0.35	2.4	14.80±0.10	1.79	11.80±0.35	6.95
F ₂	10.12±0.16	3.25	14.65±0.13	2.51	16.69±0.52	12.34	13.30±0.26	10.50
F ₃	11.97±0.04	6.02	13.98±0.25	3.90	15.28±0.45	2.50	12.94±0.35	5.15
Generations	Seed yield per plant (g)		Hundred seed weight(g)					
	Mean ± SE	Variance	Mean ± SE	Variance				
P ₁	19.61±0.22	6.21	12.81±0.12	0.34				
P ₂	21.23±0.31	2.06	12.04±0.21	0.83				
F ₁	26.17±0.23	1.89	12.58±0.10	2.14				
F ₂	18.74±0.07	2.19	11.11±0.17	4.69				
F ₃	19.80±0.05	4.25	11.75±0.51	1.98				

SE-Standard error

3. Plant height (cm)

IT- 38956-1 was dwarf parent (26.51 cm) than KBC-2 (40.88 cm) with low variability. Mean plant height of F_1 (25.14 cm) lower than the height of IT- 38956-1, there was decrease in plant height in F_3 (22.85 cm). Mean height of F_2 (27.73cm) is more or less same as that of IT-38956-1 with high variance. Both segregating populations are high variance compared to non segregating population.

4. Primary branches per plant

Minimum numbers of primary branches per plant were found in KBC-2 (4.90) and IT- 38956-1 (6.55). There was increase in variance for primary branches per plant in F_2 and F_3 compared to non segregating generation.

5. Secondary branches per plant

Both the parents produce more or same number of secondary branches per plant, F_2 producing higher number of secondary branches per plant than that the parents. The F_3 population displayed higher magnitude of variance among the segregating generation for this trait.

6. Number of pods per plant

Mean number of pods per plant in F_1 (15.15), F_2 (14.65) and F_3 (13.98) was intermediate between the parents IT- 38956-1 (13.75) and KBC-2 (15.25). Variability in F_2 population was very high compared to F_3 population.

7. Pod length (cm)

Highest pod length was observed in KBC-2 (14.18) and lowest in IT- 38956 - 1(12.55), F_1 pod length (14.80) was more than the both the parents. There was very high variability between F_2 (16.69 cm) and F_3 (15.28 cm) compared to parents. The magnitude of variation was high in F_2 compared to F_3 population. Variance among segregating population was very high in F_2 compared to F_3 .

8. Number of seeds per pod

The better parent KBC-2 exhibited more mean number of seeds per pod (15.25) compared to IT- 38956-1 (13.35). There was decrease in number of seeds per pod in F_1 (11.80). The variation for number of seeds per pod in F_2 (13.30) was more compared to F_3 (12.94). The variance was high in F_2 compared to F_3 population.

9. Seed yield per plant (g)

Highest seed yield was observed in KBC-2 (21.23 g/plant) compared to IT-38956-1 (19.61 g/plant). Mean yield per plant in F_1 (26.17 g) is highest among the parents. Mean seed yield in F_2 (18.74 g) which is less than the both the parents. Mean seed yield of F_3 (19.80 g) is highest than the F_2 . There was increased in mean seed yield in F_2 to F_3 which is less than that of both the parents, and variance was high in F_3 than the F_2 population.

10. Hundred seed weight (g)

Mean of hundred seed weight in F_1 (12.58 g) surpassed both the parents in segregating generation. Mean hundred seed weight was 11.11 g in F_2 and 11.75 g in F_3 .

4.2.2.2 Means and variances of quantitative characters in cowpea cross IT-38956-1 × CP-12

Means and variances of quantitative characters in cowpea cross IT-38956-1 × KBC-2 has been tabulated in Table 25 and these are briefly outlined below

1. Days to first flower

The parent IT- 38956-1 took 39 days for flower initiation compared to other parent CP-12 that took 36 days for flower initiation. F_1 took 50 days for flower initiation which is highest than two parents. The reduction in flower initiation days in F_2 (39.96) to F_3 (41.78), variation was also high in F_2 compared to F_3 (Table 25).

Table 25: Means, standard errors and variances ten quantitative characters in cowpea cross IT-38956-1 × CP-12

Generations	Days to first flowering		Days to maturity		Plant height (cm)		Primary branches / plant	
	Mean ± SE	Variance	Mean ± SE	Variance	Mean ± SE	Variance	Mean ± SE	Variance
P ₁	39.42±0.42	0.48	84.70±0.68	0.74	35.70±1.02	1.79	5.25±0.54	0.51
P ₂	36.66±0.53	2.63	78.85±0.41	1.09	26.30±0.61	1.57	5.19±0.36	0.56
F ₁	50.50±0.66	1.31	87.15±0.53	2.23	38.36±0.36	2.18	5.40±0.28	0.53
F ₂	39.96±0.28	13.73	85.11±0.28	13.38	32.87±0.48	17.25	6.87±0.35	1.91
F ₃	41.78±0.35	12.35	82.99±0.67	5.40	32.48±0.51	40.18	7.65±0.27	0.39
Generations	Secondary branches / plant		Pods per plant		Pod length (cm)		Seeds / pod	
	Mean ± SE	Variance	Mean ± SE	Variance	Mean ± SE	Variance	Mean ± SE	Variance
P ₁	11.40±0.44	0.46	14.15±0.40	2.13	14.15±0.23	2.13	12.90±0.22	1.03
P ₂	12.33±0.42	1.80	12.42±0.59	0.25	12.89±0.13	0.18	11.28±0.31	0.99
F ₁	11.60±0.32	0.25	14.50±0.48	2.18	15.70±0.23	0.53	14.65±0.14	2.63
F ₂	6.87±0.17	5.25	12.08±0.12	4.01	11.59±0.17	5.31	10.20±0.17	5.29
F ₃	8.93±0.24	4.91	12.04±0.25	2.77	12.17±0.26	16.5	8.23±0.42	4.23
Generations	Seed yield per plant (g)		Hundred seed weight(g)					
	Mean ± SE	Variance	Mean ± SE	Variance				
P ₁	18.36±0.21	1.46	10.32±0.04	0.25				
P ₂	21.35±0.11	2.6	11.32±0.25	0.63				
F ₁	20.96±1.84	3.42	11.30±1.36	1.23				
F ₂	17.43±0.36	22.07	10.85±0.15	4.11				
F ₃	18.28±0.14	2.74	11.76±0.24	1.15				

SE-Standard error

2. Days to maturity

CP-12 was early to mature than IT-38956-1 by 14 days but F_1 took 3 days more for maturity compared to IT-38956-1 and took 9 days more than CP-12. F_2 took one day late to mature than IT-38956-1 and took 7 days late to mature than CP-12. F_3 took 2 days early to mature than IT-38956-1 and variance was very high in F_2 compared to F_3 population.

3. Plant height

CP-12 was dwarf (26.30 cm) than IT-38956-1 (35.70 cm), mean height of F_1 (38.36 cm) higher than the height of both the parents. There was decrease in plant height in F_2 and F_3 compared to F_1 and IT-38956-1 which is having the height of 32 cm and very high variance was observed in F_3 than the F_2 population.

4. Primary branches per plant

Both the parents possessing same number of primary branches per plant *i.e.* 5, but the increase in primary branches per plant in F_2 (6.87) and F_3 (7.65) with less variation and variance from F_2 to F_3 .

5. Secondary branches per plant

Both the parents possess more or less same number of secondary branches per plant *i.e.*, IT-38956-1 (11.40) and CP-12 (12.33). There was decrease in variance for secondary branches per plant in F_2 to F_3 compared to non segregating generations but the variance was very high in F_2 population compared to all the population.

6. Number of pods per plant

The number of pods per plant was higher in parent IT-38956-1 (14.15) compared to the other parent CP-12 (12.89). Mean number of pods per plant in F_1 (14.50) is higher than both the parents, the mean of F_2 (11.59) which is lower than both the parents. There is a decrease in variability between parents to offspring's.

7. Number of seeds per pod

The mean seeds per pod of IT-38956-1(12.90) which is highest than the parent CP-12 (11.28), mean of F_1 (14.65) which is highest compared to other generations and to the parents. There was decreased variability for seeds per pod from F_2 (10.20) to F_3 (8.23) population. The variance was very high in F_3 population compared to the F_2 population.

8. Pod length (cm)

Highest pod length was observed in F_2 (15.36 cm) compared to all the population which is highest compared to parents. There was decreased variability for pod length from F_2 (11.59 cm) to F_3 (12.17 cm). The variance was high in F_3 population compared to F_2 population.

9. Seed yield per plant (g)

Among the five populations, the mean seed yield per plant was highest for CP-12 (21.35 g) compared to other generations. The mean seed yield per plant was intermediate between F_1 (20.96 g). There was increase of variability for seed yield per plant from F_2 (17.43 g) to F_3 (18.28 g) population. The variance was high in F_2 population compared to F_3 population.

10. Hundred seed weight (g)

Mean test weight of CP-12 (11.32 g) is higher than IT- 38956 (10.32 g). Mean hundred seed weight of F_1 (11.30 g) falls in between the parents. There was increased variability for test weight from F_2 (10.85 g) to F_3 (11.76 g) but variance was low in all the populations.

4.2.2.3 Means and variances for quantitative characters in cowpea cross KBC-2 × CP-12

Means and variances of quantitative characters in cowpea cross KBC-2 × CP-12 has been tabulated in Table 26 and these are briefly outlined below.

Table 26: Means, standard errors and variances ten quantitative characters in cowpea cross KBC-2 × CP-12

Generations	Days to first flowering		Days to maturity		Plant height (cm)		Primary branches / plant	
	Mean ± SE	Variance	Mean ± SE	Variance	Mean ± SE	Variance	Mean ± SE	Variance
P ₁	44.65±0.45	4.13	83.65±0.62	7.81	41.34±0.16	0.55	4.80±0.26	1.43
P ₂	36.70±0.38	1.17	78.75±0.21	0.96	26.43±0.26	1.17	5.15±1.66	0.79
F ₁	48.00±0.19	0.73	88.40±0.25	1.30	28.77±0.11	2.59	5.5±0.11	2.61
F ₂	44.66±0.28	30.09	75.45±0.33	41.27	33.49±0.47	84.00	5.40±0.08	2.75
F ₃	51.57±0.30	3.62	92.24±0.26	3.19	23.00±0.34	4.12	5.74±0.11	1.46
Generations	Secondary branches / plant		Pods per plant		Pod length (cm)		Seeds / pod	
	Mean ± SE	Variance	Mean ± SE	Variance	Mean ± SE	Variance	Mean ± SE	Variance
P ₁	10.40±0.24	1.20	15.45±0.29	1.73	14.40±0.22	1.01	12.30±0.17	0.64
P ₂	12.30±0.21	0.97	12.40±0.11	0.50	12.86±0.14	0.66	10.70±0.52	2.3
F ₁	13.05±0.22	1.99	15.50±0.11	2.63	15.87±0.10	2.35	14.45±0.12	5.64
F ₂	7.72±0.13	6.54	10.86±0.23	20.85	14.53±0.19	14.25	9.03±0.13	6.69
F ₃	9.21±0.16	1.46	12.60±0.19	2.34	14.87±0.20	2.34	8.77±0.22	2.65
Generations	Seed yield per plant (g)		Hundred seed weight(g)					
	Mean ± SE	Variance	Mean ± SE	Variance				
P ₁	10.40±0.24	1.99	11.84±0.11	0.25				
P ₂	20.82±0.46	1.81	11.32±0.05	2.4				
F ₁	24.70±0.22	1.85	11.34±0.24	3.6				
F ₂	15.85±0.19	14.53	11.29±0.42	6.8				
F ₃	18.77±0.35	4.20	11.80±0.09	1.12				

SE-Standard error

1. Days to first flower

CP-12 was found to be earliest in flower initiation (36 days) by 8 days than KBC-2, F_1 took 48 days where as F_2 took 44 days for flower initiation. Where F_3 took 51 days for flower initiation, variation was also high in F_2 compared to F_3 .

2. Days to maturity

CP-12 found to be mature earlier than the KBC-2 by 5 days, however F_1 took 88 days to maturity which is higher than the both the parents. Mean of F_2 was 75 days which falls between the parents, but F_3 mean was 92 days which is very higher than the all generations. Variance was very high in F_2 (46.27) compared to F_3 (3.19) population.

3. Plant height (cm)

CP-12 was dwarf parent (26.43 cm) than KBC-2 (41.34 cm) with very low variability, mean plant height of F_1 (28.77 cm) which is lower than the KBC-2. There was decrease in plant height from F_2 (33.49 cm) to F_3 (23.00 cm). Very high variance was observed in F_2 population.

4. Primary branches per plant

All the plant populations having the more or less same number of primary branches per plant with very low variability.

5. Secondary branches per plant

The mean of secondary branches per plant for KBC-2 and CP-12 were 10.40 and 12.30 respectively. The F_1 (13.05) was found to be more than the both parents, number of secondary branches in F_2 and F_3 was very less compared to both the parents. Mean number of secondary branches increased in segregating populations from F_2 to F_3 . F_2 displayed higher magnitude of variance among the segregating generations for this trait.

6. Number of pods per plant

Mean number of pods per plant in F_1 (15.50) is higher than the KBC-2 (15.45) and CP-12 (12.40). The mean of F_2 (10.86) was intermediate between the two parents.

There was increase in number of pods per plant in F_2 (10.86) to F_3 (12.60), it shows increase in pods per plant from F_2 to F_3 .

7. Number of seeds per pod

The better parent KBC-2 exhibited higher mean number of seeds per pod compared to CP-12 (10.70), mean of F_1 (15.87) was found to be higher among all populations and also highest than the parents. There was decreased in variability for seeds per pod from F_2 (9.03) to F_3 (8.77) population but the variance was found very high in F_2 population.

8. Pod length (cm)

Pod lengths were found to be equal in F_2 and F_3 populations. Highest pod length was observed in F_1 (15.50cm) and lowest in CP-12 (12.86 cm). Among the segregating population F_2 found to be having higher variance than F_3 .

9. Seed yield per plant (g)

Among the five populations, the mean seed yield per plant was highest for F_1 (24.70 g) compared to other generations. The mean seed yield per plant of F_2 (15.85 g) which is found intermediate between the parents. There was increase of variability for seed yield per plant from F_2 (15.85 g) to F_3 (18.77g) population.

10. Hundred seed weight (g)

The 100 seed weight for all the populations was found to be more or less same with very less variability and variance.

4.2.3 Estimation of gene effects

Joint scaling test of five generation means pertaining to the gene effects due to additive, dominance and epistatic effect such as additive $\times$ additive, dominance $\times$ dominance were estimated for yield and agro morphological characters. The results were furnished in Table 27.

4.2.3.1 Gene effects for ten quantitative characters in cowpea cross IT-38956-1 × KBC-2

The gene effects for quantitative characters in cowpea cross IT-38956-1 × KBC-2 has been tabulated in Table 27 and these are briefly outlined below

1. Days to first flower

It was clear from the Table that additive dominance model was inadequate in explaining the inheritance of days to first flower as indicated by significant chi-square value. Additive, dominance and additive × additive gene interaction were significant but it was in negative direction. The genes controlling this trait were found to be interacting with each other in a duplicate manner.

2. Days to maturity

The magnitude of dominance effect was found to be significant, simple additive dominance model was inadequate to explain the expression of days to maturity. All parameters were significant except additive gene effect while dominance × dominance effects were in negative direction with duplicate gene interaction governing this trait.

3. Plant height (cm)

Additive dominance model was inadequate in explaining the inheritance of plant height showed the non allelic interaction by significant chi-square value. Additive × additive, dominance × dominance were significant but it was in negative direction. The duplicate type of epistasis was present.

4. Primary branches per plant

Because of non significant chi-square test 3 parameters were found to be sufficient to explain all the variations among generation means for primary branches per plant.

Table 27: Gene effects for 10 quantitative characters in three cowpea crosses

Sl. No.	Characters	Crosses	Gene effects					Chi square value	Type of epistasis
			(m)	(d)	(h)	(i)	(l)		
1.	Days to first flowering								
		Cross 1	105.04**	-2.99**	-6.29**	-5.79**	7.09**	11.37*	D
		Cross 2	297.02**	6.80**	-4.01**	6.72**	23.72**	25.12**	D
		Cross 3	172.46**	-0.52	8.89**	8.27**	-12.06**	13.96**	D
2.	Days to maturity								
		Cross 1	125.21**	0.68	6.25**	13.08**	-2.24**	92.75**	D
		Cross 2	417.87**	-1.14	1.68			5.21	
		Cross 3	238.04**	0.37	-17.84**	-6.18**	10.06**	38.93**	D
3.	Plant height (cm)								
		Cross 1	317.22**	-32.64**	7.03**	-4.69**	-8.47**	22.03**	D
		Cross 2	64.84**	-0.65	17.49**	19.19**	16.59**	12.93*	C
		Cross 3	69.19**	-0.12	7.88**	7.18**	-7.82**	29.43**	D
4.	Primary branches per plant								
		Cross 1	20.45**	-3.17**	1.49			2.21	
		Cross 2	65.50**	1.94	5.00**	-1.03	1.55	24.12**	C
		Cross 3	67.58**	-2.30**	-15.20**	-12.13**	13.89**	25.12**	D
5.	Secondary branches per plant								
		Cross 1	86.45**	-1.20	6.99**			3.46	
		Cross 2	98.88**	1.37	16.12**	13.64**	-11.04**	24.12**	D
		Cross 3	122.36**	2.66**	-7.40**	-7.58**	9.44**	35.65**	D
6.	Pods per plant								
		Cross 1	16.45**	0.45	2.33**	3.83**	-4.45**	33.39**	D
		Cross 2	124.56**	3.14**	14.38**			7.67	
		Cross 3	118.00**	-1.14	9.17**			7.03	
7.	Pod length (cm)								
		Cross 1	142.50**	-3.29**	-2.48	5.35**	-4.15**	94.19**	C
		Cross 2	102.53**	18.28**	3.61**	-2.17	-0.69	29.46**	D
		Cross 3	99.60**	2.96**	10.22**			7.67	
8.	Seeds per pod								
		Cross 1	11.13**	4.18**	-3.60**			2.45	
		Cross 2	98.78**	10.42**	18.06**	10.83**	-11.91**	13.64**	D
		Cross 3	78.18**	2.21**	0.32	0.17	1.83	11.37**	C
9.	Hundred seed weight								
		Cross 1	10.96**	-1.03	-12.67**	-12.69**	-10.25**	11.37*	C
		Cross 2	54.39**	5.33**	-0.50	-1.46	-4.17**	15.13**	C
		Cross 3	92.66	-2.5*	-8.61**	-9.83**	11.71**	13.80**	D
10.	Seed yield per plant (g)								
		Cross 1	9.5**	1.23	-0.64	0.45	0.62	75.00**	D
		Cross 2	12.87**	6.68**	0.19	-1.35	4.42**	10.91*	C
		Cross 3	8.59	-2.22**	-1.87	-3.14**	-1.28	13.80**	C

*- Significance at 0.05 probability level, **- Significance at 0.01 probability level

Cross 1 –IT-38956-1 × KBC-2, Cross 2 –IT-38956-1X CP-2, Cross 3 – KBC-2 × CP-12,

D - Duplicate or Dominant epistasis, C- Complementary / Recessive gene interaction

5. Secondary branches per plant

Because of non significant chi-square test 3 parameters were found to be sufficient to explain all the variations among generation means for primary branches per plant.

6. Number of pods per plant

Significance of chi-square test indicated the inadequacy of simple additive-dominance 3 parameter model. All parameter were significant except additive gene effect. The gene controlling this trait was found to interact with each other in a duplicate type of gene interaction.

7. Pod length (cm)

Variation for pod length were not explained adequately by three parameter model. Therefore the model was extended to include additive $\times$ additive (i), dominance $\times$ dominance (j), epistatic effects. Additive, additive $\times$ additive, dominance $\times$ dominance gene interaction was found additive $\times$ additive interaction effect was significant over all the interactions with complementary type of genes controlling the traits.

8. Number of seeds per pod

Non significant chi-square test shows that the 3 parameter model was found to be sufficient in explaining all the variations among the generation's means for number of seeds per pod.

9. Seed yield per plant (g)

Five parameter model was necessary to explain the inheritance of seed yield per plant, where as significant and negative direction was found to be for dominance, additive $\times$ additive, dominance $\times$ dominance and additive was found to be negative and non significant with the duplicate type of gene interaction was present.

10. Hundred seed weight (g)

Additive-dominance was not sufficient to explain the expression of this character. All the effects were found to be non significant duplicate type of gene interaction was found to be governing this trait.

4.2.3.2 Gene effects for 10 quantitative characters in cowpea cross IT-38956-1 × CP-12

Gene effects for quantitative characters in cowpea cross IT-38956-1 × CP-12 has been tabulated in Table 27 and these are briefly outlined below

1. Days to first flower

Significant chi-square test explains the additive dominance model was found to be inadequate in explaining the inheritance of days to first flowering significance. All the five parameters m, d, h, i and l were significant and found to be in negative direction with duplicate gene effect governing this trait for all the genes.

2. Days to maturity

Failure of additive dominance model was evident from the significance of chi-square test indicating the digenic interaction effect was governing this trait. All the parameter was found to be non significant gene effect, duplicate gene effect governing this trait for all the genes.

3. Plant height (cm)

It was clear from the Table that additive dominance model is inadequate in explaining the inheritance of plant height as indicated by the significance of the chi-square value. The trait was governed by the digenic interaction of non additive genes which were negative and non significant. Additive × additive gene interaction was found to be significant with complementary gene action.

4. Primary branches per plant

A simple additive dominance model was inadequate to explain gene effects for primary branches per plant. Only dominance was found to be significant with the complementary type of gene interaction acting on this character.

5. Secondary branches per plant

Significant chi-square indicated three parameter model was found to be insufficient to explain the inheritance of secondary branches per plant. Additive interaction found to be non significant dominance, additive $\times$ additive found to be significant in positive direction were as dominance $\times$ dominance recorded significant effect but negative with duplicate type of gene action.

6. Number of pods per plant

Non significant chi square test will help in the explanation of inheritance of number of pods per plant.

7. Pod length (cm)

Three parameter model did not explain variation for pod length. Therefore the model was extended to include additive $\times$ additive (i), dominance $\times$ dominance (l), epistatic effects. Only Additive-dominance model was found to be significant with duplicate type of gene interactions.

8. Number of seeds per pod

Significant chi-square test indicated the involvement of non allelic interaction. All the parameter were significant but dominance $\times$ dominance in negative direction and duplicate type of gene interaction was controlling this trait.

9. Seed yield per plant (g)

Three parameter model could not explain variation for seed yield per plant. Therefore the model was extended to additive $\times$ additive, dominance $\times$ dominance effects. Only additive effect was found to be positive and significant, dominance $\times$

dominance effect was found significant but in negative direction. Complementary type of gene interaction was found to be controlling this trait.

10. Hundred seed weight (g)

It was clear from the Table that chi square test was significant and three parameter model did not explain the interaction of genes controlling this trait. The additive, dominance $\times$ dominance type of gene action was found to be significant. Complementary type of gene interaction was found to be controlling this trait.

4.2.3.3 Gene effects for ten quantitative characters in cowpea cross KBC-2 $\times$ CP-12

Gene effects for quantitative characters in cowpea cross KBC-2 $\times$ CP-12 has been tabulated in Table 27 and these are briefly outlined below.

1. Days to first flower

Three parameter model could not explain variation for days to first flowering, therefore the model was extended to include additive $\times$ additive, dominance $\times$ dominance and epistatic effects. The dominance, additive $\times$ additive, dominance $\times$ dominance was found to be significant. But dominance $\times$ dominance effect in negative direction with duplicate gene interaction.

2. Days to maturity

It is clear from the significant of chi-square test indicating that the three parameter model insufficient to explain the inheritance of this trait. Only dominance $\times$ dominance gene interaction was found to be significant and positive. The genes controlling this trait found to be interacting with each other in a duplicate type of gene interaction.

3. Plant height

Additive dominance model was inadequate in explaining the inheritance of plant height. All the parameter was found to be significant but dominance $\times$ dominance effect was in negative gene effect and additive effect was found to be non significant. The genes

controlling for this trait was found to be interact with each other in a duplicate type of gene interaction.

4. Primary branches per plant

A significance of chi square test revealed inadequacy of additive dominance model. Further five parameter model was used in explaining the inheritance of this trait. The parameter is found to be significant but additive, dominance, additive $\times$ additive effect was in negative direction with duplicate type of gene interaction.

5. Secondary branches per plant

A three parameter model did not explain the variation for this trait. Therefore the model was extended to include additive $\times$ additive, dominance $\times$ dominance and epistatic effects. All the five parameter was found to be significant and dominance, additive $\times$ additive effect was found to be in negative direction. The genes controlling this trait were found to be interacting with each other in a duplicate manner.

6. Number of pods per plant

Variation among generation means for number of pods per plant was sufficiently explained by five parameter model. Only dominance, additive $\times$ additive effect was found to be significant with complementary type of gene interaction.

7. Pod length (cm)

A simple additive dominance model was inadequate in explaining the pod length. All parameter were significant, while additive $\times$ additive, recorded negative gene effect. The genes controlling this trait were found to be interacting with each other in a complementary type of gene interaction.

8. Number of seeds per pod

Goodness of fit of chi-square test between observed and estimated generation means indicated the inadequacy of additive-dominance model in explaining the

inheritance of this trait. Only additive gene action was found to be significant and all other model are non significant, this trait exhibits complementary type gene interaction.

9. Seed yield per plant (g)

Variation among generation for seed yield per plant was not explained adequately by a three parameter model. A significant negative variation registered for additive, dominance and additive $\times$ additive gene action except dominance $\times$ dominance gene effect. Duplicate type of gene interaction was found to be controlling this trait.

10. Hundred seed weight(g)

Even for hundred seed weight also significance of chi square test indicated the inadequacy of three parameter model. Only additive, additive $\times$ additive was found to be significant but in negative direction. And dominance, dominance $\times$ dominance model was found to be non-significant with complementary type of gene interaction.

4.2.4 Scaling and joint scaling test

The mean and variance of six generations viz., P_1 , P_2 , F_1 , F_2 and F_3 of the three crosses of cowpea (IT- 38956-1 $\times$ KBC-2, IT- 38956-1 $\times$ CP-12 and KBC-2 $\times$ CP-12) in respect of 10 quantitative traits were used for scaling tests as per the method of Mather (1949) and Joint scaling test as per the method of Cavalli (1952) to test the presence or absence of gene interaction in the inheritance of these traits. The significance of A and B scales indicates the presence of all the three type of non-allelic interactions viz., additive $\times$ additive and dominance $\times$ dominance [$\hat{I}$]. The significance of C scale suggests dominance $\times$ dominance [$\hat{I}$] type of interaction. The significance of any one of the scaling tests indicates inadequacy of simple additive dominance model. The results of scaling tests and joint scaling test in respect of ten traits have been tabulated in Table 28 and Table 29, respectively and presented trait wise below.

1. Days to first flowering

The scaling tests ‘C’ and ‘D’ were highly negative and significant, which was further confirmed by high level of significance of chi-square value obtained in Joint

Table 28: Scaling test for ten quantitative characters for the three crosses of cowpea

Sl. No.	Character	Crosses	Scaling tests			
			A	B	C	D
1	Days to first flowering	Cross-1	3.09**±1.41	8.37**±1.54	-16.75**±3.17	-59.50**±1.83
		Cross-2	-71.99**±0.56	-32.1**9±0.60	-7.82**±0.25	-13.62**±0.32
		Cross-3	-14.31**±0.45	-3.58**±1.57	-7.59**±2.83	-47.17**±2.33
2	Days to maturity	Cross-1	2.96**±0.88	2.56**±0.84	-10.58**±2.17	-95.20**±1.82
		Cross-2	-3.36**±0.61	-2.95**±0.48	-4.82**±1.23	-55.60**±1.04
		Cross-3	-14.23**±0.02	-3.86**±0.22	-5.97**±0.26	-24.59**±1.25
3	Plant Height (cm)	Cross-1	19.30**±0.60	38.16**±0.53	-5.30**±1.39	-33.87**±2.34
		Cross-2	-26.68**±0.77	-39.42**±0.50	4.35**±1.70	-8.86**±2.61
		Cross-3	116.94**±1.09	114.04**±1.13	52.23**±4.73	-64.31**±2.90
4	Primary branches per plant	Cross-1	-16.40**±0.24	-13.43**±0.24	3.77**±0.55	-5.55**±0.55
		Cross-2	2.84**±.43	1.04±0.32	0.52±0.68	-13.93**±0.61
		Cross-3	29.51**±1.25	29.27**1.23	15.72**±3.46	-32.94**±1.75
5	Secondary branches per plant	Cross-1	-0.82±0.30	0.48±0.30	-1.73±0.69	-26.67**±0.93
		Cross-2	18.38**±0.39	17.45**±0.37	0.23±0.80	-34.12**±0.90
		Cross-3	-16.93**±0.36	-17.16**±0.35	-7.87**±1.06	-19.63**±0.67
6	Pods/Plant	Cross-1	2.46*±0.47	-0.45±0.46	-2.47*±0.92	-30.99**±0.93
		Cross-2	19.44±0.44	12.95**±0.54	7.17**±0.92	-33.03**±0.86
		Cross-3	3.61**±0.68	4.18**±0.75	-2.98**±1.50	-32.06**±0.88
7	Pod Length (cm)	Cross-1	-2.12*±0.37	1.66±0.27	-3.42**±0.95	-25.97**±1.17
		Cross-2	5.67**±0.23	-11.34**±0.18	-4.95**±0.62	-30.32**±0.73
		Cross-3	-6.14**±0.55	-7.05**±0.54	3.93**±1.21	-18.72**±0.80
8	Seeds/Pod	Cross-1	2.29**±0.32	-1.28±0.30	5.41**±0.94	-25.02**±0.90
		Cross-2	19.86**±0.32	9.93**±0.28	-6.68**±0.70	-31.44**±0.82
		Cross-3	-6.14**±0.55	-7.05±0.54	3.93±1.21	-18.72±0.80
9	Seed yield/Plant (g)	Cross-1	-1.45±0.40	0.06±0.44	-11.22**±1.37	-21.62**±1.64
		Cross-2	-8.57**±0.55	-10.82**±0.56	-8.82**±1.49	24.51**±0.87
		Cross-3	-7.39**±0.77	-5.91**±0.83	-0.57±1.68	-12.71**±1.07
10	Hundred seed weight (g)	Cross-1	-17.65**±0.19	-12.47**±0.20	-2.85**±0.60	-33.72**±0.57
		Cross-2	-7.88**±0.05	50.43**±0.05	7.97**±0.45	-54.77**±0.42
		Cross-3	-1.76±0.82	-1.94**±0.75	-3.30**±1.72	-24.80**±1.03

Cross-I: IT-38956-1 × KBC-2, Cross-II: IT-38956-1 × CP-12 and KBC-2 × CP-12

Table 29: Joint scaling test for 10 quantitative characters for the three crosses of cowpea

Sl. No.	Character	Crosses	Scaling tests			
			M	d	h	Chi square value
1	Days to first flowering	Cross-1	22.67**	-3.94**	6.35**	52.68**
		Cross-2	13.12**	-4.96**	6.45**	12.36**
		Cross-3	98.02**	6.80**	-4.01**	23.46**
2	Days to maturity	Cross-1	18.49**	3.41**	13.79**	53.49**
		Cross-2	12.35**	9.65**	8.62**	35.65**
		Cross-3	17.87**	-1.14	-2.04**	13.45**
3	Plant Height(cm)	Cross-1	31.92**	-34.95**	30.18**	66.58**
		Cross-2	23.45*	-12.41**	35.51**	51.80**
		Cross-3	64.84**	-17.49**	-19.19**	35.67**
4	Primary branches per plant	Cross-1	38.85**	-11.13**	1.82	59.52**
		Cross-2	25.96**	-1.95	-5.72**	26.65**
		Cross-3	65.50**	1.94	5.00**	13.64**
5	Secondary branches per plant	Cross-1	32.62**	6.95**	1.62	26.25**
		Cross-2	12.96**	16.26**	3.85**	12.36**
		Cross-3	98.88**	1.37	16.12**	34.65**
6	Pods/Plant	Cross-1	14.48**	3.88**	3.70**	66.92**
		Cross-2	124.56**	3.14**	14.38**	12.35**
		Cross-3	102.53**	18.28**	3.91**	47.68**
7	Pod Length(cm)	Cross-1	127.54**	0.66	-0.55	94.19**
		Cross-2	9.36**	-16.12**	-4.35**	13.53**
		Cross-3	98.78**	10.42**	18.06**	11.91**
8	Seeds/Pod	Cross-1	12.81**	3.39**	3.23**	66.69**
		Cross-2	46.23**	-18.10**	12.25**	36.25**
		Cross-3	65.23**	0.15	13.74	12.24**
9	Seed yield/Plant(g)	Cross-1	87.34**	-7.34	-12.97	78.85**
		Cross-2	33.45**	-2.33	1.14	40.82**
		Cross-3	44.40**	-1.08	-8.76**	35.64**
10	Hundred seed weight (g)	Cross-1	8.33**	1.94**	1.61**	25.68**
		Cross-2	34.12**	12.12**	-4.16**	2.56
		Cross-3	51.44**	0.02	0.93	13.65**

Cross-I: IT-38956-1 × KBC-2, Cross-II: IT-38956-1 × CP-12 and KBC-2 × CP-12

scaling test. This clearly indicated inadequacy of simple additive-dominance model and presence of digenic or still higher order epistasis in the inheritance of this trait.

2. Days to maturity

The tests 'A' and 'B' were found highly significant and negative indicating inadequacy of additive-dominance model. This was further confirmed by significance of additive and dominance components as well as high level of significance of chi-square value in joint scaling test indicating role of epistasis genetic control of the trait.

3. Plant height (cm)

The 'A' and 'B' tests were highly significant and positive. The additive and dominance components are also found to be significant and chi-square value of joint scaling test was highly significant suggesting failure of simple additive – dominance model to explain the inheritance of this trait suggesting the role of interaction in the inheritance of this trait.

4. Number of primary branches per plant

'A' and 'D' tests were highly significant and positive. However, 'C' tests and chi-square value of joint scaling test were significant at 5 per cent level. The two components in joint scaling test were also significant indicating greater role of gene interaction in the genetic control of this trait. The additive and dominance components are also found to be significant, and chi-square values of joint scaling test were also highly significant, indicating greater role of gene interaction in the genetic control of the trait.

5. Secondary branches per plant

Simple additive-dominance model failed to explain the inheritance of this trait as indicated by the significance of 'D' test, which was further confirmed by the high level of significance of additive components as well as chi-square value in joint scaling test. This strongly suggests major role of gene interaction in the inheritance of this trait.

6. Pods per plant (g)

‘A’ and ‘C’ tests are significant at one percent level and ‘D’ test significant at five percent level indicating inadequacy of additive dominance model which was further confirmed by high level of significance of chi-square value suggesting the presence of gene interaction in the genetic control of this trait.

7. Pod length (cm)

‘A’, ‘C’ and ‘D’ tests were significant and negative. While, additive and dominance components as well as Chi-square values were highly significant indicating inadequacy of simple additive-dominance model and presence of gene interaction in the genetic control of this trait.

8. Seeds per pod

‘A’ and ‘C’ tests significant ‘D’ test is negative. The additive dominance components and chi-square value of joint scaling test were also highly significant suggesting failure of additive-dominance model to explain the inheritance of trait and presence of epistasis in the genetic control of this trait.

9. Seed yield per plant (g)

‘C’ and ‘D’ tests were significant and negative. The additive-dominance components as well as chi-square value of joint scaling tests were also highly significant, which clearly indicated major role of gene interaction in the inheritance of this trait.

10. Hundred seed weight (g)

All the four tests were significant and negative. The additive-dominance components as well as chi-square value of joint scaling tests were also highly significant, which clearly indicated major role of gene interaction in the inheritance of this trait.

The same trend will also fit for Cross-II and Cross-III as that of Cross-I.

4.2.5 Number of effective factors

Minimum number of effective factors influencing a trait in F₂ population of three cowpea crosses in respect of 10 quantitative characters was estimated and results of the same are tabulated in Table 30 and briefly outlined below.

4.2.5.1 Number of effective factors in F₂ population of cowpea cross IT- 38956-1 × KBC-2

The traits viz., days to maturity(1.00), plant height(0.58), number of primary branches per plant (0.05), number of secondary branches per plant (0.06), pods per plant (1.02), pod length (0.16), seeds per pod (0.18), hundred seed weight (0.02) were controlled by one group of effective factors. On the other hand, days to first flowering (2.25) were controlled by two groups of effective factors. While, seed yield per plant (4.12) appear to be controlled by a mean of five pair of effective factors.

4.2.5.2 Number of effective factors in F₂ population of cowpea cross IT- 38956-1 × CP-12

At least one group of effective factors appear to control the inheritance of days to flowering (1.40), plant height (1.20), Days to maturity (0.05), number of primary branches per plant (1.0), number of secondary branches per plant (1.00), and hundred seed weight(1.44) appear to be controlled by one number of factor. Whereas, pods per plant (3.12), pod length (3.46) and seeds per pod (3.77) appear to be under the control of two effective factors. Contrary to this, four groups of genes for seed yield per plant (4.45) appear to be present in the genetic control of the respective traits.

4.2.5.3 Number of effective factors in F₂ population of cowpea cross KBC-2 × CP-12

At least one group of effective factors appear to control the inheritance of days to first flowering (0.02), plant height (1.29), days to maturity (1.29), number of primary branches per plant (1.10), pods per plant (0.36)and hundred seed weight (0.21) appear to be controlled by one number of factor. Whereas, secondary branches per plant (2.23), pod length (2.35) and seeds per pod (3.77), appear to be under the control of two effective

Table 30: Number of effective factors in the genetic control of ten quantitative characters in F₂ generation of three cowpea crosses

Sl. No.	Character	Number of effective factors (N) in		
		IT-38956-1 × KBC-2	IT-38956-1 × CP-12	KBC-2 × CP-12
1	Days to first flowering	2.25	1.40	0.02
2	Days to maturity	1.00	0.05	1.29
3	Plant height(cm)	0.58	1.20	0.01
4	Primary branches per plant	0.05	1.00	1.10
5	Secondary branches per plant	0.06	1.00	2.23
6	Pods per plant	1.02	3.12	0.36
7	Pod length(cm)	0.16	3.46	2.47
8	Seeds per pod	0.18	3.77	2.35
9	Seed yield per plant(g)	4.12	4.45	5.81
10	Hundred seed weight (g)	0.02	1.44	0.21

factors. Contrary to this, five groups of genes for seed yield per plant (5.81) appear to be present in the genetic control of the respective traits.

4.2.6 Potence ratio

The degree of dominance in respect of different traits computed from generation means of F_1 as well as F_2 generation in terms of potence ratio for two crosses of cowpea have been tabulated in Table 31 and briefly presented below.

4.2.6.1 Potence ratio in cowpea cross IT- 38956-1 $\times$ KBC-2

In F_1 generation, the degree of dominance in terms of potence ratio (h_1) was between zero and unity for the traits such plant height (0.18) indicating either no dominance or partial dominance in the genetic control of the traits. However, overdominance for the traits viz., days to maturity (6.11), seeds per pod (3.0) and seed yield per plant (1.81) was indicated. Since, the value of potence ratio was more than one for these traits. The characters viz., days to first flowering (-2.74), primary branches per plant (-3.42), secondary branches per plant (-5.50), pods per plant (-1.5), pod length (-0.04) and hundred seed weight (-0.93) were under partial dominance as their h_2 values were less than unity.

In F_2 generation, the potence ratio (h_2) was more than unity for characters viz., days to maturity (5.08) and pods per plant (4.74) indicated presence of overdominance. The characters viz., days to first flowering (-8.95), plant height (-0.65), primary branches per plant (-0.41), secondary branches per plant (-8.50), pod length (-2.16) and hundred seed weight (-2.88) were under partial dominance as their h_2 values were less than unity. The ratio was between zero and unity for remaining trait pods per plant (0.13) indicating no dominance or partial dominance in the genetic control of these traits.

4.2.6.2 Potence ratio in cowpea cross IT- 38956-1 $\times$ CP-12

Potence ration in F_1 generation (h_1) was more than unity indicating overdominance for the traits viz., days to first flowering (1.36), primary branches per plant (4.77), secondary branches per plant (2.50), pods per plant (2.25), pod length (1.79),

Table 31: Potence ratio for ten quantitative characters in F₁ and F₂ generations of three crosses of cowpea

Sl. No.	Character	Potence ratio in					
		IT-38956-1 × KBC-2		IT-38956-1 × CP-12		KBC-2 × CP-12	
		h ₁	h ₂	h ₁	h ₂	h ₁	h ₂
1	Days to first flowering	-2.74	-8.95	1.36	3.12	2.87	-4.07
2	Days to maturity	6.11	5.08	-4.84	4.04	-5.11	-8.16
3	Plant Height(cm)	0.18	-0.65	-4.46	8.92	3.45	8.26
4	Primary branches per plant	-3.42	-0.41	4.77	4.37	-4.04	1.05
5	Secondary branches per plant	-5.50	-8.50	2.50	2.18	5.00	6.20
6	Pods/Plant	-1.50	0.13	2.25	-1.90	-1.28	7.67
7	Pod Length(cm)	-0.04	-2.66	1.79	2.69	-2.75	4.71
8	Seeds/Pod	3.04	4.74	1.88	3.15	3.75	8.24
9	Seed yield/Plant(gm)	1.81	-2.16	1.20	0.82	-1.12	-2.23
10	Test Weight(gm)	-0.93	-2.88	-0.30	0.77	8.13	4.04

h₁ = Potence ratio in F₁ and h₂ = Potence ratio in F₂

seeds per pod (1.20) and seed yield per plant (1.20). The characters viz., days to maturity (-4.84), plant height (-4.46) and hundred seed weight (-0.30) were under partial dominance as their h_2 values were less than unity. The degree of dominance in terms of potence ratio (h_1) was between zero and unity for hundred seed weight indicating either no dominance or partial dominance in the genetic control of the traits.

The potence ratio in F_2 generation (h_2) was less than unity indicating partial dominance for the traits viz., pods per plant (-1.90), seed yield per plant (0.82) and hundred seed weight (0.77). While, the characters days to first flowering (3.12), days to maturity (4.04), plant height (8.92), primary braches per plant (4.37), secondary branches per plant (2.18), pod length (2.69) and pods per plant (3.15) traits were having more than unity indicating over dominance.

4.2.6.3 Potence ratio in cowpea cross KBC-2 × CP-12

Potence ratio in F_1 generation (h_1) was more than unity indicating over dominance for the traits viz., days to first flowering (2.87), plant height (3.45), and number of secondary branches per plant (5.0). While ratios are unity indicating partial dominance for the traits viz., primary branches per plant (-4.04), pods per plant (-1.28), pod length (-2.75) and seed yield per plant (-1.12) characters viz., days to maturity (-5.11) plant height (-4.46) and hundred seed weight (-0.30).

The potence ratio in F_2 generation (h_2) was less than unity indicating partial dominance for the traits viz., days to flowering (-4.07), days to maturity (-8.16) and seed yield per plant (-2.23). While, the characters days to first plant height (8.26), primary braches per plant (1.05), secondary branches per plant (6.20), pods per plant (7.67), pod length (4.71), pods per plant (8.24) and hundred seed weight (4.04) traits were having more than unity indicating over dominance.

4.3 Estimating the relationship between physiological parameters with the seed yield of cowpea

4.3.1 Descriptive statistics in F₃ generation of cowpea cross IT- 38956-1 × KBC-2

The descriptive statistics in F₃ population of cowpea has been tabulated in Table 32 and briefly outlined below.

1. Days to first flowering

Days to first flowering varied from 40 to 52 days with a mean of 45 days and variance of 12.02 days.

Platykurtic ($K=-1.01$) and positively skewed distribution ($S=0.20$) is an evidence of involvement of overall large number of genes with dominance and dominance based complementary interaction in the inheritance of days to first flowering.

2. Days to maturity

Days to maturity ranged from 78 to 86 days with a mean value of 82.32 and variance of 7.32 days.

Platykurtic ($K=-1.26$) and negatively skewed ($S=-0.18$) distribution indicated the involvement of large number of dominant genes having increasing effects and duplicate type of interaction in the inheritance of days to maturity.

3. Plant Height (cm)

Plant height varied from 15.20 to 30.60 cm with a mean value of 22.85 cm and variance of 23.44 cm indicating high variability for the trait.

The Platykurtic ($K=-1.28$) and positively skewed distribution ($S=0.95$) suggested involvement of relatively larger number of genes with majority of them having decreasing effects and dominance based complementary type of interaction in the inheritance of plant height.

Table 32: Descriptive statistics for twelve quantitative characters in F₃ generation of the cross IT-38956-1 × KBC-2 in Cowpea

Sl. No.	Character	Mean	Range		Variance	Skewness	Kurtosis	Kurtosis type
			Minimum	Maximum				
1	Days to first flowering	45.72	40.0	52.0	12.02	0.20	-1.01	P
2	Days to maturity	82.32	78.0	86.0	7.32	-0.18	-1.26	P
3	Plant height(cm)	22.85	15.20	30.60	23.44	0.95	-1.2	P
4	Primary branches	5.5	4.0	7.0	1.25	-0.15	1.30	P
5	Secondary branches	11.97	8.0	15.0	5.3	-0.19	1.0	P
6	Pods per plant	14.25	12.0	16.0	1.67	0.02	1.26	P
7	Pod length(cm)	15.28	12.10	18.90	3.5	0.15	0.172	P
8	Seeds per pod	15.92	8.0	18.0	9.59	1.96	0.94	P
9	SLA (cm ² /g)	174.84	103.85	423.47	130.27	0.83	1.23	P
10	SCMR	37.50	24.26	45.62	31.26	1.28	1.42	P
11	Seed yield per plant(g)	19.80	12.15	26.35	16.20	1.71	0.94	P
12	Hundred seed weight(g)	11.75	10.12	13.35	1.22	0.43	-1.33	P

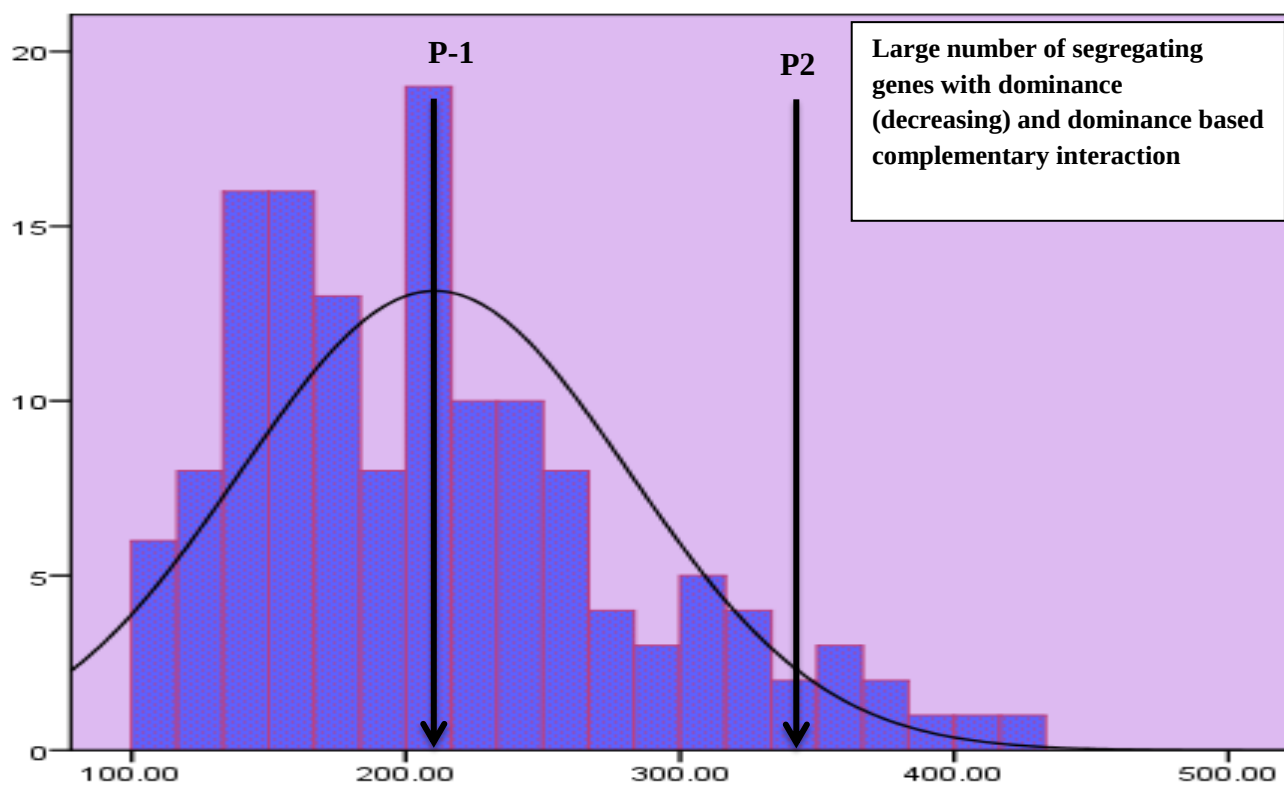


Figure 31: Platykurtic and positively skewed distribution of F_3 of IT-38956-1 $\times$ KBC-2 for SLA (cm^2/g)

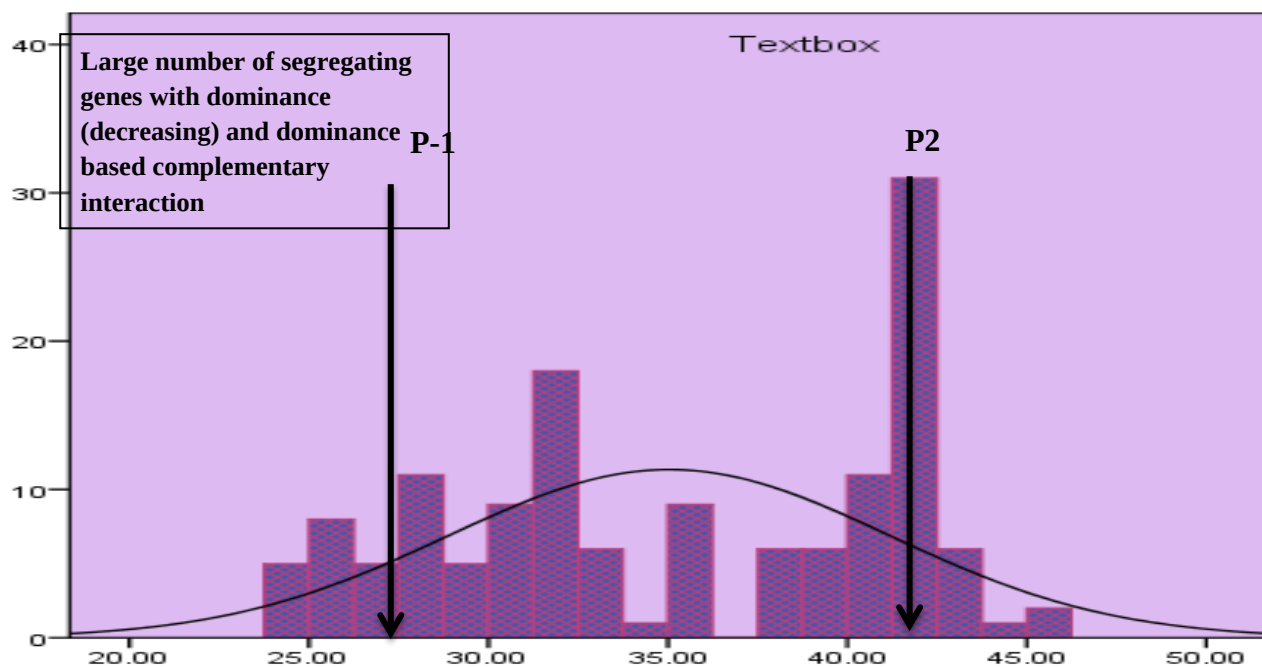


Figure 32: Platykurtic and positively skewed distribution of F_3 of IT-38956-1 $\times$ KBC-2 for SCMR

4. Number of primary branches/plant

Primary braches per plant ranged between 4.0 to 7.0 with a mean value of 5.50 and variance of 1.25.

Negatively skewed ($S=-0.15$) platykurtic ($K=1.30$) distribution is an evidence for involvement of a large number of dominant genes with majority of them having increasing effects and duplicate type of epistasis in the inheritance of pods per plant.

5. Number of secondary branches per plant

Secondary branches varied between 8.0 to 15.0 per plant with a mean value of 11.97 and variance of 5.3.

Negatively skewed ($S=-0.19$) and platykurtic ($K=1.00$) distribution is an evidence for involvement of a large number of dominant genes with majority of them having increasing effects and duplicate type of epistasis in the inheritance of pods per plant.

6. Pods per plant

Pods per plant ranged from 12.0 to 16.0 with a mean value of 14.25 and variance of 1.67.

The expression of the trait appears to be controlled by larger number of genes having decreasing effects and involvement of dominance based complementary interaction as evidenced by platykurtic ($K=1.26$) and positively skewed ($S=0.02$) distribution.

7. Pod length (cm)

Pod length varied between 12.10 to 18.90 cm per plant with a mean value of 15.28 cm and variance of 3.5 cm.

The expression of the trait appears to be controlled by larger number of genes having decreasing effects and involvement of dominance based complementary interaction as evidenced by platykurtic ($K=0.172$) and positively skewed ($S=0.15$) distribution.

8. Seeds per pod

The seeds per pod varied between 8 to 18 with a mean value of 15.92 and variance of 1.96.

Platykurtic ($K=0.94$) and positively skewed ($S=1.96$) distribution indicated involvement of relatively larger number of genes with decreasing effects and dominance based complementary type of interaction in the inheritance of seeds per pod.

9. Specific Leaf Area (cm^2/g)

The SLA varied between 103.85 to 423.47 cm^2/g per plant with a mean value of 174.84 cm^2/g and variance of 130.27 cm^2/g .

The involvement of large number of dominant genes having decreasing effects and dominance based complementary interaction in the inheritance of SLA as evidenced by platykurtic ($K=1.23$) and positively skewed ($S=0.83$) distribution (Fig. 31).

10. SPAD chlorophyll meter reading (SCMR)

SCMR varied between 24.26 to 45.62 per plant with a variance of 31.26 and mean of 37.50.

The involvement of large number of dominant genes having decreasing effects and dominance based complementary interaction in the inheritance of SCMR as evidenced by platykurtic ($K=1.42$) and positively skewed ($S=1.28$) distribution (Fig. 32).

11. Seed Yield per plant (g)

Seed yield per plant varied between 12.15 to 26.35 g per plant with a mean value of 19.80 g and variance of 16.20 g.

The involvement of large number of dominant genes having decreasing effects and dominance based complementary interaction in the inheritance of seed yield as evidenced by platykurtic ($K=0.946$) positively skewed ($S=1.71$) distribution.

12. Hundred seed weight (g)

Hundred seed weight ranged from 10.12 to 13.35 g with a mean value of 11.75 g and variance of 1.22 g.

The involvement of large number of dominant genes having decreasing effects and dominance based duplicate interaction in the inheritance of hundred seed weight as evidenced by platykurtic ($K=-1.33$) and positively skewed ($S=0.43$) distribution.

4.3.2 Genetic variability parameters in F_3 generation

Genetic variability parameters viz., phenotypic co-efficient of variation (PCV), genotypic co-efficient variation (GCV), broad sense heritability (h^2) and genetic advance as per cent of population mean (GAM) in respect of seed yield and its attributing characters in cowpea cross IT-38956-1 $\times$ KBC-2 are tabulated in Table 33 and briefly outlined below.

The PCV values were relatively higher than GCV values in respect of all the traits. However the difference between PCV and GCV values were low in respect of all the traits indicating the less environmental influence on all the characters and moderate influence on the traits.

1. Days to first flowering

The PCV (5.08 %) and GCV (2.45 %) values were low for days to first flowering, while moderate heritability (22.9 %) and low genetic advance as per cent of mean (2.96 %) indicating the major role of non additive gene action in respect of this trait.

2. Days to maturity

The PCV (14.11 %) and GCV (7.11 %) values were low to moderate for days to maturity with moderate (20.27 %) heritability and low genetic advance as per cent of mean (2.96 %) revealing non additive gene action in the control of this trait.

Table 33: Genetic variability parameters for physiological traits associated with seed yield and yield attributing traits in F₃ generation of IT-38956-1 × KBC-2 in cowpea

Genetic parameters	Days to first flowering	Days to maturity	Plant height (cm)	Primary branches/plant	Secondary branches/plant	Pods per plant
Mean	45.79	81.59	22.85	5.54	11.97	13.98
PCV (%)	5.08	2.30	14.11	15.67	24.43	27.14
GCV (%)	2.45	1.03	7.11	6.45	16.45	22.98
Heritability (%)	22.9	20.27	26.43	20.01	30.01	36.78
GA as % Mean	16.39	2.96	7.39	5.94	20.35	42.56

Genetic parameters	Pod length (cm)	Seeds per pod	SLA (cm²/g)	SCMR	Seed yield per plant (g)	Hundred seed weight (g)
Mean	15.28	12.92	74.84	37.50	19.82	11.75
PCV (%)	37.85	37.67	53.78	36.96	14.56	6.96
GCV (%)	25.38	28.57	51.69	29.59	2.95	3.47
Heritability (%)	46.89	33.57	42.65	34.95	14.11	7.89
GA as % Mean	27.59	48.58	60.25	55.26	31.23	3.57

3. Plant height (cm)

Moderate values of PCV (2.30 %) and GCV (1.03 %) were registered for the plant height. However, moderate heritability (26.45 %) and low genetic advance as per cent of mean (7.39 %) indicated the major role of non additive gene action in control of this trait.

4. Primary branches per plant

Primary braches per plant registered the moderate value of PCV (15.67 %) and low value of GCV (6.45 %). While, high moderate (20.01 %) and low genetic advance as per cent of mean (5.94 %) revealing the traits are under the control of non additive gene action.

5. Secondary braches per plant

The PCV (24.43 %) and GCV (16.45 %) value were moderate for secondary braches per plant. However, estimate of broad sense high heritability (30.01 %) and moderated genetic advance as per cent of mean (20.35 %) revealing the additive gene action controlling this trait.

6. Pods per plant

PCV and GCV registered higher values (27.14 % and 22.98 % respectively) for pods per plant. However, estimate of broad sense heritability was high (36.78 %) and genetic advance as per cent of mean (42.56 %) revealing the additive gene action in the control if this trait.

7. Pod length (cm)

PCV and GCV registered higher values (37.85 and 25.38 % respectively) for pods per plant. However, estimate of high broad sense heritability (46.89 %) coupled with high genetic advance as per cent of mean (27.59 %) revealed the additive gene action in the control if this trait.

8. Seeds per pod

PCV and GCV registered higher values (37.67 % and 28.57 % respectively) for pods per plant. However, estimate of broad sense heritability was high (33.57 %) with high genetic advance as per cent of mean (48.58 %) revealing the additive gene action in the control of this trait.

9. Specific leaf area (cm²/g)

PCV and GCV registered higher values (53.78 % and 51.69 % respectively) for pods per plant. However, estimate of broad sense heritability was high (42.65 %) and genetic advance as per cent of mean (60.25 %) revealing the additive gene action in the control of this trait.

10. SCMR

PCV and GCV registered higher values (36.96 % and 29.59 % respectively) for pods per plant. However, estimate of broad sense heritability was high (34.95 %) and high genetic advance as per cent of mean (55.26 %) revealing the additive gene action in the control of this trait.

11. Seed yield per plant (g)

Seed yield per plant registered moderate values for PCV (14.56 %) and GCV (2.95 %) coupled with low heritability (2.95 %) and genetic advance (14.11 %) indicated the predominance of non additive gene action in control on seed yield per plant.

12. Hundred Seed weight (g)

PCV (6.96 %) and GCV (3.47 %) recorded low values. However, low heritability (7.89 %) and genetic advance as per cent of mean (3.57 %) indicating the major role of non additive gene action in the control of this trait.

4.3.3 Correlation in F₃ generation of cowpea cross IT- 38956 × KBC-2

The correlation studies for the cross IT-38956-1 × KBC-2 in F₃ population are tabulated in Table 34 and briefly outlined below.

Table 34: Correlation coefficient seed yield per plant and yield attributing characters in F₃ population of the cross IT-38956-1 × KBC-2

	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂
X ₁	1.000	0.245*	0.118	-0.017	-0.101	0.234*	-0.127	-0.148	0.189	0.163	-0.101	0.326**
X ₂		1.000	0.342**	0.224*	0.139	-0.145	0.026	0.088	0.216	0.278*	0.136	0.387**
X ₃			1.000	-0.020	0.411**	0.219*	0.386*	0.243*	0.467**	0.317**	0.011	0.220**
X ₄				1.000	-0.201	0.256*	0.411**	0.246*	0.649**	0.257*	0.081	0.617**
X ₅					1.000	0.152*	0.105	0.295**	0.274*	0.196	-0.003	0.763**
X ₆						1.000	0.043	0.678**	0.416**	0.478**	0.200	0.737**
X ₇							1.000	0.727**	0.376**	0.756**	0.206	0.427**
X ₈								1.000	0.247*	0.374**	0.257	0.443**
X ₉									1.000	0.236**	-0.099	-0.269**
X ₁₀										1.000	0.139	0.164*
X ₁₁											1.000	0.398**
X ₁₂												1.000

* Significant at P = 0.05 , **Significant at P = 0.01

X₁: Days to first flowering

X₂: Days to maturity

X₃: Plant height (cm)

X₄: Primary branches per plant

X₅: Secondary branches per plant

X₆: Pods per plant

X₇: Pod length (cm)

X₈: Seeds per pod

X₉: Specific Leaf Area(cm²/g)

X₁₀: SCMR

X₁₁: Hundred seed weight (g)

X₁₂: Yield per plant (g)

4.3.3.1 Association between seed yield per plant with its component characters

Seed yield per plant was significantly and positively correlated with seeds per plant (0.544) followed by SCMR (0.415), pods per plant (0.388), primary branches per plant (0.250) and plant height (0.247). The SLA has been significant and negative (-0.269).

4.3.3.2 Association among seed per plant and attributing characters

Among the seed yield per plant and yield attributing characters, positive and significant association was observed for days to first flowering with plant height (0.342), SCMR (0.278) and primary branches per plant (0.224); primary branches per plant with SLA (0.649), SCMR (0.257), pod length (0.411), pods per plant and seeds per pod (0.246); pods per plant with seeds per pod (0.678), SCMR (0.478), SLA (0.416) and hundred seed weight (0.200); pod length with SCMR (0.756), seeds per pod (0.727), SLA (0.376) and hundred seed weight (0.206); seeds per pod with SCMR (0.374), SLA (0.247) and hundred seed weight (0.257); SLA with hundred seed weight (0.519) and SCMR (0.496); SCMR showed non-significant association with hundred seed weight (0.206).

4.3.4 Path analysis in F₃ generation

The direct and indirect effect on seed yield and attributing characters were tabulated in Table 35 and are briefly outlined below.

4.3.4.1 Association of physiological traits on seed yield of cowpea

1. Effect of SLA on seed yield

The direct effect of this trait was low and negative (-0.1045) on seed yield per plant. However, the positive indirect effect of this trait on the seed yield through traits such as., primary braches per plant (0.3047) and SCMAR (0.1154). The plant height (-0.5281) pods per plant (-0.2059) and pod length (-0.2059) is having high negative direct effect on seed yield and all other traits having the negligible indirect effect on the seed yield.

Table 35: Path analysis indicating direct and indirect effects of component characters on seed yield/plant in F₃ generation of cowpea cross IT-38956-1 × KBC-2

Character	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	'r' with Seed yield per plant
X ₁	-0.0604	0.1008	0.4085	-0.1015	-0.2001	-0.2826	0.1003	0.0561	0.1025	0.1024	0.1001	0.326**
X ₂	-0.033	0.1465	0.7536	-0.0016	-0.2988	-0.6146	0.2999	0.0718	0.0729	0.0024	-0.0121	0.387**
X ₃	-0.0326	0.1461	0.1559	-0.0017	-0.297	-0.6191	0.4007	0.0721	0.2017	0.2059	-0.012	0.220**
X ₄	0.0016	-0.0067	-0.0371	0.0353	-0.1185	0.1525	0.3456	0.0783	0.0527	0.1139	-0.001	0.617**
X ₅	-0.0203	0.0735	0.3771	0.2007	-0.5955	0.1196	0.1443	0.0662	0.2017	0.2145	-0.0188	0.763**
X ₆	-0.0214	0.1128	0.2862	-0.2068	0.0892	0.2983	0.1938	0.0341	0.0381	0.0156	-0.1025	0.737**
X ₇	-0.0227	0.0726	0.1755	0.0151	-0.2542	-0.1918	0.3066	0.1231	0.1029	0.1089	-0.0092	0.427**
X ₈	0.0204	-0.1024	0.2047	-0.2428	0.1049	0.1127	0.0247	0.1419	0.0799	0.3412	0.1026	0.443**
X ₉	0.0324	0.2047	-0.5281	0.3047	0.0089	-0.2059	-0.2029	0.0012	-0.1045	0.1154	0.1048	-0.269**
X ₁₀	-0.0239	0.0742	0.1838	0.0195	-0.2779	-0.1916	0.1998	0.0246	0.0347	0.2015	-0.0065	0.164*
X ₁₁	0.0001	0.0302	0.1545	0.0006	-0.1901	0.0006	0.1267	0.0156	0.0171	0.3014	-0.0588	0.398**

Residual effect= 0.05

* Significant at P = 0.05

**Significant at P = 0.01

X₁: Days to first flowering

X₅: Secondary branches per plant

X₉: Specific Leaf Area(cm²/g)

X₂: Days to maturity

X₆: Pods per plant

X₁₀: SCMR

X₃: Plant height (cm)

X₇: Pod length (cm)

X₁₁: Hundred seed weight (g)

X₄: Primary branches per plant

X₈: Seeds per pod

X₁₂: Seed yield per plant (g)

2. SCMR on seed yield

The direct effect of this trait on the seed yield was positive and medium (0.2015). However, the positive indirect effect of these traits on seed yield through traits such as., pods length (0.1998) and plant height (0.1838) moderate effect on seed yield and SLA (0.0347) associated with negligible effect on seed yield; secondary branches per plant (-0.2779), pods per plant (-0.1916) and days to first flowering (-0.1916) had negative indirect effect on the seed yield.

4.4 Transgressive segregants for seed yield per plant.

The present investigation lead to the identification of superior promising individual plants in segregating generations of two crosses in cowpea (IT-38956-1 × KBC-2 and IT-38956-1 × CP-12) But in cowpea cross KBC-2 × CP-12 minimum number segregants were observed. The selection of segregants (surpassing the greater parent) was made based on the seed yield in three crosses the top twenty five transgressive segregants were tabulated in the Table 36.

Table 36: Transgressive segregants identified surpassing the better parent identified for seed yield per plant in three crosses of cowpea

IT-38956-1 × KBC-2		IT-38956-1 × CP-12		KBC-2 × CP-12	
Parents	Seed yield	Parents	Seed yield	Parents	Seed yield
IT-38956-1	19.61 g/plant	IT-38956-1	18.26 g/plant	KBC-2	21.20
KBC-2	21.23 g/plant	CP-12	20.96 g/plant	CP-12	19.25
F ₂ Plant no	Seed yield	F ₂ Plant no	Seed yield	F ₂ Plant no	Seed yield
7	27.80	102	25.30	174	20.79
17	27.24	113	24.98	167	20.33
32	26.86	109	24.93	102	20.29
38	26.69	61	24.92	127	20.28
129	26.46	166	24.88	2	20.23
21	26.37	57	24.84	31	20.15
39	26.24	93	24.76	57	19.84
35	25.85	70	24.48	48	19.80
110	25.31	127	24.43	75	19.78
140	25.24	125	24.36	49	19.75
50	25.22	112	24.31	158	19.75
107	24.87	115	24.30	6	19.74
124	24.81	52	24.10	117	19.74
93	24.74	148	24.07	36	19.73
36	24.74	101	23.97	92	19.69
66	24.72	37	23.90	65	19.34
33	24.48	39	23.90	171	19.32
71	24.30	155	23.80	67	19.30
1	24.29	28	23.79	137	19.28
118	24.24	11	23.75	106	19.25
117	23.85	30	23.74	33	19.25
8	23.80	71	23.73	74	19.25
112	23.80	90	23.65	177	19.21
97	23.76	133	23.65	153	19.13
80	23.33	67	23.41	1	19.13



Discussion

V DISCUSSION

Cowpea is one of the important pulse crop grown for its protein rich seed, fodder and green manure value. Though it is drought tolerant crop the productivity levels of the crop is low. There is every need to develop agronomically superior variety with higher seed yield and drought tolerant.

Being a self-pollinated crop, genetic improvement in cowpea has been made through conventional techniques such as selection from local materials, pedigree method of breeding etc. (Patel *et al.*, 2009).

Limited studies have been reported in the selection of cowpea varieties on the basis of their tolerance to water stress. The first strategy is to screen cowpea varieties according to water use efficiency which was based on the assessment of shoot dry matter and leaf area under well watered and drought treatments in field conditions. These studies allow identifying cowpea varieties showing tolerance to water stress.

Keeping all these in view, the present study was designed to study the physiological association to yield and yield attributing characters are studied in cowpea cross IT-38956-1 $\times$ KBC-2 in F_3 population and also to study the genetic variability parameters such as heritability, genetic advance, association studies and gene action for the yield and yield attributing characters in the cowpea cross IT-38956-1 $\times$ KBC-2, IT-38956-1 $\times$ CP-12 and KBC-2 $\times$ CP-12 in F_2 population. These experiments were taken in the Dry Land Agriculture Project (DLAP), UAS, Bangalore, GKVK. The results obtained in the present investigation and conclusion drawn thereof has been discussed under following headings.

5.1 Justification for the materials and methods used in the study

5.1.1 Experiment material

In the present study three diverse parents were used to produce three crosses cross IT-38956-1 $\times$ KBC-2, IT-38956-1 $\times$ CP-12 and KBC-2 $\times$ CP-12. The parents selected for the crosses provided contrasting phenotypes for several quantitative characters. The

primary objective of the investigation was to study the association between physiological traits with the seed yield and its yield attributing characters in cowpea cross IT-38956-1 × KBC-2 and also to study the heterosis, inbreeding depression, genetic variability parameters and extent of gene action involved in cowpea for the yield and its attributing characters in three crosses. As such a study requires the two parents, their F_1 , F_2 and F_3 in each cross, the same material was utilized to estimate the gene effects for yield and quantitative characters in three crosses.

The two separate experiments were taken up at Dry Land Agriculture Project, GKVK, UAS, Bangalore. The results obtained in the present investigation and conclusion drawn thereof has been discussed under following headings.

5.2 Genetic variability parameters in three crosses of cowpea

5.2.1 Descriptive statistics

The study of descriptive statistics like mean, range and variance gives basic idea of the breeding material. The characteristics of the two F_2 populations in respect of various quantitative characters as indicated by these first and second degree statistics are discussed below.

Wide range of variability was present for the traits viz., days to first flower, days to maturity, plant height, seeds per pod and seed yield per plant studied as indicated by their respective mean and variances. Existence of low variability was observed for secondary branches per plant, pods per plant, pod length and hundred seed weight in all the three crosses.

The study of distribution properties such as co-efficients of skewness (third degree statistic) and kurtosis (fourth degree statistic) provides insight about the nature of gene action (Fisher, 1932) and number of genes controlling the traits (Robson, 1956), respectively. All the reported nature of genetic control of quantitative traits in cowpea based on the first degree (gene effects through generation mean analysis) and second degree (components of genetic variances through diallel, line × tester analysis, etc.) statistics. Skewness and kurtosis are more powerful than first and second degree statistics

which reveal interaction genetic effects (Choo and Reinbergs, 1982). The skewed distribution of a trait in general suggests that the trait is under the control of non-additive gene action, especially epistasis and influenced by environmental variables (Pooni *et al.*, 1977; Kimberg and Bingham, 1998; Roy, 2000). While, positive skewness is associated with complementary interaction and negative skewness is associated with duplicate (additive $\times$ additive) gene interactions predominantly in the same directions. Complete ambi-directional epistasis however produces kurtosis while distribution stays symmetrical around mean (Pooni *et al.*, 1977).

The genes controlling the trait with skewed distribution tend to be predominantly dominant irrespective of whether they have increasing or decreasing effects on the expression of trait. In general, the distribution pattern of F₂ populations of three crosses suggested that dominance and dominance based epistasis is the major cause for significant variation and abnormal distribution of majority of the traits investigated in the present study.

The traits with leptokurtic and platykurtic distribution are controlled by fewer and a large number of genes, respectively. Kurtosis is negative or close to zero in the absence of gene interactions and is positive in the presence of gene interactions (Pooni *et al.*, 1977; Choo and Reinbergs, 1982). The inferences on the relative number of genes and nature of genetic control of different traits in F₂ generation of three cowpea crosses are discussed below.

Platykurtic and positively skewed distribution suggested the involvement of relatively large number of segregating genes with majority of them having decreasing effects and dominance based complementary type of interaction in the inheritance of days to first flowering, plant height, primary branches per plant, secondary branches per plant, pod length, seeds per pod, seed yield per plant and test weight in IT-38956-1 $\times$ CP-12 cross and for days to first flowering, days to maturity, plant height, primary branches per plant, secondary branches per plant, pod length and seeds per pod in case of IT-38956-1 $\times$ CP-12 cross and for days to maturity, plant height, primary branches per plant, secondary branches per plant, pod length, seeds per pod and seed yield per plant in case

of KBC-2 $\times$ CP-12. Maximizing the genetic gain in respect of the traits with positively skewed distribution requires intense selection from the existing variability. However, negatively skewed platykurtic distribution is an evidence for involvement of a large number of dominant genes with majority of them having increasing effects and duplicate type of epistasis in the inheritance of days to maturity, secondary branches per plant and pods per plant in IT-38956-1 $\times$ CP-12 cross; seed yield per plant and hundred seed weight in IT-38956-1 $\times$ CP-12; days to first flowering and hundred seed weight in KBC-2 $\times$ CP-12. These traits have evolved with dominance and dominance based duplicate epistasis which helps to protect the individual plants from deleterious alleles arising from existing variability (Roy, 2000).

5.2.2 Genetic variability parameters

Estimation of variability parameters for any population is a pre-requisite for any breeding programme aimed at improving yield, quality and other important characters under consideration. Unless a major portion of variation is heritable, attempts to improve characters by selection would be futile. The success in a crop improvement programme depends on the ability of the breeder to define and assemble the required genetic variability and select for yield indirectly through yield associated and highly heritable characters after eliminating the environmental components of phenotypic variation (Mather, 1949). Therefore, firstly it is necessary to have information on both PCV and GCV, so that the heritability, which helps the breeder to predict the expected genetic advance possible by selection for characters, can be computed.

Knowledge on genetic advance that is expected by applying selection pressure to a segregating population is useful in designing effective breeding programme. The evaluation of the segregating progenies helps in estimation of various genetic and non-genetic components of variance. The study of variability provides an opportunity for selecting the desirable genotypes. Heritability is a fraction of variance in phenotypic expression that arises from genetic effects. The nature of the selection units and sampling errors also influences greatly the magnitude of heritability estimates. The heritability estimates in segregating generations helps to know genetic variance, genotype-

environment interaction and progress to be expected from selection. A most misleading estimate of phenotypic variance for yield under natural conditions would have been estimated from a single test, resulting in the confounding of the interaction variances with progeny variance. The estimates of genetic advance may be biased upward, if phenotypic variance contains a fraction of whether genetic variance due to non-additive effects (dominance or epistasis) if present (Hanson *et al.*, 1956).

The range in mean values does not reflect the total variance in the material studied. Hence, actual variance has to be estimated for the characters to know the extent of existing variability. The genotypic variance measures the magnitude of genetic variability present in the crop and phenotypic variance indicates the amount of variation which is due to phenotypic values. The absolute values of phenotypic and genotypic variance cannot be used for comparing the degree of variability in different characters because the characters differ in the unit of measurement. Hence, the co-efficient of variation (PCV and GCV) which is calculated by considering the respective means have been used for the comparisons. High values of these parameters indicate wider variability and *vice versa*. In the same context, narrow differences between the phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) implies lesser effect of environment on these traits.

Broad sense heritability gives an idea about portion of observed variability attributable to genetic differences. The difference between PCV and GCV estimates indicates the relative influence of environment on the character, which in turn decides the extent of their heritability. If the difference is low for a character then the influence of environment is less coupled with high heritability. Wide differences indicate considerable influence of the environment, thus resulting in low heritability estimates. According to Johnson *et al.* (1955) heritability estimates along with genetic gain would be more useful than the former alone in predicting the effectiveness of selecting the best individual. Therefore, it is essential to consider the predicted genetic advance along with heritability estimate as a tool in selection programme for better efficiency.

In the present study, the range of variability created in the cross was quite moderate for all the characters studied except pods per plant, primary branches per plant and hundred seed weight exhibited low variability across all three crosses. Whereas, it may not be equally effective for a character which exhibited narrow range of variability.

5.2.2.1 Genetic variability parameters in cowpea cross IT-38956-1 × KBC-2

In general, PCV values were relatively higher than GCV values in F₂ generation for the cross IT-38956-1 × KBC-2 coupled with negligible differences which indicated less environmental influence on all the traits and was confirmed with the earlier studies of Jana *et al.* (1983), Girish *et al.* (2006), Ramesh Kumar *et al.* (2009), Kumar P *et al.* (2013), Tigga K *et al.* (2014), Kharde *et al.* (2014) and Inuwa *et al.* (2015)

Days to first flowering exhibited low values of GCV and PCV in F₂. These results are in conformity with those of Ramesh Kumar *et al.* (2009). Heritability in broad sense for this trait was high coupled with low genetic advance as per cent of means indicated predominant role of non-additive gene action and these results are in accordance with that of Tigga K *et al.* (2014).

Days to maturity exhibited lower values of GCV and PCV and differences between them was high, which indicated the influence of more environmental factors on expression of this trait. The broad sense heritability was high coupled with low genetic advance indicating the predominant role of non-additive gene action. The results of heritability and genetic advance in the present study are in total agreement with the reports of Kumar R *et al.* (2009), Kumar P *et al.* (2013) and Tigga K *et al.* (2014).

Plant height exhibited moderate estimates of GCV and PCV high which difference indicating environmental influence on expression of this trait. Kumar P *et al.* (2013) and Tigga K *et al.* (2014) reported similar results for this trait. High broad sense heritability coupled with low genetic advance as per cent of mean indicated the predominant role of non-additive gene action and high scope for further improvement of this trait through simple selection in F₂ population. Similar, results have also been

reported by Tigga K *et al.* (2014) who have noticed the role of non-additive gene action for plant height.

Primary branches per plant registered moderate PCV and GCV values considerable difference between them indicating substantial influence of environment on this trait. The results of PCV and GCV were in agreement with earlier report of Singh *et al.* (2004), Singh *et al.* (2010) and Tigga K *et al.* (2014). Moderate heritability coupled with low genetic advance expressed as per cent of mean indicated the role of non-additive gene action in the genetic control. Results of the present study are in conformity with the results of Girish *et al.* (2006) and Kumar P *et al.* (2013) who have reported the role of non additive gene action controlling the trait primary branches per plant.

Secondary branches per plant registered the moderate PCV and GCV values with narrow difference indicating low influence of environment on this trait expression. Broad sense heritability estimates exhibited higher values coupled with high genetic advance as per cent of mean for this trait. Thus, high heritability coupled with high genetic advance indicated role of additive gene action, which may act as useful index for improvement of this trait through simple selection. These, results are in agreement with earlier reports of Kumar R *et al.* (2009), Kumar P *et al.* (2013), Tigga K *et al.* (2014) and Bhawna Pandey and Singh Y V (2015) for higher heritability and genetic advance.

Pods per plant registered moderate values of GCV and PCV with narrow difference in both the crosses indicating low influence of environment on expression of this trait. However, the broad sense heritability estimates were high coupled with high genetic advance expressed as per cent of mean indicating predominant role of additive gene action in both crosses. Bhawna Pandey and Singh Y V (2015) reported similar results for heritability and genetic advance. Hence, this trait can be effectively used for selecting desirable segregants owing to its high heritability combined with high genetic advance.

Pod length recorded the moderate value of PCV and GCV with high difference between them. The expression of this trait was influenced by environment. However, the

moderate heritability and low genetic advance expressed as per cent of mean indicated this trait is controlled by the non additive gene action in F₂ population. This was in accordance with the earlier observations made by Yadav *et al.* (2004), Eswaran *et al.* (2007), Subbaiah *et al.* (2013) and Bhadru and Navale (2012).

Seeds per pod recorded moderate values of PCV and GCV with moderate difference indicating substantial influence of environment on trait expression. Broad sense heritability and genetic advance estimates were also high in both crosses indicating preponderance of additive gene action in genetic control of this trait.

Seed yield per plant recorded moderate to high values of PCV and GCV with narrow difference indicating low influence of environment on this trait expression. Broad sense heritability estimates exhibited moderate values coupled with moderate genetic advance as per cent of mean for this trait indicating the non additive type of gene action controlling this trait in F₂ population. This was in accordance with the earlier observations made by Yadav *et al.* (2004), Eswaran *et al.* (2007), Subbaiah *et al.* (2013) and Bhadru *et al.* (2012).

The trait, hundred seed weight registered moderate values of PCV and GCV with narrow difference between them in both crosses, indicating less influence of environment on expression of this trait. However, the estimates of heritability and genetic advance expressed as per cent of mean were moderate indicating the role of non additive gene action in F₂ generation.

5.2.2.2 Genetic variability parameters in cowpea cross-II (IT-38956-1 × CP-12)

In general, PCV values were relatively higher than GCV values in F₂ generation for the cross IT-38956-1 × CP-12 coupled with negligible differences indicated less environmental influence on all the traits. These results are supported by the earlier studies of Kumar K *et al.* (2009), Kumar P *et al.* (2013) and Tigga K *et al.* (2014).

Days to first flowering exhibited moderate values of GCV and PCV in F₂. This was in conformity with the study of Kumar R *et al.* (2009). Heritability in broad sense for

this trait was high coupled with moderate genetic advance as per cent of means indicated predominant role of non-additive gene action and this result was in accordance with Tigga K *et al.* (2014).

Days to maturity exhibited lower values of GCV and PCV and differences between them was low. This expression of this trait was less influenced by environment. The broad sense heritability was high coupled with high genetic advance as per cent of mean indicated predominant role of additive gene action. This may be useful for exploitation of heterosis. The results of heritability and genetic advance in the present study are in total agreement with the reports of Kumar R *et al.* (2009), Kumar P *et al.* (2013) and Tigga K *et al.* (2014).

Plant height exhibited moderate estimates of GCV and PCV with high difference indicating environmental influence on expression of this trait. Kumar P *et al.* (2013) and Tigga K *et al.* (2014) reported parallel results for this trait. High broad sense heritability coupled with high genetic advance as per cent of mean indicated the predominant role of additive gene action and revealing the scope for further improvement of this trait through simple selection in F₂ population. Similar, results were reported by Tigga K *et al.* (2014) which they also attributed to non-additive gene action.

Primary branches per plant registered high PCV and GCV values with high difference between them indicating substantial influence of environment on this trait. High heritability coupled with high genetic advance indicated the role of additive gene action in the genetic control. Results of present study are in similar kind of reports by Kumar P *et al.* (2013) who also attributed to additive gene action.

Secondary branches per plant registered the high PCV and GCV values with high difference for nodes per plant indicating influence of environment on this trait expression. Broad sense heritability estimates exhibited higher values coupled with high genetic advance as per cent of mean for this trait. Thus, high heritability coupled with high genetic advance indicated role of additive gene action, which may act as useful index for improvement of this trait through simple selection These, results are in

agreement with earlier reports of Kumar R *et al.* (2009), Kumar P *et al.* (2013), Tigga K *et al.* (2014) and Bhawna Pandey and Singh Y V (2015) for higher heritability and genetic advance.

Pods per plant registered moderate values of GCV and PCV with high difference indicating high influence of environment on expression of this trait. However, the broad sense heritability estimates were high coupled with high genetic advance expressed as per cent of mean indicating predominant role of additive gene action in both crosses. Bhawna Pandey and Singh Y V (2015) reported similar results for heritability and genetic advance. This trait can be effectively used for selecting desirable segregants owing to its high heritability combined with high genetic advance.

Pod length has recorded high value of PCV and GCV with high difference between them showed that the expression of this trait was influenced by environment. However, the high broad sense heritability and genetic advance estimates indicated the usefulness of this trait in selection of desirable segregants due to its genetic control by additive gene action in F_2 population.

Seeds per pod recorded moderate values of PCV and GCV with moderate difference between them indicating substantial influence of environment on trait expression. Broad sense heritability and genetic advance estimates were also high in both crosses indicating pre dominant role of additive gene action in genetic control of this trait. Higher estimates of heritability and genetic advance indicating simple selection may be sufficient in deriving desirable segregants in F_2 population. These results are in total agreement with the earlier report made by Bhadru *et al.* (2012)

Seed yield per plant recorded moderate to high values of PCV and GCV with high difference between them indicating high influence of environment on this trait expression. Broad sense heritability estimates exhibited moderate values coupled with low genetic advance as per cent of mean for this trait indicating the additive type gene action controlling this trait in F_2 population. This was in accordance with the earlier

observations made by Yadav *et al.* (2004), Eswaran *et al.* (2007), Subbaiah *et al.* (2013) and Bhadru *et al.* (2012).

Hundred seed weight registered low values of PCV and GCV with narrow difference between them in both crosses, indicating less influence of environment on trait expression. However, the estimates of heritability and genetic advance expressed as per cent of mean were moderate indicating role of non additive gene action.

5.2.2.3 Genetic variability parameters in cowpea cross-III (KBC-2 × CP- 12)

In general, PCV values were relatively higher than GCV values for the cross KBC-2 × CP-12 coupled with moderate differences indicated lesser environmental influence on all the traits this was confirmed with the study of Kumar R *et al.* (2009), Kumar P *et al.* (2013) and Tigga K *et al.* (2014).

Days to first flowering exhibited lower values of GCV and PCV in F₂. Heritability in broad sense for this trait was high coupled with moderate genetic advance as per cent of means indicated the predominant role of non-additive gene action and this result was in accordance with Tigga K *et al.* (2014).

Days to maturity exhibited lower values of GCV and PCV and differences between them were low. This expression of this trait was less influenced by environment. The broad sense heritability was moderate coupled with moderate genetic advance as per cent of mean indicated predominant role of non additive gene action.

Plant height exhibited high estimates of GCV and PCV with high difference indicating environmental influence on expression of this trait. Praveen Kumar *et al.* (2013) and Tigga K *et al.* (2014) reported parallel results for this trait. High broad sense heritability coupled with moderate genetic advance as per cent of mean indicated the predominant role of non additive gene action. Similar results were reported by Tigga K *et al.* (2014) who also attributed the role of non-additive gene action.

Primary branches per plant registered high PCV and GCV with high difference between them indicating substantial influence of environment on this trait. The results of

PCV and GCV were in agreement with earlier report of Tigga K *et al.* (2014). High heritability coupled with moderate genetic advance expressed as per cent of mean indicating the role of additive gene action in the genetic control. Results of present study in context of the earlier reports of Girish *et al.* (2006) and Kumar P *et al.* (2013) which they also attributed to additive gene action.

Secondary branches per plant registered the high PCV and GCV values with moderate difference indicating influence of environment on this trait expression. Broad sense heritability estimates exhibited higher values coupled with moderate genetic advance as per cent of mean for this trait. Thus, high heritability coupled with moderate genetic advance indicated the role of additive gene action, which may act as useful index for improvement of this trait through simple selection in F_2 population. These, results are in agreement with earlier reports of Kumar P *et al.* (2009), Kumar P *et al.* (2013) and Tigga K *et al.* (2014) and Bhawna Pandey and Singh (2015) for higher heritability and genetic advance.

Pods per plant registered high values of GCV and PCV with high difference indicating high influence of environment on expression of this trait. However, the broad sense heritability estimates were high coupled with moderate genetic advance expressed as per cent of mean indicating predominant role of additive gene action in both crosses. Bhawna Pandey and Singh Y V (2015) reported similar results for heritability and genetic advance. Hence, this trait can be effectively used for selecting desirable segregants owing to its high heritability combined with high genetic advance.

Pod length recorded the moderate value of PCV and HCV with high difference between them indicated this trait was influenced by environment. However, the high broad sense heritability and moderate genetic advance estimates indicating usefulness of this trait in selection of desirable segregants due to its genetic control by additive gene action in F_2 population.

Seeds per pod recorded moderate values of PCV and GCV with moderate difference indicating substantial influence of environment on trait expression. Broad

sense heritability and genetic advance estimates were also high indicating preponderance of additive gene action in genetic control of this trait. Similar report made by Bhadru and Navale (2012) for higher estimates of heritability and genetic advance indicating simple selection may be sufficient in deriving desirable segregants in F_2 population.

Seed yield per plant recorded high values of PCV and GCV with low difference indicating low influence of environment on this trait expression. Broad sense heritability estimates exhibited high values coupled with high genetic advance as per cent of mean for this trait indicating the additive type gene action controlling this trait in F_2 population. This was in accordance with the earlier observations made by Yadav *et al.* (2004), Eswaran *et al.* (2007), Subbaiah *et al.* (2013) and Bhadru and Navale (2012).

Hundred seed weight registered low values of PCV and GCV with narrow difference between them in both crosses, indicating less influence of environment on trait expression. However, the estimates of heritability and genetic advance expressed as per cent of mean were moderate indicating role of non additive gene action in F_2 generation.

5.2.3 Character association

The potential progress expected in accomplishing the objectives demands knowledge of inter-relationships among various traits and component characters contributing yield. This helps breeder in selection schemes. Character associations may vary with environmental conditions. Association of yield components of quantitative nature, which is quite useful as basis of selection. As breeder has to handle very large population in achieving the objectives, it is impossible to evaluate each and every genotype in the field for yield and/or quality. Therefore, it is necessary to have the estimates of correlation of yield with other traits for which the genotypes could be assessed visually or measured easily. Thus, correlation analysis helps in examining the possibility of improving yield through indirect selection of its component traits which are highly correlated. In the present study, character association among all the characters related to seed yield per plant in F_2 population of three crosses (IT-38956-1x KBC-2, IT-38956-1 $\times$ CP-12 and KBC-2 $\times$ CP-12) were estimated and results are discussed below.

5.2.3.1 Association between seed yield with its component characters

Seed yield per plant was significantly and positively associated with all the yield attributing traits in all the crosses except for plant height and seed per pod in KBC-2 × CP-12. According to Falconer (1981), the phenotypic variability of quantitative traits in a population usually has an environmental component. So, it is inferred that those characters with positive correlations are influenced and controlled by similar gene combinations and environmental factors. This is in accordance with the earlier reports of Alege and Mustapha (2007) and Khadre *et al.* (2014).

5.2.3.2 Association among seed yield and its attributing characters

5.3.3.2.1 Association among seed yield and its attributing characters of cowpea cross IT-38956-1 × KBC-2

Among the seed yield and its attributing characters in the cross, positive and significant association of days to first flowering with days to maturity, plant height, biomass, secondary branches per plant, pods per plant, pod length and test weight; days to maturity with plant height, secondary branches per plant, pods per plant, seeds per pod and test weight; plant height with secondary branches per plant, pod length, pods per plant and hundred seed weight; primary branches per plant with secondary branches per plant, pod length, seeds per pod and hundred seed weight; secondary branches per plant with pod length, seeds per pod and hundred seed weight; pod length with seeds per pod and hundred seed weight; seed per pod with hundred seed weight. These findings are in conformity with the report of Khadre *et al.* (2014), Jana *et al.* (1983), Mishra *et al.* (1994), Vardhan and Savithramma (1998) and Vidya and Oomen (2002). Contrary to association of days to flowering and number of seeds per pod recorded negative direct effect were reported by Mishra *et al.* (1994), Venkatesan (2003), Biradar *et al.* (1993) and Kharde *et al.* (2014).

To improve the seed yield in cowpea, it is important to give more importance to the traits such as secondary branches per plant, pods per plant, pod length and seeds per pod, as these traits had positive and significant association with seed yield.

5.2.3.2.2 Association among seed yield and its attributing characters in cowpea cross IT-38956-1 × CP-12

Among the seed yield and its attributing characters in the cross, positive and significant association of days to first flowering with days to maturity, plant height, biomass, secondary branches per plant, pods per plant, pod length and hundred seed weight; days to maturity with plant height, secondary branches per plant, pods per plant, seeds per pod and test weight; plant height with secondary branches per plant , pod length, pods per plant and hundred seed; primary branches per plant with secondary branches per plant, pod length, seeds per pod and hundred seed weight; secondary branches per plant with pod length, seeds per pod and hundred seed weight; pod length with seeds per pod and hundred seed weight; seed per pod with hundred seed weight were observed.

5.2.3.2.3 Association among seed yield and its attributing characters in cowpea cross KBC-2 × CP-12

Among the seed yield and its attributing characters in the cowpea cross KBC-2 × CP-12, negative and significant association of days to first flowering with days to maturity, plant height, secondary branches per plant and hundred seed weight; positive significant association of days to maturity with pods per plant and hundred seed weight; negative significant association of primary branches per plant with secondary branches per plant and seeds per pod; primary branches per plant showed negative significant association with secondary branches per plant, pod length and seeds per pod; secondary branches per plant with hundred seed weight; pod length with hundred seed weight were observed.

On the other hand the days to first flowering, primary branches per plant and seeds per pod showed negative association with seed yield per plant.

5.2.4 Path co-efficient analysis

As the correlation estimate is the sum total of direct and indirect effects of an independent characters on a dependent characters, it is quite possible that a correlation

(Positive or negative) may be of small magnitude and non-significant in spite of its direct effect and/or some of the indirect effects are operating in the opposite direction. Therefore, path analysis is required to partition the correlation estimate into direct and indirect effects so as to get a correct picture of the association of characters. Further, for the same reason, as many independent characters as possible, whether or not they are showing significant correlations with the dependent characters are to be considered for path co-efficient analysis.

The path analysis is a useful technique to understand more clearly the association among different variables as recorded by simple correlation values. It helps to partition the overall association of particular variables with dependent variable into direct and indirect effects. When the influence of a set of variables on the dependent variables is to be understood, it is possible with the help of path analysis to estimate the extent of direct contribution of a particular variable and the extent of its indirect contribution through other variables in a set to the total influence it has on the dependent variable. While dealing with a more complex character like yield, it enables the breeders to specially identify the important component traits of such a nature and differential emphasis can be laid on those characters for selection. The results obtained for the association analysis for direct and indirect effects on the seed yield are discussed below.

5.2.4.1 Path analysis in F₂ generation of the cowpea cross IT-38956-1 × KBC-2

Direct and indirect effects of component characters on seed yield resulted from path analysis indicated maximum positive direct effect of pod length followed by secondary branches per plant and plant height. Though, pods per plant and seeds per pod exhibited low positive direct effect, its indirect effect *via.*, days to first flowering, days to maturity and primary branches per plant exhibited negative correlation with the seed yield per plant. The similar results were reported by Apte *et al.* (1987), Damarany (1994), Idahosa *et al.* (2010), Manggoel *et al.* (2012) and Nwosu *et al.* (2013).

While the pod length exerted high positive indirect effect via plant height followed by seeds per pod and secondary branches per plant

The days to first flowering showed the indirect high positive effect towards the seed yield per plant through the pod length followed by plant height, low positive effect towards the seed yield through the pods per plant, secondary branches per plant and primary branches per plant. These results are in accordance with the earlier reports of Birder *et al.* (1996), Venkatesan (2003), Alege and Mustapha (2007), Abadyomi and Abidoye (2009) and Kharde *et al.* (2014).

5.2.4.2 Path analysis in F₂ generation of the cross IT-38956-1 × CP-12

The results of path analysis for seed yield per plant indicated high positive direct effect of seeds per pod followed by pod length, days to first flowering and pods per plant on seed yield per plant. However, a primary branch per plant, secondary branches per plant and hundred seed weight shows low positive direct effect. On the other hand, days to maturity and plant height showed negative direct effect with seed yield.

5.2.4.3 Path analysis in F₂ generation in cowpea cross KBC-2 × CP-12

The results of path analysis for seed yield per plant indicated high positive direct effect of pod length followed by secondary branches per plant, seeds per pod and pods per plant on seed yield. However, plant height and primary branches per plant showed low positive direct effect. On the other hand, days to first flowering, days to maturity and hundred seed weight had negative direct effect with seed yield. Days to first flowering showed the negative direct effect but showed positive indirect effect through the pod length followed by plant height.

5.3 Gene action for quantitative characters

Generation mean analysis (Mather and Jinks, 1983) was adopted to study the gene action for yield and other quantitative characters as it allows estimation of all the three types of gene actions additive, dominance and epistasis. Since cowpea is a self pollinated crop crossing is difficult and consequently production of enough seeds for rising backcross generation is difficult. Therefore five generation mean analysis which involves two parents (P₁ & P₂), their F₁, F₂ and F₃ in each cross was chosen for the study instead

of six generation mean analysis which requires two backcross generations (BC_1 , BC_2), in addition to P_1 , P_2 , F_1 and F_2 in each cross.

The four parameters viz., non-significant heterosis in F_1 , lack of inbreeding depression from F_1 to F_2 , lack of inbreeding depression from F_2 to F_3 and high heritability, indicate preponderance of additive gene action over non-additive gene action, while significance of any one of the first three parameters or low heritability indicate the reverse. However, the type of gene action involved is finally based on the actual estimates of d , h , i and l . This is because the significance or otherwise of the first three parameters *i.e.* (i), (ii) and (iii) depends on the net effects of the positive and negative polygenes which may be dominant or epistatic in nature involved for a character. So also, if the heritability estimated is of broad sense, its high or low magnitude may not correspond with the magnitudes of d , h , i and l . For the same reason, the indication given by the first three parameters may not be of same type and may not coincide with the indication of gene action given by heritability value, keeping these points in view, the reason pertaining to gene effects are discussed below character-wise and cross-wise.

The gene effects that are significant only are discussed. Further, the sign of the effects (+ve or -ve) is ignored because irrespective of the sign, higher magnitude of an effect as compared to another effect indicates that it is involved to a greater extent than the other.

5.3.1 Days to first flowering

1. Cross 1 (IT-38956-1 $\times$ KBC-2)

In this cross, for days to first flowering initiation, the heterosis in F_1 and inbreeding depression from F_1 to F_2 and F_2 to F_3 were significant indicating that non additive gene action is preponderant over additive gene action. Though, $[d]$ was significant, its magnitude was more than i , which was also significant.

2. Cross 2 (IT-38956-1 × CP-12)

In this cross, F_1 showed significant heterosis over mid parent and better parent, inbreeding depression from F_1 to F_2 as well as F_2 to F_3 were significant, The significant [h], [i] and [l] values were higher in magnitude than non-significant [d] value indicates the non additive gene action for days to flowering.

3. Cross 3 (KBC-2 × CP-12)

Heterosis over mid parent and better parent are significant, inbreeding depression from F_1 to F_2 and F_2 to F_3 were significant, indicating that non additive gene action is more than additive gene action for this character which was confirmed by the fact that significant [i] and [l] values were higher in magnitude than [d].

5.3.2 Days to maturity

1. Cross 1 (IT-38956-1 × KBC-2)

Heterosis over mid parent and better parent were significant, inbreeding depression from F_1 to F_2 and F_2 to F_3 were non-significant indicating that non additive gene action is more than additive gene action for this character which was confirmed by the fact that significant [h], [i] and [l] values were higher in magnitude than [d].

2. Cross 2 (IT-38956-1 × CP-12)

In this cross, the F_1 did not show significant heterosis over mid parent, inbreeding depression from F_1 to F_2 as well as F_2 to F_3 were also not significant indicating additive gene action for this character and also the gene action effects were also found to be non significant.

3. Cross 3 (KBC-2 × CP-12)

Though, (a) mid parent heterosis (b) inbreeding depression from F_1 to F_2 and F_2 to F_3 were significant, and (c) heritability was high in F_2 and F_3 indicating more of non additive gene action than additive gene action governing this character which was confirmed by the higher magnitudes of [l] and [i] as compared to [d].

5.3.3 Plant height (cm)

1. Cross 1 (IT-38956-1 × CP-12)

Heterosis over mid parent and better parent, inbreeding depression from F_1 to F_2 and F_2 to F_3 were significant, indicating preponderance of non additive gene action over additive gene action for this character. Contrary to this, magnitude value of d is more than the $[h]$, $[i]$ and $[l]$.

2. Cross 2 (IT-38956-1 × CP-12)

Heterosis over mid parent and better parent were non-significant, inbreeding depression from F_1 to F_2 were significant and F_2 to F_3 were non-significant values indicating that role of non-additive gene action than additive gene action for this trait which was confirmed by the fact that the value of $[i]$ was higher in magnitude than that of $[d]$.

3. Cross 3 (KBC-2 × CP-12)

In this cross, for days to maturity, heterosis over mid parent and better parent were significant, in F_1 and inbreeding depression from F_2 to F_3 were significant indicating that non additive gene action is more involved than non additive gene action for this trait. But $[h]$ value was higher in magnitude than $[d]$.

5.3.4 Primary branches per plant

1. Cross 1 (IT-38956-1 × CP-12)

The heterosis over the mid parent and better parent were significant. The inbreeding depression from F_1 to F_2 and F_2 to F_3 was significant. However, significant heterosis over mid parent and inbreeding depression from F_1 to F_2 indicated that non additive gene action was more involved than additive gene action for this character which was confirmed by the fact that $[i]$ value was higher in magnitude than $[d]$ though $[h]$ was smaller than $[d]$ and non-significant chi-square test.

2. Cross 2 (IT-38956-1 × CP-12)

In this cross, for primary branches per plant, the inbreeding depression from F_1 to F_2 and F_2 to F_3 were significant. Nevertheless, heterosis over mid parent and better parent was significant which meant that, for this character, non-additive gene action was involved to a greater extent than additive gene action. To support this, magnitude of [h] and [i] value was more than the [d] and non-significant.

3. Cross 3 (KBC-2 × CP-12)

Heterosis over mid parent and inbreeding depression from F_1 to F_2 was significant though the inbreeding depression from F_2 to F_3 was not significant, indicating the involvement of non additive gene action to a greater extent than additive gene action for this trait which was confirmed by the fact that significant [h] and [i] values were higher in magnitude than [d].

5.3.5 Secondary branches per plant

1. Cross 1 (IT-38956-1 × KBC-2)

In this cross, for secondary branches per plant the heterosis over mid parent and better parent were significant and inbreeding depression from F_1 to F_2 and F_2 to F_3 were significant indicating that non additive gene action is more than additive gene action. This was confirmed by the fact that [i] and [h] values were significant whereas [d] was not significant.

2. Cross 2 (IT-38956-1 × CP-12)

In this cross, the heterosis over mid parent and better parent were significant, inbreeding depression from F_1 to F_2 as well as F_2 to F_3 were also significant. Heritability was high in F_2 and moderate in F_3 indicating that non additive gene action is predominant over additive gene action for this character. This was confirmed by the fact that [i] and [h] values were significant where as [d] was not significant.

3. Cross 3 (KBC-2 × CP-12)

In this cross, for secondary branches per plant, heterosis over mid parent and inbreeding depression from F_1 to F_2 were significant, though (a) the inbreeding depression from F_2 to F_3 was not significant, indicating that non additive gene action is more than additive gene action for this character which was confirmed by the fact that [i] and [l] values were higher magnitudes than [d].

5.3.6 Number of pods per plant

1. Cross 1 (IT-38956-1 × CP-12)

Though the heterosis over mid parent and better parent were significant, inbreeding depression from F_1 to F_2 and F_2 to F_3 was significant and, indicating that non additive gene action is more than additive gene action for this character which was confirmed by the fact that [i] and [l] value was higher in magnitude than [d] value.

2. Cross 2 (IT-38956-1 × CP-12)

In this cross, the F_1 showed significant heterosis over better parent and mid parent, inbreeding depression from F_1 to F_2 was significant and F_2 to F_3 were non significant, indicating that non additive gene action was more involved than additive gene action for this character. This indication was supported by [h] and [i] values being of higher magnitude than [d] value.

3. Cross 3 (KBC-2 × CP-12)

Heterosis over mid parent and better parent were significant though , inbreeding depression from F_1 to F_2 as well as F_2 to F_3 were significant, indicating that non additive gene action is more than additive gene action for this character. However, this indication was not confirmed as evident from the non-significance of magnitude value of [d] lower than the [h] and [i] magnitude value.

5.3.7 Pod length (cm)

1. Cross 1 (IT-38956-1 × KBC-2)

In this cross, F_1 did not show significant heterosis over better parent, inbreeding depression from F_1 to F_2 was not significant, indicating that non additive gene action is more than additive gene action for this character which was confirmed by the fact that higher magnitude value of [h] and [i] than the magnitude [d] value.

2. Cross 2 (IT-38956-1 × CP-12)

Heterosis over mid parent and better parent in F_1 was significant though, inbreeding depression from F_1 to F_2 and F_2 to F_3 were significant, indicating that the character was governed to a great extent by non-additive gene action than additive gene action. On contrary to this is the magnitude of [d] value was significant and higher than the all values.

3. Cross 3 (KBC-2 × CP-12)

Heterosis over mid parent and better parent in F_1 was significant though, inbreeding depression from F_1 to F_2 and F_2 to F_3 were significant, indicating that the character was governed to a great extent by non-additive gene action than additive gene action. This indication was confirmed by the fact that [d] was significant and lower than the all values.

5.3.8 Seeds per pod

1. Cross 1 (IT-38956-1 × KBC-2)

Heterosis over mid parent and better parent in F_1 was significant though, inbreeding depression from F_1 to F_2 and F_2 to F_3 were significant, indicating that the character was governed to a great extent by non-additive gene action than additive gene action for this character which was confirmed by the fact that magnitude of [I] value which was higher in magnitude value than [d].

2. Cross 2 (IT-38956-1 × CP-12)

In this cross, heterosis over mid parent and inbreeding depression from F_2 to F_3 was significant, indicating the preponderance of non additive gene action over additive gene action which was confirmed by the higher magnitude value of [h] than the value of [d].

3. Cross 3 (KBC-2 × CP-12)

Though the inbreeding depression from F_1 to F_2 was non significant and F_2 to F_3 was significant and the heterosis over mid parent was significant which meant non-additive gene action was operating to a greater extent than additive gene action for this character. Contradictory to this, [d] was the only gene effect that was significant.

5.3.9 Seed yield per plant (g)

1. Cross 1 (IT-38956-1 × KBC-2)

Heterosis over mid parent and better parent were significant, inbreeding depression from F_1 to F_2 and F_2 to F_3 were significant which indicated that non additive gene action for this character is more than additive gene action but this was confirmed by the fact that d was non significant for this character and higher magnitude values of [h], [i] and [l] than the magnitude of [d] value.

2. Cross 2 (IT-38956-1 × CP-12)

In this cross, for seed yield per plant the heterosis in F_1 over mid parent, inbreeding depression from F_1 to F_2 and F_2 to F_3 were significant which indicating that non additive gene action was predominant over additive gene action. But this was not confirmed because except [d] other gene effects were not significant and lesser.

3. Cross 3 (KBC-2 × CP-12)

Heterosis over mid parent and better parent were significant, inbreeding depression from F_1 to F_2 and F_2 to F_3 were significant which indicated that non additive gene action for this character is more than additive gene action but this was confirmed by

the fact that [d] was non significant for this character and higher magnitude values of [h], [i] and [l] than the magnitude of [d] value.

5.3.10 Hundred seed weight (g)

1. Cross 1 (IT-38956-1 × KBC-2)

Heterosis over mid parent and better parent was non significant, inbreeding depression from F_1 to F_2 as well as F_2 to F_3 generations were significant, indicating that non additive gene action was predominant over additive gene action for this character which was confirmed by the higher magnitude of [l], [i] and [h] values than [d] value even though all the effects were non significant

2. Cross 2 (IT-38956-1 × CP-12)

Though the inbreeding depression from F_1 to F_2 and F_2 to F_3 were significant, heterosis over mid parent and better parent were significant which meant that for this character, non-additive gene action was operating to a greater extent. On the contrary to the magnitude of [d] value is more than the all other values.

3. Cross 3 (KBC-2 × CP-12)

Heterosis over better parent, and inbreeding depression from F_2 to F_3 were significant, where indicated that non-additive gene action was governing this character to a greater extent than additive gene action. This was confirmed by the higher magnitudes of [h] and [l] than [d] value.

A comprehensive consideration of the discussion on the results pertaining to heterosis, inbreeding depression, heritability and gene action presented alone revealed that for almost all the characters in all the three crosses, non additive gene action was found to have greater role than additive gene action. It may be noted that this conclusion has been reached by ignoring the signs (+ve or -ve) of the effects and considering their absolute magnitudes once they are significant. This is appropriate for knowing the involvement of different types of gene action for each character. In general, for suggesting the further on the utilization of the three crosses of the present investigation,

the signs of the significant gene effect also needs to be considered, in addition to their magnitudes.

In the present study, non additive gene action was found operating to a greater extent than additive gene action for days to first flowering, days to maturity, secondary branches, number of pods per plant, seed yield and hundred seed weight the same results are confirmed by several earlier workers (Ningappa, 1979; Jatsara, 1980; Marangappanavar, 1984; Srikantaradhya, 1984; Kabi Raj, 1986; Patil and Bhapkar, 1986; Patil and Patil, 1986; Singh and Dabas, 1986; Patil and Patil, 1987; Arun Kumar, 1989; Shakarad, 1989; Savithramma, 1991 a and b; Madhusudan , 1994; Shakarad *et al.*, 1995; Bhushana, 1996; Balaraju, 1997; Girish, 2000); Selvam *et al.*, 2000; Khanum, 2001 and Venkatesan *et al.*, 2003). But for the same characters, Sohoo *et al.*, 1971; Singh *et al.*, 1977; Tikka *et al.*, 1977; Pandita *et al.*, 1979; Sreekumar *et al.*, 1979; Bhaskaraiah *et al.*, 1980; Chikkadevaiah *et al.*, 1980; Dharmalingam and Kadambavanasundaram, 1984; Vaid and Singh, 1984; Apte *et al.*, 1987; Patil and Shete, 1987; Patil and Bhaviskar, 1987; Sangwan and Lodhi, 1995; Vijendara Das, 1996; Girish, 2005; Anbumalarmathi *et al.*, 2005; Lal *et al.*, 2007 and Patel *et al.*, 2016 reported preponderance of additive gene action over non non-additive gene action. Such contradictory results were possible depending on genetic material used in different studies.

The mean values of F_1 's when compared with their respective parents indicated the degree of the dominance for a character. As far as degree of dominance is concerned for characters for which non-additive gene action was confirmed, no-dominance was observed for days to maturity, seeds per pod and seed yield per plant. Partial degree of dominance was observed for days to first flowering, primary branches per plant, secondary branches, pods per plant and pod length in cross 1. In cross 2, over-dominance was observed for days to first flowering, primary branches per plant, secondary branches, pods per plant, pod length, seeds per pod and seed yield. While partial dominance was observed for days to maturity, plant height and hundred seed weight. In cross 3, over-dominance was observed for days to first flower, plant height and secondary branches, while partial dominance was observed for primary branches per plant, pods per plant, pod length and seed yield per plant.

Selection of seed yield should be differed to advanced segregating generations as it is predominantly under the control of dominance and dominance based gene action. Perhaps, one or two cycles of biparental mating in early segregating generations are useful to break conserved linkage blocks which are considered to be cause for non additive gene action.

Although, generation mean analysis is valuable for detection and estimation of additive, dominance and epistatic gene effects, it does have limitations. Linkage affects epistatic gene effects and causes more biased estimation of additive $\times$ additive and dominance $\times$ dominance gene effects. Inferences based on the magnitudes of additive effects are not advisable, because the distribution of positive and negative gene effects in the parents may result in different degrees of cancellation of effects in the expression of the generation means. For the same reason, the magnitudes of additive gene effects do not necessarily reflect the magnitude of additive variance. However, dominance $[\hat{h}]$ and dominance $\times$ dominance $[\hat{l}]$ are independent of the degree of gene distribution due to which the combined estimates of dominance $[\hat{h}]$ and dominance $\times$ dominance $[\hat{l}]$ could be considered to be the best representative of sign and magnitude of individual $[\hat{h}']$ s and $[\hat{l}']$ s, respectively. Hence, these are the only components which can safely be used practically to determine the type of epistasis where may have influence on the observed performance of generations (Mather and Jinks, 1982). For the same reason, emphasis has been given to the characters which are governed by such gene effects for suggesting appropriate breeding method that could be followed to achieve higher expression of such characters.

5.4 Number of effective factors

Minimum number of effective factors influencing a trait in F_2 population of three crosses of Cowpea in respect of 10 quantitative characters was estimated and results of the same are discussed here.

In IT-38956-1 $\times$ KBC-2 cross, the traits viz., days to maturity (1.00), plant height (0.58), number of primary branches per plant(0.05), number of secondary branches per

plant(0.06), pods per plant(1.02), pod length(0.16), seeds per pod(0.18), hundred seed weight were controlled by one group of effective factors. On the other hand, days to flowering (2.25) were controlled by two groups of effective factors. While, seed yield per plant (4.12) appear to be controlled by a mean of five pair of effective factors

In cross, IT-38956 $\times$ KBC-2, at least one group of effective factors appear to control the inheritance of days to flowering (1.40), plant height (1.20), days to maturity (0.05), number of primary branches per plant (1.0), number of secondary branches per plant (1.00), and hundred seed weight (1.44). Whereas, pods per plant (3.12), pod length (3.46) and seeds per pod (3.77) appear to be under the control of two effective factors. Contrary to this, four groups of genes for seed yield per plant (4.45) appear to be present in the genetic control of the respective traits.

In the cross KBC-2 $\times$ CP-12, at least one group of effective factors appear to control the inheritance of days to first flowering (0.02), plant height (1.29), Days to maturity (1.29), number of primary branches per plant(0.01), pods per plant (0.36) and hundred seed weight (0.21) appear to be controlled by one number of factor. Whereas, secondary branches per plant (2.23), pod length (2.35) and seeds per pod (3.77), appear to be under the control of two effective factors. Contrary to this, five groups of genes for seed yield per plant (5.81) appear to have influence in the genetic control of the respective traits.

It can be inferred from the above results that as the complexity of trait increases (from attributing traits to yield) the number of factors governing the major traits like yield increasing arithmetically, thereby confirming the polygenic nature of the complex traits.

5.5 Potence ratio

The degree of dominance in respect of different traits computed from generation means of F_1 as well as F_2 generation in terms of Potence ratio for three crosses (Table 32) of Cowpea is discussed below.

In F_1 generation of IT-38956-1 $\times$ KBC-2, the degree of dominance in terms of potence ratio (h_1) was between zero and unity for the traits such plant height (0.18) indicating either no dominance or partial dominance in the genetic control of the traits. However, over dominance for the traits viz., days to maturity (6.11), seeds per pod (3.0) and seed yield per plant (1.81) was indicated. The characters viz., days to first flowering (-2.74), primary branches per plant (-3.42), secondary branches per plant (-5.50), pods per plant (-1.5), pod length (-0.04) and hundred seed weight (-0.93) were under partial dominance as their h_2 values were less than unity

In F_2 generation of IT-38956-1 $\times$ KC-2, the potence ration (h_2) was more than unity for characters viz., days to maturity (5.08) and pods per plant (4.74) which indicated the presence of over dominance. The characters viz., days to first flowering (-8.95), plant height (-0.65), primary branches per plant (-0.41), secondary branches per plant (-8.50), pod length (-2.16) and hundred seed weight (-2.88) were under partial dominance as their h_2 values were less than unity. The ratio was between zero and unity for remaining trait pods per plant (0.13) indicating no dominance or partial dominance in the genetic control of these traits.

In cross IT-38956-1 $\times$ CP-12, Potence ration in F_1 generation (h_1) was more than unity indicating over dominance for the traits viz., days to first flowering (1.36), primary branches per plant (4.77), secondary branches per plant (2.50), pods per plant (2.25), pod length (1.79), seeds per pod (1.20) and seed yield per plant (1.20). The characters viz., days to maturity (-4.84), plant height (-4.46) and hundred seed weight (-0.30) were under partial dominance as their h_2 values were less than unity. The degree of dominance in terms of potence ratio (h_1) was between zero and unity for hundred seed weight indicating either no dominance or partial dominance in the genetic control of the traits.

In cross IT-38956-1 $\times$ CP-12, the potence ration in F_2 generation (h_2) was less than unity indicating partial dominance for the traits viz., pods per plant (-1.90), seed yield per plant (0.82) and hundred seed weight (0.77). While, the characters such as days to first flowering (3.12), days to maturity (4.04), plant height (8.92), primary braches per

plant (4.37), secondary branches per plant (2.18), pod length (2.69) and pods per plant (3.15) showed more than unity indicating over dominance.

In cross KBC-2 $\times$ CP-12, the Potence ration in F_1 generation (h_1) was more than unity indicating over dominance for the traits viz., days to first flowering (2.87), plant height (3.45), and number of secondary branches per plant (5.0). While the ratios were unity indicating partial dominance for the traits viz., primary branches per plant (-4.04), pods per plant (-1.28), pod length (-2.75) and seed yield per plant (-1.12) characters viz., days to maturity (-5.11) plant height (-4.46) and hundred seed weight (-0.30).

In cross KBC-2 $\times$ CP-12, the potence ration in F_2 generation (h_2) was less than unity indicating partial dominance for the traits viz., days to flowering (-4.07), days to maturity (-8.16) and seed yield per plant (-2.23). While, the characters days to first plant height (8.26), primary braches per plant (1.05), secondary branches per plant (6.20), pods per plant (7.67), pod length(4.71), pods per plant(8.24) and hundred seed weight(4.04) traits were having more than unity indicating over dominance.

5.6 Comparison of nature of gene action resolved from lower and higher order statistics

Nearly all of the current quantitative genetic theories are based on first and second degree statistics. Fisher *et al.* (1932) called our attention the usefulness of third degree statistics in the study of polygenic traits. The fourth degree statistics (Kurtosis) can be applied to genetic variance component analysis, in the unbiased estimation of variance components and estimation of number of genes controlling the inheritance of a quantitative character (Robson, 1956). When nature of gene action indicated by generation mean analysis which is based on the first degree statistics compared with the nature of gene action provided by the skewness and kurtosis values, in cross IT-38956 $\times$ KBC-2 for the traits viz., days to maturity, pods per plant and seed yield per plant; in cross IT-38956 $\times$ CP-12 for the traits viz., plant height and primary braches per plant and in cross KBC-2 $\times$ CP-12 for the traits viz., days to first flowering, pod length and seeds per pod. This deviation may be attributed to the limitations of generation means as

indicated under the heading 5.3, which is purely based on the first degree statistics *i.e.*, based on mean effects and it is not reliable to greater extent.

The results obtained from the skewness and kurtosis, which are of third and fourth degree statistics and found to be more powerful than the lower order statistics like means as it is analyzed through variance approach and it suggests the method of selection to fasten the gain. When, the population shows negative skewness, the gain is faster with mild selection and less rapid with intense selection, while the reverse is true if the population shows positive skewness. Hence, the nature of gene action predicted through higher degree statistics are more authenticated than judged by the lower degree statistics, which is only indicative (Roy, 2000). However, these inferences need to be confirmed by analyzing large population and also through advanced variance analysis.

5.7 Extent of association between the physiological trait and seed yield in cowpea cross IT-38956 × KBC-2 in F₃ population

Various approaches used for the assessment of genetic variability in water use efficiency (WUE) such as gravimetry method and gas exchange method which have their own limitations. Though, gravimetry is quite accurate and integrates diurnal and seasonal variations, it is very cumbersome and time consuming and hence cannot be used for large scale screening. The gas exchange measurements are rapid but they are time instantaneous, hence estimates of water use efficiency through specific leaf area (SLA), SPAD chlorophyll meter reading (SCMR) assumes greater importance as they are suitable for rapid screening and more affordable and do not hamper the accuracy of determining the water use efficiency.

In the present study, the cowpea cross IT-38956 × KBC-2 was advanced up to F₃ generation to study the extent of variability and association of physiological characters with reference to the Specific Leaf Area (cm²/g) and SPAD chlorophyll meter readings were estimated and analyzed by statistical analysis.

Wide range of variability was present for the two physiological characters as indicted by their respective mean and variances.

The skewness and kurtosis provides insight about the nature of gene action platykurtic and positively skewed distribution explains the involvement of relatively large number of segregating genes with majority of them having decreasing effects and dominance based complementary type of interaction present in the inheritance of SLA and SCMR character in the F_3 population of the cross IT-38956 $\times$ KBC-2, reports are lacking to support these observations in cowpea.

Genetic variability parameters for the SLA and SCMR exhibited higher values of GCV and PCV, coupled with high heritability and genetic advance as percent of mean indicated the predominant role of additive gene action. Hence, these traits can be effectively used for selecting desirable segregants owing to its high heritability combined with high genetic advance.

The other parameters such as secondary branches per plant, pods per plant, pod length, and seeds per pod exhibited the higher values of PCV and GCV. Coupled with the high heritability and genetic advance indicated the additive gene action controlling these traits.

The character association was found to be significant and positively associated with the seed yield of cowpea. The association of SLA with the seed yield was negative and significant. This may be due to the higher leaf area leads to the only more vegetative growth and which will reflect on the reduced reproductive phase leads to the lesser yield. SCMR was also found to be positive and significantly correlate with the seed yield per plant, which may be due to higher chlorophyll content results in the higher seed yield.

The path analysis revealed the direct and indirect effects on the seed yield. The SLA is having high negative direct effect on the seed yield and also indirect positive contribution through the traits such as, primary branches per plant and days to maturity. The SLA which reflect in the production of higher biomass which is having the negative effect on the seed yield per plant. The production of higher biomass leads to the prolonged vegetative phase and delayed reproductive phase which leads to the lowering the seed yield.

SCMR is indicated the positive, direct and low significant effect on seed yield. The indirect positive contribution through plant height, pod length and SLA. Increase in plant height leads to increases the biomass of the plant, which resulted in higher number of pods and longer pods with more number of seeds per pod resulted in the higher seed yield. The secondary braches per plant is having a moderate negative effect for the seed yield per plant, in which the higher production of secondary leaves will leads to the lesser pods and seeds per pod leads to decrease in the seed yield per plant.

5.8 Identification of Transgressive segregants

Transgressive genotypes are identified as those genotypes, which surpassed both the parents in a desirable direction for any of the character, in segregating generations, especially in F_2 population. Combinations of favorable genes (positive alleles) from different parents and additive gene action are the main reasons for the occurrence of transgressive segregants.

In the present study for two cowpea cross IT-38956 $\times$ KBC-2 and IT-38956 $\times$ CP-14 the transgressive segregants for the seed yield has been observed, but the seed yield in the cross KBC-2 $\times$ CP-12 which does not surpass the parents.

FUTURE LINE OF WORK:

- ❖ The genetic studies may be conducted by using more number of crosses having large population size through advanced biometrical tools having variance approach.
- ❖ Physiological basis of inheritance may be confirmed by use of large population with the use of molecular markers.
- ❖ The F_3 mapping population may be advanced to develop advanced mapping populations like Recombinant Inbred Lines (RIL'S)
- ❖ Identified desirable segregants may be forwarded for further generations to identify the breeding lines for seed yield per plant.



Summary

VI SUMMARY

The present investigation was undertaken during 2008-2010 at Dry Land Agriculture Project, GKVK, UAS, Bangalore in Cowpea to study the association of physiological traits with the yield and yield attributing characters in the cross IT-38956-1 $\times$ KBC2 and to study variability parameters in F_2 generation of three crosses of Cowpea viz., IT-38956-1 $\times$ KBC-2, IT-38956-1 $\times$ CP-12 and KBC-2 $\times$ CP-12 and Generation mean analysis of the three cross of cowpea.

The summary of the finding of the present study is presented below.

1. Genetics of seed yield and yield attributing characters in the three cowpea crosses

Ten quantitative characters viz., days to first flowering, days to maturity, plant height, primary branches per plant, secondary branches per plant, pods per plant, pod length, seeds per pod, seed yield per plant and test weight were analyzed by following standard biometrical techniques.

The results showed in general, the mean and variance in respect of these 10 quantitative characters in three F_2 population viz., IT-38956-1 $\times$ KBC-2, IT-38956-1 $\times$ CP-12 and KBC-2 $\times$ CP-12 indicated wide variability for the traits such as plant height, days to maturity, pod length, seeds per pod and seed yield per plant; moderate to low variability for primary branches per plant, secondary branches per plant, pods per plant and test weight in all the crosses.

The skewness and kurtosis in three crosses of F_2 population for 10 quantitative characters studied indicated the presence of complementary type of gene interaction in the inheritance of days to first flowering, plant height, number of primary branches per plant, pod length, seeds per pod, seed yield per plant and hundred seed weight in the cross IT-38956-1 $\times$ KBC-2: for days to first flower, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, pods per plant, pod length, seeds per pod and hundred seed weight in the cross IT-38956-1 $\times$ CP-

12 and for days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, pods per plant, pod length and seeds per pod in the cross KBC-2 $\times$ CP-12. However, duplicate type of gene interaction was noticed for days to maturity, and number of secondary branches per plant in IT-38956-1 $\times$ KBC-2: for days to maturity for the cross IT-38956-1 $\times$ CP-12 and in days to first flowering and hundred seed weight in cross KBC-2 $\times$ CP-12. However, the cross IT-38956-1 $\times$ CP-12 showed absence of epistasis for pod length.

Higher per cent of GCV and PCV were observed for traits such as plant height, secondary branches per plant, pods per plant, seeds per pod and seed yield per plant in all the crosses. While, in all the crosses, all the characters except primary branches per plant and hundred seed weight all these characters exhibited high heritability coupled with medium to low genetic advance as per cent of mean indicated the predominance of non additive gene action in the genetic control of these traits.

Correlation studies in F_2 generation in all the three crosses revealed high significant positive correlation of seed yield per plant with secondary branches per plant, pods per plant, pod length and seeds per pod, is directly give more importance for these traits in selection schemes.

Path analysis in F_2 generation of three crosses indicated maximum positive direct effect of pod length, secondary branches per plant and seeds per pod on seed yield per plant.

The five generations means of the three cross indicated that, the F_2 means were lesser than the F_1 means and mid parental values in respect of all the traits except days to first flowering, days to maturity, pod length, number of seeds per pod and test weight indicating high degree of inbreeding depression. These results indicated predominant role of non-additive gene action which includes both dominance as well as epistatic interactions.

The F_1 means exceeded mid parental and better parent values in majority of the characters except for number of pods per plant, pod length and number of seeds per plant indicated the presence of both partial and over dominance.

The scaling tests as well as Chi Square test from joint scaling test were highly significant in all the three cross for all the ten characters, indicated the inadequacy of simple additive-dominance model.

The five generation mean analysis carried out for ten quantitative characters in IT-38956-1 $\times$ KBC-2, IT-38956-1 $\times$ CP-12 and KBC-2 $\times$ CP-12 crosses indicated significance of non additive or epistasis gene effects. However, all the traits except primary branches per plant, secondary branches per plant and number of seeds per pod in cross-I (IT-38956-1 $\times$ KBC-2) showed the additive gene action.

Based on the same signs and opposite signs of $[\hat{h}]$ and $[\hat{l}]$, the action of complementary type (same sign) of gene interaction in the inheritance of trait was observed for seed yield per plant, while, duplicate type (opposite sign) of gene interaction in the inheritance of traits was observed for days to first flowering, days to maturity, plant height, number of pods per plant and test weight in cross-I (IT-38956-1 $\times$ KBC-2). The action of complementary type (same sign) of gene interaction in the inheritance of trait was observed for plant height, primary branches per plant and seed yield per plant, while duplicate type (opposite sign) of gene interaction in the inheritance of trait was observed for days to first flowering, days to maturity, secondary branches per plant, number of pods per plant, pod length and number of seeds per pod in cross-II (IT-38956-1 $\times$ CP-12). The action of complementary type (same sign) of gene interaction in the inheritance of trait was observed for number of pods per plant, pod length, number of seeds per pod and hundred seed weight; while duplicate type (opposite sign) of gene interaction in the inheritance of trait was observed for days to first flowering, days to maturity, plant height, primary branches per plant, secondary number of pods per plant and seed yield per plant in cross-III (KBC-2 $\times$ CP-12).

Minimum number of effective factors influencing a trait in F₂ population of these three crosses of cowpea estimated in respect of 10 quantitative characters ranged from one to five pairs.

Potence ratio for three crosses of cowpea in F₁ as well as F₂ generation revealed that, presence of over-dominance and partial dominance for almost all the traits in F₁ generation of all the crosses. While, in majority of the traits were partially dominant in F₂ generation of cross-I (IT-38956-1 × KBC-2), Cross-II (IT-38956-1 × CP-12) and Cross-III (KBC-2 × CP-12).

High heterosis coupled with low inbreeding depression in respect of secondary branches per plant, number of pods per plant, number of seeds per pod and seed yield indicated additive and/or additive × additive variance which is fixable in segregating generations. However, the remaining characters viz., days to first flowering, days to maturity, plant height, primary branches per plant, exhibited high magnitude of inbreeding depression accompanied by high better parent heterosis indicated the operation of non-additive gene action including dominance and additive × additive or dominance × dominance gene interactions which can't be fixed in segregating population.

2. Influence of Physiological traits on seed yield and yield attributing characters in cowpea cross IT-38956-1 × KBC-2

Observations were recorded on twelve quantitative characters viz., days to first flowering, days to maturity, plant height, primary branches per plant, secondary branches per plant, pods per plant, pod length, seeds per pod, SLA , SCMR, seed yield per plant and test weight were analyzed following standard biometrical techniques. More emphasis were given for the SLA and SCMR traits.

The physiological traits associated with the drought tolerance such as Specific leaf Area (SLA) and SCMR readings were considered for the study in the F₃ generation of the cross IT-38956-1 × KBC-2. In general both the characters are exhibited the high GCV and PCV coupled with the high heritability and genetic advance as indicated by per cent of mean indicated the predominance of additive gene action controlling the traits.

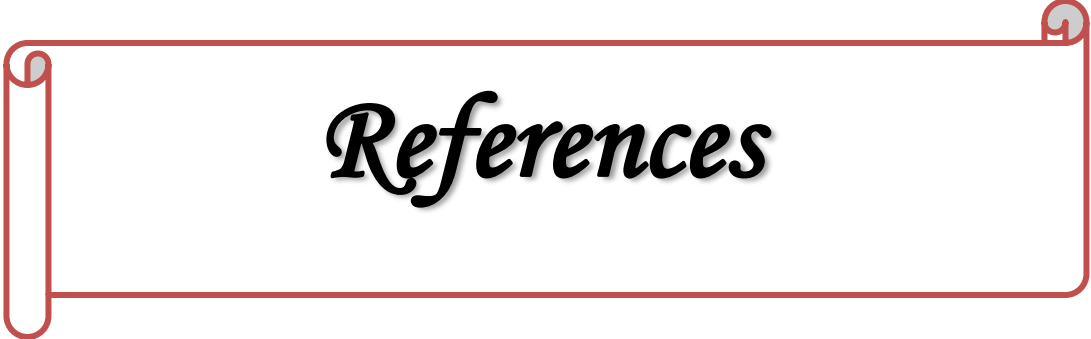
The skewness and kurtosis indicated the involvement of large number of dominant genes having decreasing effects and dominance based complementary interaction exist in the inheritance of this trait.

These traits were positive and significantly correlated with the seed yield per plant which is confirmed by the direct and indirect effects of these characters on seed yield per plant.

The present experiment in cowpea indicated the predominant role of non additive gene action, over dominance and dominant based complementary gene actions controlling the inheritance of the maximum characters. The characters such as, pods per plant, pod length and seeds per pod are having the direct relationship with seed yield of the plant so the selection with these characters for the next segregation generation will help full to improve the seed yield of the plant. The physiological parameters such as

SLA and SCMR has been found to be weak association with the seed yield indicated that independent genetic control for the expression of seed yield per plant, such strong inverse relationship is advantageous for genetic enhancement of cowpea for drought tolerance through this characters.

In all the crosses, superior segregants for seed yield per plants were identified in the F_2 generation, which can be advanced to further generations to study and select for credibility.



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* Originals are not seen