## Combination breeding for high protein cowpea

(Vigna unguiculata L. Walp)

By Sarath P.S. 2013-11-132



Department of Plant Breeding and Genetics
COLLEGE OF HORTICULTURE
KERALA AGRICULTURAL UNIVERSITY
VELLANIKKARA, THRISSUR – 680 656
KERALA, INDIA
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### **THESIS**

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### **DECLARATION**

I hereby declare that the thesis entitled "COMBINATION BREEDING FOR HIGH PROTEIN COWPEA (*Vigna unguiculata* L. Walp)" is a bonafide record of research done by me during the course of study and the thesis has not previously formed the basis for the award of any degree, diploma, fellowship or other similar title, of any other University or Society.

 Vellanikkara
 Sarath P.S

 22-09- 2015
 2013-11-132

### CERTIFICATE

Certified that this thesis entitled "COMBINATION BREEDING FOR HIGH PROTEIN COWPEA (*Vigna unguiculata* L. Walp)" is a record of research work done independently by Sarath P.S (2013-11-132) under my guidance and supervision and that it has not previously formed the basis for the award of any degree, diploma, fellowship or associateship to him.

Vellanikkara

22-09-2015

Dr. Jiji Joseph

Associate Professor and

Chairperson (Advisory Committee)

Department of Plant Breeding & Genetics

College of Horticulture, KAU

Vellanikkara, Thrissur

### **CERTIFICATE**

We, the undersigned members of the Advisory committee of **Mr. Sarath P. S** (2013-11-132), a candidate for the degree of **Master of Science in Agriculture** agree that the thesis entitled "Combination breeding for high protein cowpea (*Vigna unguiculata L. Walp*)" is submitted by him in partial fulfillment of the requirement for the degree.

Dr. Jiji Joseph
Associate Professor
Dept. of Plant Breeding and Genetics
College of Horticulture, KAU, Vellanikkara, Thrissur
(Chairman)

Dr. C. R. Elsy Professor and Head Dept. of Plant Breeding and Genetics College of Horticulture Vellanikkara, Thrissur (Member) Dr. Salikutty Joseph Professor Department of Olericulture College of Horticulture Vellanikkara, Thrissur (Member)

Dr. Rose Mary Francies Associate Professor Seed Technology Unit College of Horticulture Vellanikkara, Thrissur (Member) **External Examiner:** 

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## Introduction

### 1. INTRODUCTION

Cowpea (*Vigna unguiculata* L .Walp) is one of the most important legume crops in the world and is a major food crop in Africa, Latin America and India because of its high protein content (Kareem and Taiwan, 2007). Production of this crop was estimated to be 11.8 million ha with 5.4 million tons of dried grains (FAO, 2007). Cowpea has the unique ability to fix nitrogen even in poor soil. It is also shade tolerant and compatible as an intercrop in a number of cereals and root crops, as well as with cotton, sugarcane and several other crops.

Coupled with these attributes, its quick growth and rapid ground coverage have made cowpea an essential component of sustainable agriculture in marginal lands and regions of the tropics (Singh *et al.*, 1997). In the cultivated cowpea, four cultivated groups have been identified, (1) *Vigna unguiculata* grain type, which is the major group, (2) *Vigna biflora* or *catjang*, which is differentiated mainly by its small erect pods and is grown in Southeast Asia, (3) *Vigna sesquipedalis*, the yard long bean, which is differentiated mainly by its very long pods and growth habit and is grown for its fresh pods in Asia and (4) *Vigna textilis*, which was grown in West Africa for the textile fibres obtained from its long peduncles (Baudoin and Marechal, 1985).

Exploitation of genetic potential of wild and close relatives of cowpea, enhancing cowpea productivity had not been well documented (Singh *et al.*, 1997). The varietal requirements in terms of plant type, seed type, green pod colour, maturity and use are extremely diverse from region to region, making breeding programmes more complex than any other crop (Davis *et al.*, 2003). The seed colour preference and use pattern differ from region to region. Maturity, growth habit and photosensitivity requirements depend upon the cropping system. Thus no single variety can be suitable for all conditions.

Protein deficiency has been reported as one of the main sources of nutritional problems in the developing world (FAO, 2007). According to Ghaly *et* 

al. (2010), two debilitating diseases, marasmus and kwashiorkor occur in children who suffer protein malnutrition. About one billion people are still reported to be suffering from protein deficiency and malnutrition worldwide (FAO, 2007).

This report also revealed that leafy vegetable protein is about half the vegetable protein present in the human diet and probably amounts to more of the world total protein than do fish. In addition, only a minute percentage (8-20%) of plant protein from animal's consumption can be recovered as protein supplement for human nutrition. Thus, more efficient ways of utilizing plant protein must be found. Interestingly, several studies have revealed nutritional differences among genotypes of different species of cowpea. Identifying high yielding varieties of cowpea with high protein content will not only contribute to food security and alleviate poverty but could also contribute to the alleviation of protein deficiencies.

Earlier research showed that little attention has been made on the genetic improvement of cowpea for improved protein content. Hence, a breeding programme to develop cowpea with high protein content will be a fruitful venture. For formulation of a breeding programme, the knowledge with regard to heterosis, combining ability, genetic diversity and gene action is essential. The state and national programme on the improvement of pulses emphasize the urgency of generating variability for high genetic potential.

To achieve a major breakthrough in the genetic improvement of cowpea, emphasis should be laid on the varietal improvement with definite objective of improving yield and the nutritional quality *viz.*, protein content. Hence, present investigation in *Vigna unguiculata* L .Walp has been done with the objective of

• Combination breeding to transfer high protein trait to high yielding genotypes in cowpea

# Review of literature

### 2. REVIEW OF LITERATURE

Cowpea (*Vigna unguiculata* L. Walp) is an ancient grain legume crop widely grown in Africa, Asia and South America. Cowpea is used as forage and vegetable crop mainly in the tropics. Itis a source of protein, a vital nutrient for healthy growth in humans and livestock. Its leaves, green pods and grain are consumed as a dietary source of protein (Ghaly *et al.*, 2012). Grain legumes have been described as one of the most important crops in many countries providing about one-quarter of the world's dietary protein. They are essential source of protein for about 700 million people particularly in the developing countries of South America, Africa and Asia, where plants provide 83 per cent of total protein in the average diet (Nagl *et al.*, 2013).

The cowpea seed contains about 23 per cent protein and 57 per cent carbohydrate, while the leaves contain between 27 to 34 per cent protein. The leaves and seeds also serve as sources of high protein feed and fodder for livestock (Tarawali *et al.*, 2010). Because of its high protein, vitamins and minerals content, cowpea plays an important role in both human and animal nutrition (Mishra *et al.*, 2009). In most of the developing countries, the cost of animal protein is too high and is unaffordable to most families (Ghaly *et al.*, 2010). Hence, there is an urgent need arises to increase current agricultural practices in marginal lands in order to bring a lasting solution to the menace of protein deficiency and world food shortage. The protein content of cowpea ranges from 18 to 40 per cent. This clearly indicates that there is wide scope for improvement of protein content in cowpea.

Success in breeding for cowpea depends on the genetic variability and method of selection and genetic potential of the parents involved in the breeding programme. Important findings, which are relevant to the objectives of the present study in cowpea, are briefly reviewed under the following headings.

- 2.1 Studies on variability in cowpea
- 2.2 Heritability and genetic advance in cowpea
- 2.3 Combining ability in cowpea
- 2.4 Heterosis in cowpea

### 2.1 Studies on variability

Range is the difference between high and low values of observation in a population. It is the simplest but a crude measure of variability. It is commonly used as a measure of variability in plant breeding population and its computation is very easy. Enhancing variability is one of the initial steps in breeding programme. This become essential in self pollinated crops like cowpea, where the variability is low.

Lartey and Ofori, (2000) collected fourty five cowpea accessions randomly from cowpea germplasm from four major cowpea producing regions of Ghana. They observed that variability within regions was not significant, but there were significant differences among the regions for all the characters. The accessions from northern region were early to flower and harvest with short life while, those from upper east region were the last to flower and harvest.

Nwofia *et al.* (2012) observed highly significant variations between cowpea genotypes for plant height, number of branches, pods per plant, pod length, seeds per pod, dry matter and yield based on their work with twelve cowpea genotypes for two years.

Inuwa *et al.* (2013) observed wide variability in cow pea genotypes for duration of vegetative and reproductive phase, seeds per pod, number of pods per plant, weight of pod, 100 seed weight and yield.

Sivakumar *et al.* (2013) observed wide range of variation for many of the traits in cowpea. The plant height varied from 58.9 cm (VU 24) to 182.97 cm (VU 22), primary branches 5.22 (VU 19 and VU 21) to 7.44 (VU 11), days to first flowering from 31.29 (VU 6) to 38.40 (VU14), days to first harvest from 40.69 (VU 24) to 47.71 (VU 14), pod length 12.40 cm (VU 24) to 32.53 cm (VU 20), pod girth from 1.83 cm (VU 24) to 2.93 cm (VU 1), pod weight from 4.83 g (VU 24) to 12.44 g (VU 20), pods per plant from 23.35 (VU 22) to 70.30 (VU 8) and yield per plant from 150.86 g (VU 15) to 310.41 g (VU 6).

Shanko *et al.* (2014) observed significant difference between genotypes for days to flowering and maturity, plant height, number of primary and secondary branches, number of pods per plant, seeds per pod, 100 seed weight and yield per plant based on their study of 49 genotypes of cowpea.

Chavan *et al.* (1989) reported high level of variability in cowpea genotypes. They observed that the protein content in cowpea was ranging between 18.30 to 35.00 percent. Larger seeds exhibited less protein as compared to the smaller seeds (Kachare, 1986). The protein content in twenty six strains of cowpea showing variation in seed coat colour were reported by Sharma *et al.* (2013). They observed that genotypes with white and brown hilum had a protein per cent of 20.2 to 25.03, while buff coloured genotypes had protein content ranging from 17.24 to 24.15 per cent. Protein content of 19.43 to 25.55 per cent was observed in brown coloured genotypes and white coloured genotypes had 20.65 to 22.58 per cent protein.

Guptha, (2010) reported that protein content was ranging from 23.44 to 28.23 per cent with an average value of 25.82 per cent in wild cowpea genotypes. In cultivated varieties, the seed protein content ranged from 22.34 per cent to 25.54 per cent with an average value of 23.59 per cent.

## 2.1.1 Components of genetic variation

Variability in a population is measured by phenotypic and genotypic coefficient of variability (PCV and GCV). Assessment of PCV and GCV of the material under study is essential for a sound and successful plant breeding programme. The relevant literature pertaining to the variability studies with respect to cowpea is documented below.

Sl no	Character	PCV	GCV	Reference
		High	High	Ushakumar i <i>et al.</i> ,2010
				Chaudhariet al.,2013
1	Plant height	Moderate	Moderate	Borah and Khan, 2003
				Chauhan, 2008
		Low	Low	Sobha and Vahab, 2000
				Mannivannan and Sekhar, 2005
		High	Moderate	Rajaravindran and Vijedradas, 2000
	Days to 50% flowering		Moderate	Patel <i>et al.</i> , 2007
		Moderate	Moderate	Tyagi <i>et al.</i> , 2000
2				Chaudhari et al., 2013
2				Hazra <i>et al.</i> , 2007
		Low	Low	Sivakumar et al., 2013
				Sivakumai et al., 2013
		High	High	Yadav <i>et al.</i> , 2005
				Indarsingh et al., 2007
3	Days to maturity	High	_	
		IIIgii	Low	Rewaleet al., 1995

	High	High	Mannivannan and Sekhar, 2005
amber of anches per	Moderate	Moderate	Indarsingh <i>et al.</i> , 2007 Chaudhari <i>et al.</i> ,2013
	Low	Low	Sharma et al., 2013
	High	High	Bhavesh et al., 2012
	Moderate	Moderate	Indarsingh et al., 2007
d lenth			Rewale et al., 1995
	Low	Low	Anbuselvam et al., 2010
1 6	High	Moderate	Selvakumar, 2014
	TT' 1	TT' 1	Sharma et al., 2013
ca per pou	High	High	Chaudhari et al., 2013
	Moderate	Moderate	Mahalakshmi, 2007
ındred seed			Ushakumari <i>et al.</i> ,2010
eight	Low	Low	Mannivannan and Sekhar, 2005
	High	High	Kukar and Sagwan, 2005
			Anbuselvam et al., 2010
	Moderate	Moderate	Selvalakshmi, 2000
d yield			Satishkumar, 2010
	Low	Low	Raju <i>et al.</i> , 2008 Chaudhari <i>et al.</i> , 2013
	nches per nt delenth d	Inches per nt Low High Moderate I lenth Low High Moderate I lenth Low High Moderate I lenth Low High Moderate I lenth Low High Moderate I lenth Low Moderate I lenth Low High Moderate I lenth Low Mod	mches per nt Low Low High High Moderate  How Low High Moderate Low Low High Moderate  High Moderate  High Moderate  High High Moderate  High High  High Moderate  Moderate  Moderate  Moderate  Moderate  Moderate  High High  High  High  High  High  High  High  High  High  High  High  High  High

		High	High	Guptha, 2010
				Satishkumar, 2010
9	Pod weight	Low	Low	Malarvizhi, 2004
				Sharma et al., 2013
		High	High	Sobha and Vahab, 2000
				Karpe et al., 2006
		Moderate	Moderate	Boukar et al., 2011
	Seed yield			Dalsaniya et al., 2013
10	per plant			
				Indonsingly of all 2007
		Low	Low	Indarsingh et al., 2007
				Mishra et al., 2009
		TT' 1	TT: 1	M.1. :1: 2004
		High	High	Malarvizhi, 2004
				Ushakumari <i>et al.</i> ,2010
	Protein	Moderate	Moderate	Guptha, 2010
11	content			Bhavesh et al., 2012
		Low	Low	Rewale et al., 1995
				Indarsingh et al., 2007

## 2.2 Heritabiity and genetic advance

The degree to which the variability of a quantitative trait may be transmitted to the progeny is referred to as heritability. Lush (1949) proposed heritability in narrow sense, as the ratio of additive variance to total variance. Burton and Devane (1953) proposed the expected gain from selection as a product of heritability, phenotypic standard deviation and selection differential. According to Johnson *et al.* (1955) high heritability and

high genetic gain are more useful than high heritability alone in predicting the performance of the progenies of the selected lines.

Hanson *et al.*(1956) defined heritability in broad sense as the ratio of genotypic variance to total variance in non-segregating populations. The genetic advance would be high, if the heritability was due to additive gene action (Panse and Khargonkar, 1957). Though heritability estimates represent the relative genetic strength of character and indicate the efficiency of selection system, still their scope is restricted as they are prone to changes with change in environments, materials etc., (Falconer, 1981). Heritability was classified as suggested by Johnson *et al.* (1955) in to low (0-30%), moderate (30.1-60%) and high (>60%) and the Genetic gain was categorized as suggested by Johnson *et al.* (1955) as low (0-10%), moderate (10.1-20%) and high (>20%).

The heritability estimates recorded and reported by various workers for different characters are tabulated hereunder.

Sl	Character		Genetic	
no		Heritability	advance as	References
			percentage of	
			mean	
		High	High	Borah and Khan, 2003
1	Plant height			Ushakumari <i>et al.</i> ,2010
		Moderate	High	Mannivannan and Sekhar, 2005
		Low	Low	Guptha, 2010
				Mishra <i>et al.</i> , 2009
		*** 1	TT' 1	
		High	High	Karpe <i>et al.</i> , 2006
2	Days to 50%			Sharma et al., 2013
	flowering	Low	Low	Kumar and Sagwan, 2005
				Anbuselvamet al., 2010

		High	High	Tyogi et al. 2000
3	N. 1 2			Tyagi <i>et al.</i> , 2000
3	Number of .	Moderate	Moderate	Guptha, 2010
	primary	Woderate	Wioderate	Rangaiah and Manadevu, 2001
	branches per plant	Low	Low	Chauhan, 2008
	piant	Low	LOW	Neema et al., 1995
				Indarsingh et al., 2007
		High	High	Patel et al., 2007
4	Days to	High	Low	Kumar and Sagwan, 2005
	maturity			Anbuselvam et al., 2010
				Borah and Khan, 2003
5	Pod length	High	High	Indarsingh et al., 2007
		High	High	Mannivannan and Sekhar,
6	Number of			2005
	pods per plant	Moderate	Moderate	Bhavesh et al., 2012
				Ponmariammal and
		Low	Low	Vijendradas, 2000
				Indarsingh et al., 2007
				Singh et al., 2009
		High	High	Borah and Khan,2003
7	Hundred seed			Kumar and Sagwan, 2005
	weight	Moderate	Moderate	Chauhan, 2008
				Sawant, 1995
		Low	Low	
				Mishra <i>et al.</i> , 2009

		High	High	Yadav et al., 2005
				Indarsingh et al., 2007
8	Pod yield	Moderate	Moderate	Chauhan., 2008
				Gupta, 2010
		Low	Low	Selvakumar et al., 2014
				Chauhan., 2008
9	Pod weight	High	High	Gupta, 2010
		Low	Low	Patel et al., 2007
10	Seed yield per	High	High	Tyagi et al., 2000
	plant			Yadav <i>et al.</i> , 2005
		Moderate	Moderate	Indarsingh et al., 2007
				Anbuselvam et al., 2010
		Low	Low	Mishra et al., 2009
				Selvakumar, 2014
		High	High	Kumar and Sagwan, 2005
				Anbuselvamet al., 2010
11	Protein content	Moderate	Moderate	Bhavesh et al., 2012
				Shanko <i>et al.</i> , 2014
		Low	Low	Kukar and Sagwan, 2005
				Nwofiaet al., 2012

### 2.3 Combining ability and gene action

The ability to accurately predict the parental combinations that produce superior hybrids is crucial to the success of any breeding programme. The combining ability analysis gives useful information regarding selection of parents in terms of the performance of their hybrids. Further, it serves as a powerful tool to elucidate the nature and magnitude of various type of gene action involved in the expression of quantitative traits (Dhillon, 1975). The concept of combining ability in terms of genetic variation was first given by Sprague an Tatum (1942) using single crosses in maize. They defined the term general combining ability to indicate the performance of a line or population in several hybrid combinations and specific combining ability (sca) was used to designate the dose effects in certain combinations, which significantly departed from what would be expected on the basis of the average performance of the lines involved. They attributed general combining ability to additive gene effect and specific combining ability to dominance and epistatic interactions.

Henderson, (1952) defined specific combining ability as the deviation of the average of indefinitely large number of progenies of two individuals or lines from the values which would be expected on the basis of the known *gca* of the two individuals or lines and the maternal ability of the female parent. Sprague and Federex, (1952) and Rojas and Spragu, (1952) found that the general combining ability involved both additive effects as well additive x additive interactions. This view was later confirmed by Carnalam *et al.*(I960).High *gca* effects were related to additive gene action and additive x additive interaction which represented fixable genetic components of variation (Griffing, 1956a, 1956b). Kempthorne, (1957) precisely defined the general combining ability and the specific combining ability in terms of covariance of half sibs and full sibs in random mating population.

An attempt was made to assess the combining ability of 12 hybrids along with parents generated in Line x Tester model by Thiyagarajan *et al.* (1993).

Based on the values of variance due to GCA and SCA they reported that gene action was predominantly non-additive for days to 50 percent flowering, days to maturity, plant height, pod length, seeds per pod, 100-grain weight and yield per plant and primarily additive for primary branches per plant and pods per plant. The genotypes Co4, C87, C152 and CoVu4 were good general combiners for a number of traits. The crosses Co3  $\times$  C152, Co3  $\times$  CoVu4, Co4  $\times$  C152, V87  $\times$  C152 and KC199  $\times$  KC195 were observed to have higher SCA effects for some of the yield components.

Sawarkar *et al.* (1999) conducted a study of combining ability on twenty one hybrids produced by diallel mating without reciprocals in cowpea. Preponderance of additive type of gene action was observed for all the characters. The best genotype on the basis of general combining ability (gca) effects and *per se* performance for pod yield and its contributing characters was Punjab-263 followed by Arka Garima. Similarly the best hybrid on the basis of specific combining ability (sca) effect and *per se* performance for pod yield was Punjab-263 × Arka Garima, followed by Punjab-263 × Gujarat-1 and GC-82-7 × Arka Garima.

Ten cowpea lines (KBC 2, GC 3, CAUTFTC 27, HCS 91, V 240, V322, V 381, V 419, V 575 and V585) and 3 testers (CO 2, CO 4 and CO 6) were crossed in a line × tester design by Bastian *et al.* (2000) .The variance for general combining ability and specific combining ability showed that gene action was predominantly non-additive for all 12 characters studied. Genotypes V 575, V 381, V 585 and CO 6 were found to be good general combiners. The cross V 575 × CO 6 had higher specific combining ability effects for most of the characters.

Line x tester analysis performed on thirty F<sub>1</sub>'s using ten lines and three testers by Pal *et al.* (2002). Results showed that NDCP-13, Red Seeded, Kala Zamala and Pusa Komal were good general combiners for days to 50% flowering, while NDCP-13, Red Seeded, RCV-7 and Pusa Komal were good general combiners for days to first green pod picking.

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Patel *et al.* (2007) studied 32 crosses from four lines and eight testers. Based on gca performance among femal linesPusaPhalguni was found to be good general combiner followed by GC-4, whereas among the male lines, CPD-19 was found superior combiner. The study of sca effects has shown that crosses with one good and one poor, average or good general combiners and even poor and poor general combining parents would produce hybrids with good specific combinations.

An attempt was made to assess the combining ability of four lines (TC 2000-1, TC-2000-2, TC 2000-3 and TC-2000-4) and six elite cowpea varieties (GC-2, GC-3, GC-4, Pus Phalguni, RC-19 and V-240) as testers in a line × tester fashion by Mishra *et al.* (2009). All the characters had significant differences except branches/plant in testers among lines and testers. Among the lines TC2000-4 proved the good general combiner for earliness, maturity, pods/plant, pod length, 100-seed and seed yield. Non-additive effects were relatively more important for seed yield and most of its components.

Kadam *et al.* (2013) conducted an experiment in cowpea to study the combining ability in vegetable cowpea for green pod yield and its component characters. Magnitude of general combining ability (gca) variances was smaller than the specific combining ability (sca) variances for all the traits indicating the preponderance of non-additive gene effects for all the characters. General combining ability effects revealed that the five parents *viz.*, GC-0203, GC-0502, Subhra, GC-4 and Anand Cowpea-1 were the good general combiners for green pod yield per plant. The same genotypes had good general combining ability effects for the yield attributes like pods per plant, seeds per pod and 100-seed weight. Specific combining ability revealed that three top yielding hybrids *viz.*, GC-0203 × Anand Cowpea-1, Subhra × GC-4 and GC-0203 × PusaKomal expressed significant sca effects for green pod yield and days to maturity and test weight.

Six lines (ICP-26, ICP-38, ICP-42, ICP-45, ICP-49 and ICP-54) and four testers (Pusa Komal, Arka Garima, Indira Hari and Khalleshwari) were crossed by Sharma and Mehta, (2014) for protein content and green pod yield. ICP-26 and Khalleshwari were best general combiners and ICP-38 × Arka Garima and ICP-54 × Khalleshwari were identified as best specific combiner. The ratio of GCA variance to SCA variance was found more than unity, which indicated the preponderance of additive gene action for protein content in cowpea.

Selvakumar *et al.* (2014) crossed six lines and five testers in L × T fashion and 30 hybrids were synthesized. Genotypes GC 3, Co 6, ACM 05-07, RC 101, Co(CP)7, and ACM 05-02 belonging to *Vigna unguiculata* were used as lines. Vellayani Local, Ettumanoor Local, Vyjayanthi and Vellayani Jyothika belonging to *Vigna unguiculata* spp. *sesquipedalis* and VBN-belonging to *Vigna unguiculata* were used as testers. The result indicated the presence of both additive and non-additive genetic components for traits yield per plant, seeds per pod, test weight, pod weight, days to first flowering, days to first harvest and days to last harvest. Based on the general combing ability, the parents GC 3, RC 101, Vyjayanthi and Vellayani Jyothika were selected as good combiners. The most promising specific combiners for yield and yield components were GC 3 × Vellayani local, GC 3 × Vellayani Jyothika, ACM 05-07 × VBN 2, ACM 05-07 × Vyjayanthi, RC 101 × Vellayani Jyothika and ACM 05-02 × Vyjayanthi.

The estimates of gene action/ relevant literature reported by different authors about cowpea are presented below.

Sl no	Character	Report on gene action	References
1	Plant height	Additive  Non-additive	Kumar and Sagwan, 2005 Chaudhari <i>et al.</i> , 2013
		Additive and non-additive	Indarsingh <i>et al.</i> , 2007 Selvakumar <i>et al.</i> , 2014 Selvalakshmi, 2000 Satish, 2010
2	Days to 50% flowering	Additive  Predominance of non- additive genetic variance  Non-additive	Raju <i>et al.</i> , 2008 Ushakumari <i>et al.</i> ,2010 Thiyagarajan <i>et al.</i> , 1995 Karpe <i>et al.</i> , 2006
		Non-additive	Raju <i>et al.</i> , 2008 Mishra <i>et al.</i> , 2009
3	Days to maturity	Additive  Non-additive	Rajkumar, 2005  Bhavesh et al., 2012  Boukar et al., 2011  Shanko et al., 2014
4	Number of primary branches per plant	Additive and non-additive  Non additive	Kumar and Sagwan, 2005 Mishra et al., 2009 Raju et al., 2008 Sharma et al., 2013

5	Pod length	Predominance of non-additive  Non-additive	Selvalashmi, 2000 Raju <i>et al.</i> , 2008 Satishkumar, 2010 Bhavesh <i>et al.</i> , 2012
6	Number of pods per plant	Additive  Non-additive	Bushana et al., 2004 Kumar and Sagwan, 2005 Boukar et al., 2011 Inuwa et al., 2013
7	100 seed weight	Additive  Additive and non- additive	Indarsingh et al., 2007 Mishra et al., 2009 Tyagi et al., 2000 Chaudhari et al., 2013
8	Pod yield per pant	Additive  Non-additive	Kumar and Sagwan, 2005 Satish, 2010 Rangaiah and Manadevu, 2001 Karpe et al., 2006
9	Pod weight	Additive  Predominance of non-additive	Mannivannan and Sekhar, 2005 Boukar et al., 2011 Raju et al., 2008 Bhavesh et al., 2012

		Additive gene effect	Karpe <i>et al.</i> , 2006 Patel <i>et al.</i> , 2007
10	Seed yield per plant	Non -additive	Kumar, 2005
			Guptha, 2010
		Additive and non-additive	Mishra <i>et al.</i> , 2009 Sharma <i>et al.</i> , 2013
		Additive	Ushakumari <i>et al.</i> , 2010
11	Seed protein content		Guptha, 2010
		Predominance of non- additive genetic variance	Inuwa et al., 2013
		C	Dalsaniya et al., 2013
		Non -additive	Satish, 2005
			Mahalakshmi, 2007

#### 2.4 Heterosis

Heterosis conventionally refers to the increased or decreased vigour of F1 over the mid parental value. Fonseca and Patterson, (1968) coined the new term heterobeltiosis denote the heterosis over the better parent value. Information on the magnitude of heterosis will be useful from standpoint of breeding methodology.

Notwithstanding its wide occurrence, heterosis is not manifested with same intensity in all the crop species and for all the characters. It is relatively more pronounced for characters related to fitness. A large number of crosspollinating species show heterosis, of course with varying degree but its magnitude is relatively less in self pollinated crops. Mather, (1973) attributed this differential expression of heterosis among crops to the type of genic balance that a crop has acquired during the process of its evolution.

Several workers had demonstrated the existence of varying degrees of heterosis for yield and other traits in green legumes. The presence of heterosis indicates the ability of the parents to combine well in a hybridization programme. For varietal breeding programmes, more knowledge of the extent of heterosis of no-use and so it is necessary to understand the cause of heterosis in F1. Higher expression of F1 are due to non-additive (non-fixable) type of gene action. Thus combining ability helps in identifying desirable cross combination.

The result on heterosis for various traits in cowpea reported by earlier workers are reviewed below

### **Estimates of heterosis**

Character	Relative	Heterobeltiosis	Author (s)
	Heterosis		
	-12.25 to 13.6	-16.32 to 10.59	Lesly, 2005
Plant height	-3.75 to 3.83	-17.79 to 3.31	Yadav et al., 2005
	-24.49 to 60.13	-34.93 to 54.63	Patel <i>et al.</i> , 2007
	22.09 to 43.13	5.6 to 20.1	Mannivannan and Sekhar, 2005
	-12.05 to 45.56	-14.49 to 86.67	Ajeigbe et al., 2008
Branch	-11.25 to 90.02	-15.49 to 14.48	Indarsingh et al., 2007
number	16.12 to 120.13	-26.74 to 70.03	Anbuselvam <i>et al.</i> , 2010
	13.93 to 30.20	-7.05 to 5.73	Rewale <i>et al.</i> , 1995
	-6.15 to 0.80	-5.82 to 1.34	Mahalakshmi, 2007
Days to flowering	-7.25 to 1.25	-3.5 to 8.24	Ushakumari <i>et</i> al.,2010
	-15.46 to -5.4	-4.5 to 7.4	Tyagi et al., 2000
	-1.15 to 4.8	3.2 to 24.35	Chaudhari et al., 2013
	-29.92 to 13.62	-30.13 to 2.96	Sharma <i>et al.</i> , 2013
Days to maturity	-2.5 to 20.93	-5.23 to 17.38	Bhavesh et al., 2012
	-6.2 to 152.93	-8.25 to 10.20	Rewale et al., 1995
	13.63 to 92.20	-14.05 to 165.13	Anbuselvam <i>et al.</i> , 2010

Pod	-20.76 to 30.02	25.76 to 22.53	Tyagi <i>et al.</i> , 2000
number	-18.76 to 64.93	-35.65 to 56.49	Kukar and Sagwan, 2005
	-40.80 to 156.43	56.75 to 175.56	Chauhan, 2008
	-2.45 to 5.32	-17.02 to 22.42	Rajaravindran and Vijedradas, 2000
Pod length	-0.32 to 3.75	-2.75 to 3.31	Patel et al., 2007
	-9.91 to 26.05	-12.03 to 15.63	Mahalakshmi, 2007
	-6.72 to 5.76	-11.13 to 3.23	Sivakumar et al., 2013
	-5.92 to 7.72	-4.62 to 8.96	Gupta, 2010
Pod weight	-2.63 to 10.93	-16.23 to 3.94	Hazra <i>et al.</i> , 2007
	-10.01 to 30.23	-4.93 to 15.63	Bushana et al., 2004
	-8.93 to 22.23	-10.13 to 6.69	Inuwa et al., 2013
	0.38 to 6.69	-6.25 to 6.79	Tyagi <i>et al.</i> , 2000
Seeds per pod	-0.82 to 3.48	-2.96 to 3.31	Singh et al., 2009
	-7.02 to 50.22	-10.05 to 23.21	Shanko <i>et al.</i> , 2014

	1.27 to 8.25	-9.25 to 5.02	Yadav et al., 2005
Test weight	1.23 to 9.23	-5.60 to 3.25	Chaudhari et al.,2013
	-19.22 to 15.63	-21.45 to 8.5	Rajkumar, 2005
	-8.23 to 2.05	-36.73 to 11.76	Karpe et al., 2006
	-1.89 to 2.45	-4.67 to 1.65	Nwofia et al., 2012
	-0.63 to 3.31	-7.25 to 2.21	Bushana et al., 2004
Protein content	-16.69 to 38.98	-18.37 to 38.68	Patel <i>et al.</i> , 2007
	-30.46 to 40.05	-28.63 to 28.64	Sivakumar et al., 2013
	-15.16 to 44.47	-26.75 to 38.13	Kukar and Sagwan, 2005
Grain yield per plant	1.77 to 35.67	-8.5 to 28.81	Anbuselvam <i>et al.</i> , 2010
	-4.20 to 26.93	-28.81 to 187.63	Indarsingh et al., 2007
	-30.41 to 48.64	-33.31 to 27.81	Mishra <i>et al.</i> , 2009
	12.39 to 64.73	-10.91 to 38.63	Karpe et al., 2006

## Materials and methods

#### 3. MATERIALS AND METHODS

The study entitled on "Combination breeding for high protein cowpea (*Vigna unguiculata* L. Walp) )" was carried out at the Department of Plant Breeding and Genetics, College of Horticulture, Vellanikkara during the period August 2014 - April 2015. The objective of the study was to transfer high protein trait to high yielding genotypes in cowpea through combination breeding. The study was undertaken in three different steps 1) Preliminary screening of the genotypes based on the seed protein content. 2) Hybridisation of the selected varieties in line x tester design 3) Evaluation of F1 hybrid along with parents. The materials used and methodologies adopted in the study are presented in this chapter.

#### 3.1 Materials

## 3.1.1 Experimental site

The field experiments were conducted at the Department of Plant Breeding and Genetics, College of Horticulture Vellanikkara, Thrissur, Kerala. The area is situated at 29<sup>o</sup> 102' North latitude and 75<sup>o</sup> 462' East longitudes at an altitude of 215.2 m above MSL. The soil of the experimental site was red loam belonging to Vellanikkara series which comes under the Order Oxisol.

#### 3.1.2 Experimental material

The materials used for the study consisted of 22 cowpea genotypes collected from TNAU Coimbatore, NBPGR Vellanikkara, KAU Thrissur and UAS Banglore. The details of the genotypes used are presented in Table 1.

## 3.2 Methods

The research programme comprised of evaluation of twenty two cowpea genotypes and selection of 10 varieties having high seed protein content followed by hybridization of six female parents (line) with four male parents in an line x tester mating design during November 2014. Then the resultant hybrids were evaluated along with parents.

Table 1. Parents used in the study

Sl.no	Varieties	Plant habit	Source	
1	Vellayani Jyothika	Trailing	KAU, Thrissur	
2	Bhagyalakshmi	Bushy	KAU, Thrissur	
3	Anaswara	Semi trailing	KAU, Thrissur	
4	Vyjayanthi	Trailing	KAU, Thrissur	
5	Lola	Trailing	KAU, Thrissur	
6	Kanakamony	Semi trailing	KAU, Thrissur	
7	Hridya	Bushy	KAU, Thrissur	
8	Kashi kanchan	Bushy	IVRI, Varanasi	
9	Sharika	Trailing	KAU, Thrissur	
10	Co-2	Bushy	TNAU, Coimbatore	
11	Co-4	Bushy	TNAU, Coimbatore	
12	Co-6	Bushy	TNAU, Coimbatore	
13	Co(cp)7	Bushy	TNAU, Coimbatore	
14	AV-5	Semi trailing	UAS, Banglore	
15	PKB-3	Semi trailing	UAS, Banglore	
16	PKB-4	Semi trailing	UAS, Banglore	
17	NBPGR 1	NBPGR 1 Bushy		

18	NBPGR2	Bushy	NBPGR., Vellanikkara
19	NBPGR3	Bushy	NBPGR., Vellanikkara
20	CP-1	Semi trailing	Local landrace
21	CP-2	Bushy	Local landrace
22	CP-3	Bushy	Local landrace

# 3.2.1 Experiment I: Evaluation of cowpea genotypes

Twenty two cowpea genotypes as presented in Table.1 were raised during August 2014. The field experiment was laid out in randomized block design with two replications. The plot size was five meter square and plants were raised at a spacing of 30 x 10 cm<sup>2</sup> for bushy type. Trailing and semi traling type were raised at a spacing of 2 x 2 m<sup>2</sup> on pandal, three plants per pit. Standard cultural and plant protection practices were followed according to package of practices recommendations: Crops by Kerala Agricultural University (KAU, 2011). The crop was harvested when the 90 per cent of the pods in the plants were dried. All the observations were recorded after harvest except days to flowering. The seed protein content of these varieties were estimated by Lowry's method and ten varieties showing high seed protein content were selected for hybridisation programme.

## 3.2.2 Observations recorded

Following biometric observations enumerated below were recorded in Experiment I. Observations were recorded on ten plants chosen at random in each entry

#### 3.2.2.1 Days to flowering

Number of days taken for the first flowering in each plot was recorded.

#### 3.2.2.2 Height of plant (cm)

Height of plant was recorded at the time of harvest from ground level to the growing point of the plant and expressed in centimeters.

## 3.2.2.3 Number of branches and pod bearing branches per plant

Number of branches and pod bearing branches per plant were recorded at time of harvest from each replication.

## 3.2.2.4 Number of pods per plant

Number of pods per plant were counted and recorded from each treatment.

## **3.2.2.5** Length of pod (cm)

Length of pod was measured using a scale and expressed in centimeter from 10 pods in all the flowering plants after harvest.

### 3.2.2.6 Number of seeds per pod

The number of seeds per pod was counted from ten pods in all the twenty two genotypes after harvesting.

## **3.2.2.7** The test weight (g)

Weight of 100 grains was taken at random from each cultures and expressed in grams.

## **3.2.2.8** Grain yield (g)

The weight of grain per plant after hulling was taken and expressed in grams.

#### 3.2.2.10 Protein content

Protein content was estimated by Lowry's method and is expressed as percentage (Sadasivam and Manickam, 1996). The procedure followed is detailed

below. 500 mg of fine powder of cowpea grain was made by pestle and mortar. Then it was homogenized in 25 ml phosphate buffer (pH – 7.4). The supernatant was collected after centrifugation. This was used as sample solution. 0.2 ml of sample solution was pipetted out into a test tube and made up to 1 ml by adding distilled water. A blank was set up with 0.1 ml distilled water. Then 5 ml of alkaline copper sulphate (50 ml of 2 per cent sodium carbonate in 0.1 N sodium hydroxide, mixed with 1 ml of 0.5 per cent copper sulfphate in 1 per cent potassium sodium tartarate) reagent was added to each tube and mixed well, incubated at room temperature for 10 minutes. Then 0.5 ml of Folin-Ciocalteau reagent was added and kept in darkness for 30 minutes. Similarly 0.2 ml to 1ml standard protein solution (0.2mg BSA/ml) was also pipetted out into test tubes and volume made up to 1ml with distilled water. Reagents were added as in the case of test tube sample to develop blue colour. Blue colour developed was read in a spectrophotometer at 660nm. A standard curve using the standard protein absorbance against concentration was plotted and from this the protein content in the sample was calculated and expressed in percentage.

#### 3.2.3 Experiment II: Hybridization Programme

The selected 10 genotypes were sown in pots during November 2014 with each variety were sown in five pots. Staggered sowing of each variety was done at weekly intervals from 10/11/2014 to 25/12/2014 to ensure synchronized flowering between male and female plants and pollen availability for hybridization. Standard cultural and plant protection practices were followed according to package of practices recommendations: Crops by Kerala Agricultural University (KAU, 2011). Hybridisation between the lines and testers were done by emasculation followed by hand pollination.

## **3.2.3.1** Crossing

The flowers were emacuated in the evening and pollinated in early morning of the following day as described by Krishnaswamy *et al.* (1945). It was observed that

anthesis occurred in the morning between 6.30 am to 7.00 am. The process of opening of corolla took 45-60 minutes. Anther mature and start dehiscing about 7-8 hours before opening of corolla. For hybridization of cowpea, emasculation can be effective if it is completed 20 hrs before the flower opening. Flower buds of lines that would likely to open in the next day were selected. The buds were grasped between the thumb and forefinger of the left hand. The point of a dissecting needle was inserted just under the standard in a slanting position along the top of the bud. The left side of the standard and the left wing petal was pushed outward. The left half of the kneel was cut open and anthers were removed without hurting the pistil. Then the standard and wing petal press gently to bring them to original position. The entire raceme was covered with a butter paper to avoid pollen contamination. The pollination was done in the next morning by collecting the open flowers from the pollen parents. The stamina column was brought out by pressing the kneel with fingers and they were rubbed against the stigma of the emasculated flowers. The crossed buds were labeled and covered. A total of twenty four cross combinations were made and the set seeds were collected separately. The cross combinations generated is detailed in Table 2

Table 2. Designation of genotypes resulting from Line x Tester mating design

Line/ Tester	AV-5 (T1)	PKB-3 (T2)	PKB-4 (T3)	Sharika (T4)
V. Jyothika (L1)	H1	H2	Н3	H4
Bhagyalakshmi (L2)	Н5	Н6	Н7	Н8
Anaswara (L3)	Н9	H10	H11	H12
Vyjayanthi (L4)	H13	H14	H15	H16
Lola (L5)	H17	H18	H19	H20
Kanakamony (L6)	H21	H22	H23	H24

# 3.2.4 Experiment III; Evaluation of F1 hybrids

The hybrids were raised along with parents during April 12 and 13. The field experiment was laid out in randomized block design. Standard cultural and plant protection practices were followed according to package of practices recommendations: Crops by Kerala Agricultural University (KAU, 2011).

The biometric observations were enumerated as in evaluation of genotypes.

# 3.3 Statistical Analysis

The data collected for all the biometrical traits were subjected to an analysis of variance suggested by Panse and Sukatme (1954).

Source	d.f.	Mean square	<b>Expected mean squares</b>
Replication	(r-1)	$\mathbf{M}_{\mathrm{r}}$	$\sigma^2 e + g. \ \sigma^2 r$
Genotype	(g-1)	$\mathbf{M}_{\mathrm{g}}$	$\sigma^2 e + r. \ \sigma^2 g$
Error	(r-1)	$\mathbf{M}_{\mathrm{e}}$	$\sigma^2$ e

Where,

 $r = number \ of \ replications$ 

g = number of genotypes

 $M_r$  = replication mean squares

 $M_{\rm g}=$  genotypes mean squares

M<sub>e</sub>= error variance

# **3.3.1** Estimation of genetic parameters:

These were estimated according to the method suggested by Lush (1949).

Genotypic variance 
$$(\sigma^2 g) = (M_g - M_e)/r$$

Phenotypic variance 
$$(\sigma^2 p) = \sigma^2 g + \sigma^2 e$$

## 3.3.1.1 Coefficient of variation

The components namely, phenotypic, genotypic and environmental variances were used for estimation of coefficient of variation at both phenotypic and genotypic levels for all the traits were computed by following the formula as suggested by Burton and De vane (1953).

# Phenotypic coefficient of variation (PCV)

$$\begin{array}{c} \sigma_p \\ PCV(\%) = ---- x \ 100 \\ \hline \overline{X} \end{array}$$

# **Genotypic coefficient of variation (GCV)**

$$GCV(\%) = ---- x 100$$

$$\overline{X}$$

Where,  $\overline{X}$  = grand mean of the trait

 $\sigma_P$  = phenotypic standard deviation

 $\sigma_{\text{g}} = \text{genotypic}$  standard deviation

The PCV and GCV were classified as suggested by Sivasubramanian and Madhavamenon (1973) into low (0-10%), moderate (10.1-20%) and high (>20%).

# Heritability (h<sup>2</sup>)

Heritability (Broad sense) for all the traits were computed by the formula suggested by Lush (1940).

$$\sigma^2 g$$

$$h^2 = ---- x \ 100$$

$$\sigma^2 p$$

Where,

h<sup>2</sup> = heritability (broad sense)

 $\sigma_{\rm g}^2$  = genotypic variance

 $\sigma_p^2$  = phenotypic variance

Heritability was classified as suggested by Johnson *et al.* (1955) in to low (0-30%), moderate (30.1-60%) and high (>60%).

## Genetic Advance (GA)

Genetic advance was estimated according to the formula given by Johnson *et al.* (1955).

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

Where,

 $h^2 = heritability$ 

 $\sigma p$  = phenotypic standard deviation

K = standardized selection differential at given intensity and it is 2.06 at 5 per cent intensity of selection.

# Genetic gain

Genetic gain = 
$$(GA / \overline{X}) \times 100$$

Where,

GA = Genetic advance

 $\overline{X}$  = General mean

Genetic gain was categorized as suggested by Johnson *et al.*, (1955) as low (0-10%), moderate (10.1-20%) and high (>20%).

# 3.3.2 Combining ability analysis

The data for all the biometrical traits were subjected to analysis of variance appropriate for line x tester design as suggested by Kempthrone (1957). The mean squares due to different sources of variation were obtained and the genetic expectations were worked out using the following analysis of variance (Nadarajan and Gunasekaran, 2008)

# 3.3.2.1 Analysis of variance for combining ability

Source	d.f. N	Mean squa	res Expected mean squares
Replication	(r-1)		
Hybrids	(lt-1)		
Lines	(1-1)	$MS_1 \sigma e^2$	+ r(Cov. FS- 2Cov.HS) + rt (Cov. HS)
Testers	(t-1)	$MS_2$	$\sigma e^2$ + r(Cov. FS- 2Cov.HS) + rl (Cov. HS)
Lines x testers	(l-1) (t-1	$MS_3$	$\sigma e^2 + r \text{ (Cov. FS} - 2\text{Cov.HS)}$
Error	(r-1) (lt-	1) MS <sub>4</sub>	$\sigma e^2$
Total	(rlt-1)	$MS_5$	

Where,

- r Number of replications
- 1 Number of lines
- t Number of testers

# Estimation of gca and sca effects

The *gca* and *sca* effects for each cross were estimated. The analysis was done in the following model (Nadarajan and Gunasekaran, 2008).

$$X_{ijk} = \mu + g_i + g_j + s_{ij} + e_{ijk}$$

Where,

X<sub>ijk</sub> - Value of the ijk<sup>th</sup> observation

μ - Population mean

g<sub>i</sub> - gca effect of the i<sup>th</sup> line Italics

 $g_j$  - gca effect of the  $j^{th}$  tester

sij - sca effect of the ij<sup>th</sup> hybrid

eijk- error effect associated with ijkth observation

1 - number of lines

i - number of testers

k - number of replications

The individual effects of *gca* and *sca* were obtained from the two way table of lines versus testers in which each figure was a total over replications as follows

$$\begin{split} \mu &= x/rlt \\ g^{}_i &= x_i/rt - x../rlt \\ g^{}_j &= x_j/rl - x../rlt \\ s^{}_i &= x_{ii}/r - x_i/rt - x_i/rl + x../rlt \end{split}$$

The standard errors pertaining to gca and sca effects were calculated from the square root of the variance effects as indicated below.

- a) Standard error effects for lines SE (gi) =  $(\sigma e^2/rt)^{1/2}$
- b) Standard error effects for testers SE  $(g_j) = (\sigma e^2/rl)^{1/2}$
- c) Standard error effects for hybrids SE (sij) =  $(\sigma e^2/r)^{1/2}$

#### 3.3.3 Estimation of Heterosis

Magnitude of heterosis was estimated over mid-parent, better parent as well as standard parent (Nadarajan and Gunasekaran, 2008).

#### **Relative Heterosis**

The superiority of  $F_1$  over the mid parental value was estimated as:

$$di = \frac{F - MP}{MP} \times 100$$

where,

F – mean value of hybrid

MP – mid parental value

# Heterobeltiosis (dii)

Superiority or inferiority of F<sub>1</sub> over better parent was calculated as

$$dii = \frac{F - BP}{BP} \times 100$$

where,

BP – mean value of better parent

# Standard heterosis (diii)

Superiority or inferiority of F<sub>1</sub> over standard parent was calculated as

$$diii = \frac{F - SV}{SV} \times 100$$

where,

SV – mean value of the standard variety. For each character best performing tester was used as standard.

# Test of significance

Significance of estimates of heterosis was tested at error degrees of freedom as suggested by Turner (1953).

't' for relative heterosis = 
$$\frac{F - MP}{\sqrt{\frac{Me}{r} x^{3/2}}} x 100$$

't' for heterobeltiosis = 
$$\frac{F-BP}{\sqrt{\frac{Me}{r} \times 2}} \times 100$$

't' for standard heterosis = 
$$\frac{F - SV}{\sqrt{\frac{Me}{r} \times 2}} \times 100$$

Where ' $M_e$ ' was error variance and 'r' was the number of replication.



Plate 1. Bushy type cowpea in beds



Plate 2. Trailing type cowpea on pandal



Plate 3. Variability in pod length in cowpea genotypes



Plate 4. Variability in seeds of cowpea genotypes



Plate 5. Emasculation and hybridisation



Plate 6. Tagging and labelling



Plate 7. Bagging



Plate 8. Crossed pod

# Results

## **RESULTS**

An experiment was conducted to evaluate 22 cowpea genotypes based on the protein content. From this evaluated genotypes, 10 high protein containing genotypes were selected. These genotypes were crossed in line x tester design. The result obtained for the study as presented below.

- 4.1 Evaluation of cowpea genotypes
- 4.1.1 Variability in cowpea genotypes

## 4.1.1.1Analysis of variance

Data on twenty two genotypes for yield, yield related traits and seed protein content were analyzed for bushy, semi trailing and trailing types for all the characters. For seed protein content data were analysed together. The results of the study on the variability of different traits are explained below.

## 4.1.1.2 Mean performance of cowpea genotypes

Out of the 22 genotypes evaluated, 12 genotypes belonged to bushy type, six were semi trailing and four were trailing type. So the mean performance of Cowpea genotypes for various biometrical traits are presented in three catagories and given in Table 3a, Table 3b and Table 3c respectively. In the bushy type the number of branches per plant did not show any variation (Table 4a). For semi trailing type the number of branches per plant and test weight did not show significant variation (Table 4b). But in trailing type the characters except plant height, number of pods per plant, pod weight and grain yield per plant did not show variation (Table 4c).

## **4.1.1.2.1 Plant height (cm)**

Bushy type CP-3 (53.8 cm) registered maximum plant height and minimum plant height was in Hridya (30.53 cm). Mean value of plant height in bushy type was 41.88 cm. In case of semi trailing genotypes, longest plants were observed in CP-1 (148.41 cm) while shortest in AV-5 (90.5 cm). Mean value of plant height in semi trailing type was 115.36 cm. The highest value for plant height in trailing type was for Vellayani Jyothika (254.48) which was on par with Lola (248.33 cm) and lowest value for plant height was observed for Sharika (213.37). Mean value for this trait was 235.42 cm in trailing type.

#### 4.1.1.2.1.2 Number of branches

Number of branches per plant did not show any variation in all the three groups of plants. In bushy type, Hridya (4.51) registered minimum number of branches and maximum was in Co(cp)7 (6.63). In semi trailing genotypes, Kanakamony (6.73) exhibited minimum number of branches where as maximum in CP-1 (8.34). In trailing type, Sharika exhibited less number of branches and Lola (9.39) registered maximum branch number.

## 4.1.1.2.3 Days to flowering

In bushy type, Co-6 (51.14) was late to flower which was on par with NBPGR-2 (51.08). Early flowering in bushy type was exhibited by Hridya with a value of 27.19 days. Mean value for this trait for bushy type was 44.07 days. CP-1 with a value of 55.08 days showed maximum value for days to flowering for semi trailing type while minimum value for days to flowering was shown by AV-5 (36.68 days) which was on par with PKB-3 (37.32) and PKB-4 (37.33). Mean value for this trait in semi trailing was 41.17 days. In trailing type there was no significant variation

for days to flowering. Sharika (49.20) exhibit early flowering while Lola with a value of 54.94 days was late to flowering.

# 4.1.1.2.4 Days to first harvest

In bushy type, Co-6 (65.75) exhibited maximum value for days to first harvest which was on par with Co(cp)7 with a value of 64.30 days and minimum value registered by Hridya (27.19 days). The mean value for days to first harvest in bushy type was 57.31 days. In semi trailing type longest days to harvest was shown by CP-1(67.47 days) and shortest days to harvest possessed by AV-5 (47.18 days) with a mean value of 54.16 days. In the trailing type days to last harvest did not show any variation. Vellayani Jyothika (66.68) was early to harvest where as Vyjayanthi (70.20) was registered late to first harvest. The mean value for this trait in trailing type was 68.36.

#### 4.1.1.2.5 Days to last harvest

. In bushy type Kashikanchan registered highest value for days to last harvest with a value of 114.24 days and the minimum value for this trait was showed by Hridya (65.85 days). The mean value for this trait for bushy type was 96.49 days. In the case of semi trailing types maximum value for this trait was registered by CP-1 (124.30 days) and minimum value was possessed by Kanakamony with a value of 91.25 days. The mean value was 108.33 days for semi trailing type. In trailing type no significant difference between the genotypes for days to last harvest was observed. Sharika registered minimum days to last harvest with 121.00 days where as the maximum days to harvest registered by Vyjayanthi (123.10). Mean value for this trait for trailing type was 121.85 days.

## **4.1.1.2.6 Pods per plant**

Co-6 with a value of 19.9 registered highest number of pods in bushy type and the minimum value recorded by NBPGR-2 (10.79). The mean value for pods per plant in bushy types was 16.65. In semi trailing type PKB-3 (63.63) recorded highest value for pods per plant which was on par with AV-5 with a value of 60.31. The mean value for pods per plant in semi trailing was 46.99. The highest number of pods per plant in trailing type was in Lola (60.07) which was statistically on par with Vellayani Jyothika (58.24) and Vyjayanthi (51.37) while lowest number of pods per plant was in Sharika with a value of 45.16. The mean value for pods per plant in trailing was 53.71.

## **4.1.1.2.7** Length of pod (cm)

In bushy type, CP-2 (22.74 cm) registered maximum value for pod length which was on par with CP-3 (20.65 cm). The minimum value recorded by Hridya (12.26 cm) for pod length. The mean value for pod length bushy types was 18.22 cm. CP-1 recorded longest pod in semi trailing type (48.77 cm) and the shortest was by Kanakamony with a length of 18.10 cm. The mean value for pod length semi trailing types was 28.19 cm. In trailing type no significant difference between the genotypes for length of pod. Shortest pods in trailing type was registered by Sharika (40.76 cm) where as the longest pod was registered by Lola with a pod length of 53.83cm. The mean value for this trait in trailing type was 50.11 cm.

## **4.1.1.2.8** Pod weight (g)

In bushy type, higher pod weight was registered by NBPGR 1 (10.88g) which was on par with CP-2 (10.75g) and NBPGR 2 (10.04g) and the lowest value for this trait exhibited by Hridya (2.65g). The mean value for pod weight in bushy types was 7.88g. In semi trailing type maximum value for pod weight was exhibited by PKB-3

with a value of 21.07g and the lowest value by Kanakamony (10.03g). The mean value for pod weight was 16.40g. The highest value for pod weight was registered by Lola (27.04 g) in trailing type which was on par with Vellayani Jyothika (25.03g) and Vyjayanthi (24.07g) and lowest value for pod weight was recorded by Sharika (18.06 g). The mean value for pod weight in trailing type was 23.55g.

## **4.1.1.2.9** Seeds per pod

In bushy type, Co-2 with a value of 14.11 exhibited highest value for seeds per pod which was on par with Co-4 (14.03) and Bhagyalakshmi (14.03). The lowest value was registered by Hridya (7.92). The mean value for this trait for bushy types was 11.05. In semi trailing type PKB- 3 with a value of 20.10 registered maximum value for this trait which was on par with AV-5 (20.08) and the minimum value was recorded by CP-1 (13.77). The mean value for seeds per pod in semi trailing types was 17.84. In trailing type no significant difference between the genotypes for seeds per pod was observed. Vellayani Jyothika (17.85) registered lowest value for seeds per pod. Highest value for seeds per pod was registered by Lola (22.28). The mean value for this trait in trailing type was 19.76.

## **4.1.1.2.10** Test weight (g)

In bushy type maximum test weight value was registered by Kashi kanchan (13.53g) which was on par with Co-6 (13.5g) and Co(cp) 7 with a value of 13.20g. The mean value for test weight in bushy type was 11.15 g. In semi trailing type PKB-3 with a value of 23.04 g exhibited highest test weight and the lowest was in Kanakamony (12.03g). The mean value for test weight in semi trailing was 17.90 g. There was no significant difference between the genotypes for test weight in trailing type.

## 4.1.1.2.11 Grain yield per plant (g)

In bushy type, CP-2 (40.70g) showed highest grain yield per plant and lowest value was registered by Hridya with a value of 9.31 g which was on par with Bhagyalakshmi (10.77g), Co-2 (10.01g) Co-4 (10.01g) and Co-6 (11.38g). The mean value for this trait in bushy type was 20.26 g. PKB-3 registered maximum value for grain yield per plant in semi trailing type with a value of 175.40g and the minimum value was possessed by CP-1 with a value of 54.63g. The mean value for grain yield per plant in semi trailing was 125.59g. In trailing type highest grain yield per plant was noticed in Lola (154.49g) which was on par with Vyjayanthi (145.49g) and Vellayani Jyothika (135.73g). The lowest grain yield per plant was exhibited by Sharika with a value of 100.24g. The mean value for this trait in trailing type was 134.10g.

# **4.1.1.2.12** Protein content (%)

The highest value for protein content was exhibited by PKB-3 (28.50 per cent) which was on statistically on par with PKB-4 (28.49), Bhagyalakshmi (27.96), Lola (27.75) and Anaswara (27.60). The lowest value was exhibited by NBPGR-1 (18.15). The mean value for the trait was 23.39 per cent.

Table 3a. Mean performance of genotypes for bushy type

Genotypes	Plant height (cm)	No. of branches	Days to first flowering	Days to first harvest	Last harvest	No. of pod/plant	Length of pods (cm)	Pod weight (g)	Seeds/ pod	Test weight (g)	Grain yield/ plant (g)	Protein content (%)
Bhagyalaksmi												
	37.8c <sup>de</sup>	4.71	33.87 <sup>d</sup>	46.15 <sup>d</sup>	91.75 <sup>e</sup>	12.29 <sup>cd</sup>	15.45 <sup>de</sup>	4.05 <sup>ef</sup>	14.03 <sup>a</sup>	9.93 <sup>cd</sup>	10.77 <sup>e</sup>	27.96 <sup>a</sup>
Co(cp)7												
	42.63 <sup>bc</sup>	6.63	46.66 <sup>b</sup>	64.30 <sup>a</sup>	100.7 <sup>d</sup>	18.46 <sup>ab</sup>	21.40 <sup>ab</sup>	7.01 <sup>bc</sup>	12.29 <sup>b</sup>	13.20 <sup>a</sup>	12.38 <sup>e</sup>	20.34 <sup>cde</sup>
Co-2	.2.00	0.02	.0.00	0.1.00	10017	101.10	21110	7101	12,27	10.20	12.50	20.5
	35.11 <sup>def</sup>	5.69	44.45 <sup>bc</sup>	58.93 <sup>bc</sup>	98.88 <sup>d</sup>	18.55 <sup>ab</sup>	19.11 <sup>bcd</sup>	6.01 <sup>cd</sup>	14.11 <sup>a</sup>	12.03 <sup>ab</sup>	10.01 <sup>e</sup>	20.17 <sup>de</sup>
Co-4	55111	0.05		50.75	70.00	10.00	17,111	0.01	1.112	12.00	10.01	20.17
	34.74 <sup>def</sup>	6.00	41.04°	54.97 <sup>c</sup>	102.60 <sup>c</sup>	18.93 <sup>ab</sup>	19.50 <sup>abc</sup>	5.01 <sup>de</sup>	14.03 <sup>a</sup>	12.11 <sup>ab</sup>	10.01 <sup>e</sup>	20.89 <sup>cd</sup>
Co-6	J, .	0.00		0,	102.00	10.75	19.00	5.01	11100	12.11	10.01	20.09
							_					
	36.21 <sup>cdef</sup>	5.57	51.14 <sup>a</sup>	65.75 <sup>a</sup>	99.32 <sup>d</sup>	19.91 <sup>a</sup>	15.82 <sup>cd</sup>	7.11 <sup>bc</sup>	11.79 <sup>b</sup>	13.05 <sup>a</sup>	11.385 <sup>e</sup>	20.89 <sup>cd</sup>
Hridya												
77 111 1	30.53 <sup>f</sup>	4.51	27.19 <sup>e</sup>	38.14 <sup>e</sup>	65.85 <sup>g</sup>	18.05 <sup>ab</sup>	12.26 <sup>e</sup>	2.65 <sup>f</sup>	7.92 <sup>d</sup>	6.81 <sup>d</sup>	9.31 <sup>e</sup>	21.62 <sup>bc</sup>
Kashikanchan												
	46.94 <sup>b</sup>	6.30	44.26 <sup>bc</sup>	56.77 <sup>c</sup>	114.24 <sup>a</sup>	18.3 <sup>ab</sup>	18.10 <sup>bcd</sup>	$7.80^{b}$	11.88 <sup>b</sup>	13.53 <sup>a</sup>	26.47 <sup>d</sup>	22.83 <sup>b</sup>
CP-2												
	55.10 <sup>a</sup>	5.83	45.94 <sup>b</sup>	59.38 <sup>bc</sup>	91.67 <sup>e</sup>	16.67 <sup>b</sup>	22.74 <sup>a</sup>	10.75 <sup>a</sup>	11.90 <sup>b</sup>	11.89 <sup>ab</sup>	40.70 <sup>a</sup>	19.39 <sup>ef</sup>
CP-3												
	53.80 <sup>a</sup>	5.37	45.96 <sup>b</sup>	55.58°	89.62 <sup>f</sup>	14.02°	20.65 <sup>ab</sup>	9.85ª	10.04 <sup>c</sup>	10.56 <sup>bc</sup>	34.26 <sup>b</sup>	19.43 <sup>ef</sup>
NBPGR 1												
	31.39 <sup>ef</sup>	4.59	45.92 <sup>b</sup>	57.98 <sup>c</sup>	89.23 <sup>f</sup>	12.7 <sup>cd</sup>	18.19 <sup>bcd</sup>	10.88 <sup>a</sup>	8.93 <sup>cd</sup>	8.85 <sup>d</sup>	24.88 <sup>d</sup>	18.15 <sup>f</sup>
NBPGR 2												
	45.93 <sup>b</sup>	5.23	51.08 <sup>a</sup>	63.24 <sup>ab</sup>	100.66 <sup>d</sup>	10.79 <sup>d</sup>	15.63 <sup>de</sup>	10.04 <sup>a</sup>	9.79 <sup>c</sup>	10.08 <sup>cd</sup>	28.78 <sup>cd</sup>	19.77 <sup>de</sup>
NBPGR 3												
	40.96 <sup>bcd</sup>	6.26	41.13°	55.47°	108.7 <sup>b</sup>	16.875 <sup>b</sup>	17.04 <sup>e</sup>	9.60 <sup>a</sup>	8.88 <sup>cd</sup>	10.61 <sup>bc</sup>	32.74 <sup>bc</sup>	19.48 <sup>e</sup>

Table 3b. Mean performance of cowpea genotypes for semi trailing type

Genotypes	Plant height (cm)	No. of branches	1 st flowering	1 st harvest	Last harvest	No. of pod	Length of pod (cm)	Pod weigh t (g)	Seeds/ pod	Test weigh t (g)	Grain yield/ plant (g)	Protein content (%)
Anaswara												
	121.68 <sup>b</sup>	6.90	40.68 <sup>b</sup>	55.35 <sup>b</sup>	114.70 <sup>b</sup>	45.15 <sup>c</sup>	$32.38^{b}$	16.06 <sup>c</sup>	18.03 <sup>ab</sup>	15.20	117.72 <sup>d</sup>	27.60 <sup>a</sup>
kanakamony												
	131.15 <sup>b</sup>	6.73	39.96 <sup>bc</sup>	54.39 <sup>bc</sup>	91.25 <sup>e</sup>	41.21 <sup>d</sup>	$18.10^{d}$	10.03 <sup>d</sup>	18.04 <sup>ab</sup>	12.03	100.86 <sup>e</sup>	25.38 <sup>b</sup>
CP-1												
	148.41 <sup>a</sup>	8.34	55.08 <sup>a</sup>	67.47 <sup>a</sup>	124.3 <sup>a</sup>	16.07 <sup>e</sup>	48.77 <sup>a</sup>	16.07 <sup>c</sup>	13.77 <sup>c</sup>	13.43	54.63 <sup>t</sup>	20.65°
AV-5	90.50 <sup>d</sup>	6.85	36.68 <sup>d</sup>	47.18 <sup>d</sup>	105.3 <sup>cd</sup>	60.31 <sup>a</sup>	24.50°	19.08 <sup>b</sup>	20.08 <sup>a</sup>	21.84	166.34 <sup>b</sup>	25.34 <sup>b</sup>
PKB-3												
	107.25 <sup>c</sup>	6.83	$37.32^{cd}$	51.72 <sup>bcd</sup>	110.17 <sup>bc</sup>	63.63 <sup>a</sup>	$23.40^{c}$	21.07 <sup>a</sup>	$20.10^{a}$	21.90	175.40 <sup>a</sup>	$28.5^{a}$
PKB-4												
	93.15 <sup>d</sup>	7.10	37.33 <sup>cd</sup>	48.89 <sup>cd</sup>	104.3 <sup>d</sup>	55.60 <sup>b</sup>	22.03°	$16.10^{c}$	17.04 <sup>b</sup>	23.04	138.64 <sup>c</sup>	$28.49^{a}$

Table 3c. Mean performance for cowpea genotypes for trailing type

Genotypes	Plant height (cm)	No of branch es	1 st floweri ng	1 st harvest	Last harvest	No. of pod	Length of pod (cm)	Pod weight (g)	Seeds/	Test weigh t (g)	Grain yield/ planlt (g)	Protein content (%)
Vellayani Jyothika									-			
	254.48 <sup>a</sup>	8.01	50.47	66.68	121.10	58.24 <sup>a</sup>	52.49	25.03 <sup>a</sup>	17.85	22.60	135.73 <sup>a</sup>	26.07
Vyjayanthi	225.52 <sup>bc</sup>	8.04	52.83	70.20	123.10	51.37 <sup>ab</sup>	53.37	24.07 <sup>a</sup>	20.13	20.51	145.49 <sup>a</sup>	27.05
Lola	248.33 <sup>ab</sup>	9.39	54.94	69.11	122.21	60.07 <sup>a</sup>	53.83	27.04 <sup>a</sup>	22.28	22.86	154.94 <sup>a</sup>	27.75
Sharika	213.37°	7.78	49.2	67.48	121.00	45.16 <sup>b</sup>	40.76	18.06 <sup>b</sup>	18.79	18.95	100.24 <sup>b</sup>	27.10

Table 4a. Analysis of variance for different characters in bushy type cowpea

Character	df	Treatment sum of squares	Mean sum of squares	F value
Plant height	11	1501.39	136.49**	14.47
No. of branches	11	276.54	25.14	8.13
Days to flowering	11	1029.27 23.28		23.28
Days to first harvest	11	1312.85	119.35**	27.97
Days to last harvest	11	3271.95 297.45**		402.96
No. of pods per plant	11	204.27	18.57**	13.64
Length of pods	11	185.57	16.87**	6.38
Pod weight	11	165.22	15.02**	36.47
Seeds per pod	11	102.74	9.34**	18.68
Test weight	11	59.29	59.29 5.39**	
Grain yield per plant	11	2914.67	264.97	75.16
Protein content	11	146.52	13.32	38.14

<sup>\*</sup> significant at 5% level

<sup>\*\*</sup> significant at 1% level

Table 4b. Analysis of variance for different characters in semi trailing type cowpea

Character	df	Treatment sum of squares	Mean sum of squares	F value
Plant height	5	5117.40	1023.48**	49.39
No. of branches	5	142.15	28.43	10.11
Days to flowering	5	489.55	97.91**	63.41
Days to first harvest	5	522.25	104.45**	18.19
Days to last harvest	5	1213.85	242.77**	51.63
No. of pods per plant	5	3013.95	602.79**	227.54
Length of pods	5	1238.30	247.66**	116.97
Pod weight	5	139.8	27.96**	67.47
Seeds per pod	5	54.70	10.94**	12.11
Test weight	5	61.6	12.32	15.13
Grain yield per plant	5	2700.83	245.53**	120.13
Protein content	5	88.8	17.76**	36.43

<sup>\*</sup> significant at 5% level

<sup>\*\*</sup> significant at 1% level

Table 4c. Analysis of variance for different characters in trailing type cowpea

			8 11 1			
Character	df	Treatment sum of squares	Mean sum of squares	F value		
Plant height	3	2228.31	742.77**	10.54		
No. of branches	3	75.39	25.13	12.11		
Days to flowering	3	601.15	120.23	45.27		
Days to first harvest	3	480.96	160.32	17.63		
Days to last harvest	3	631.02	210.34	45.25		
No. of pods per plant	3	458.73	152.91**	10.21		
Length of pods	3	468.39	156.13	112.14		
Pod weight	3	89.52	29.84**	13.94		
Seeds per pod	3	36.78	12.26	13.11		
Test weight	3	45.75	15.25	15.27		
Grain yield per plant	3	2235.69	745.23**	100.13		
Protein content	3	66.69	22.23	14.13		

<sup>\*</sup> significant at 5% level

<sup>\*\*</sup> significant at 1% level

## 4.2 Evaluation of hybrids and parents

## 4.2.1 Analysis of variance

The analysis of variance (Tables 5a, 5b) revealed that there existed significant difference among the genotypes for most of the characters studied with exception of number of branches. Significant difference between genotypes were observed with respect to plant height, days to flowering ,days to first and last harvest, length of pods, pod weight and number of pods per plant. grain yield per plant and protein content.

## 4.2.2 Mean performance of parents and hybrids

Mean performance of parents and hybrids for various traits are given in Table 6a & Table 6b and detailed below

#### **4.2.2.1 Plant height (cm)**

Among all the lines, testers and hybrids, this trait varied from 35.22 cm (H5) to 270.15cm (H20) with a grand mean of 147.06 cm. In the parental line, the mean value for this trait ranged from 37.88 cm (L2) to 254.48 cm (L1) where as in testers, it ranged from 70.5cm (T1) to 213.37cm (T4). Mean value of hybrid ranged from 35.22 cm (H5) to 270.15 cm (H20).

## 4.2.2.2 Number of branches per plant

There was no significant difference between number of branches among the parents and hybrids.

#### 4.2.2.3 Days to flowering

Days to flowering ranged from 30.16 (H10) to 60.65 (H20) among parents and hybrids. Grand mean estimated for this trait was 44.31. In the parental lines this trait varied between 33.87 (L2) to 54.94 (L5) while among testers the range was between 36.68 (T1) and 49.2 (T4). Among hybrids it varied between 30.16 (H10) and 60.65 (H20).

## **4.2.2.4** Days to first harvest

Range for days to first harvest varied between 43.11 (H22) and 73.65 (H16) in the parents and hybrids. Among the lines, this trait varied from 46.15 (L2) to 69.11 (L5) and among the testers, it varied from 47.18 (T1) to 67.48 (T4). Among hybrids the range was between 43.11 (H22) and 73.65 (H16).

## 4.2.2.5 Days to last harvest

Overall range for days to last harvest was between 90.28 (H5) and 140.49 (H20). A grand mean of 11.69 was registered for this trait. Among lines this was varied between 91.75 (L2) to 123.18 (L4) where as in testers, it was between 104.34 (T3) and 121.05 (T4). In hybrids, this trait ranged between 90.28 (H5) and 140.49 (H20).

## 4.2.2.6 Number of pods per plant

Number of pods per plant ranged between 75.17 (H2) and 12.29 (L2) among parents and hybrids. Grand mean of this trait was 46.14. In the line, the mean value for this trait ranged from 12.29 (L2) to 60.07 (L5) while in testers, it varied from 45.16 (T4) to 63.63 (T2). Mean value of hybrids ranged from 15.05 (H7) to 75.17 (H2).

## **4.2.2.7** Length of pods (cm)

Longest pods were observed in H3 (62.29 cm) and shortest in L2 (15.45 cm) among all the genotypes. Estimated grand mean for this trait was 36.25 cm. Among lines this trait varied from 15.45cm (L2) to 53.83cm (L5), while in testers length of pod varied between 22.03cm (T3) and 40.76 cm (T4). Mean value of length of pods among hybrids ranged from 15.69 cm (H6) and 62.29 cm (H3).

#### **4.2.2.8 Pod weight (g)**

Estimates for pod weight varied between 31.12 g (H4) and 4.05 g (L2) among parents and hybrids. Grand mean estimated for this trait was 18.32 g. In the lines, it

varied from 4.05 g (L2) to 27.04 g (L5) where as in testers, it ranged from 16.10 g (T3) to 21.07 g (T2). Among the hybrids, the range was between 5.01 g (H7) and 31.12 g (H4).

## **4.2.2.9** Seeds per pod

Seeds per pod ranged between 13.28 (H6) and 22.5 (H19) among parents and hybrids. A grand mean of 18.49 was registered for this trait. Among lines, this trait varied between 14.03 (L2) to 22.28 (L5), where as in testers it was between 17.04 (T3) to 20.1(T2).

# **4.2.2.10** Test weight (g)

Among lines, testers and hybrids test weight was ranged from 9.85g (H7) to 27.36g (H3). Grand mean estimated was 21.42g. In the line, this trait varied between 9.93g (L2) and 22.86g (L5), while in testers it varied from 18.95g (T4) and 23.04g (T3). Among the hybrids the range was between 9.85g (H7) to 27.36g (H3).

## 4.2.2.11Grain yield per plant

Yield per plant ranged from 10.77~g~(L2) to 180.25~g~(H20) among all the genotypes. Grand mean estimated was 129.06~g. In the lines this trait varied between 10.77g~(L2) to 154.94~g~(L5), while in testers it varied from 100.24~g~(T4) to 175.40~g~(T2). Among hybrids the range was between 19.29~g~(H6) to 180.25~g~(H20).

## **4.2.2.12 Protein content (%)**

Overall range of protein content was between 23.43 per cent (H20) to 31.1 (H22). A grand mean of 27.70 per cent was registered for this trait. Among the lines, this trait varied between 25.38 (L6) to 28.18 per cent (L2) where as, in testers it varied from between 25.34 (T1) and 28.5 per cent (T2). In hybrids this trait ranged between 23.43 (H20) to 31.1 per cent (H22).

## 4.2.3 Phenotypic and genotypic coefficient of variation

The PCV and GCV were classified as suggested by Sivasubramanian and Madhavamenon, (1973) into low (0-10%), moderate (10.1-20%) and high (>20%). Phenotypic coefficient of variation ranged from 16.39 per cent to 96.35 per cent corresponding to the traits, days to first harvest and grain yield per plant. Days to first harvest (16.39), days to last harvest (16.89), protein content (16.67) and days to flowering (18.89) recorded moderate PCV. All other characters exhibited high PCV (Table 7). Genotypic coefficient of variation ranged from 10.03 of days to last harvest to 84.06 per cent of grain yield per plant. Number of branches per plant (15.86), days to first flowering (12.99), days to first harvest (12.20) days to last harvest (10.03) and protein content (14.69) exhibited moderate GCV, while all other traits registered high GCV estimates. Difference between PCV and GCV estimates was maximum for pod weight (30.15%), followed by number of pod per plant (18.12%) and test weight (16.27%). However, the difference between PCV and GCV was low in case of days to first harvest (4.19%), seeds per pod (5.17%), days to flowering (5.9%) and protein content (1.98%).

## 4.2.4 Heritability and genetic advance as percentage of mean

Heritability estimates ranged from 31.18 per cent of pod weight to 81.89 per cent of plant height. Traits, pod weight (31.18%), days to last harvest (35.32%), number of branches per plant (46.89%), days to first flowering (47.29%), number of pods per plant (54.41%), test weight (36.53%) and days to first harvest (55.43%) recorded moderate heritability, while all other traits exhibited high heritability estimates. Genetic advance as per cent of mean estimates varied from 12.29 per cent to 151.09 per cent for days to harvest and grain yield per plant, respectively. Moderate estimates were observed for days to last harvest (12.29%), days to first harvest (18.72%) and days to flowering (18.40%). Other traits recorded high estimates of genetic advance as per cent of mean.

## 4.3 Studies on combining ability

## 4.3.1 Analysis of variance

ANOVA for combining ability (Table 8) show that lines vary for plant height, days to flowering, days to first harvest, days to last harvest, number of pods per plant, seeds per pod, grain yield per plant and protein content. Testers did not vary for these traits. Hybrids vary for plant height, days to flowering, days to first harvest, days to last harvest, number of pods per plant, length of pod, test weight, seeds per pod, grain yield per plant and protein content. The line x tester interaction significant for number of pods per plant, length of pods, pod weight, seeds per pod, test weight, grain yield per plant and protein content.

#### **4.3.2** Estimation of variance

The estimates of variance due to general and specific combining ability in the line x tester design for various traits are given below.

## 4.3.2.1 Combining ability effects

The general combining ability (gca) effect of lines and testers and specific combining ability effect (sca) of hybrid for various traits are given in Table 9 and Table 10, respectively.

## **4.3.2.1.1** Plant height (cm)

The gca effect of parents ranged from -105.98 (L2) to 76.69 (L4) among lines. Two lines, L4 (76.69) and L5 (61.65) showed significant gca effect where as four lines L1 (-50.56), L2 (-105.98), L3 (-54.67), L6 (-28.15) showed negative significance. The gca effect of testers ranged between -59.16 (T1) to 55.50 (T4). Three testers T1, T2 and T4 with estimates -59.16, 6.85, 55.50 exhibited significant gca effects. The sca effect among hybrids varied from -77.19 (H17) to 54.47 (H5). Eleven hybrids recorded significant positive sca effect.

Table 5a. Analysis of variance for evaluation of hybrids and parents

Source	df		Mean sum of squares								
		Plant height	No. of branches	Days to 1 st	Days to 1	Days to last harvest	Pods / plant				
Replication	1	53.76	2.28	45.94	0.72	362.35	124.05				
Treatment	33	13710.38**	4.58	157.59**	215.96**	365.76**	717.26**				
Error	33	55.11	0.31	16.30	24.43	28.59	5.95				

Table 5b. Analysis of variance for evaluation of hybrids and parents

	df	Mean sum of squares						
Source			T	Γ		1	1	
		Length of pods	Pod weight	Seeds/ pod	Test weight	Yield per plant	Protein %	
Replication	1	0.54	3.55	8.84	0.91	581.88	9.02	
Treatment	33	549.83**	131.50**	13.96**	25.96**	5715.41**	8.42**	
Error	33	7.88	1.46	1.35	1.9	29.36	0.76	

<sup>\*</sup> significant at 5% level

<sup>\*\*</sup> significant at 1% level

Table 6a. Mean performance of parents and hybrids for different traits

Genotypes	Plant height (cm)	No. of branches	Days to 1 st flowering	Days to 1 st harvest	Days to last harvest	Pods / plant
L <sub>1</sub>	254.48	8.00	50.47	66.68	121.12	58.24
$L_2$	37.88	4.71	33.87	46.15	91.75	12.29
$L_3$	121.68	6.90	40.68	55.35	114.76	45.15
$L_4$	225.52	8.04	52.83	70.20	123.18	51.37
$L_5$	248.33	9.39	54.94	69.11	122.21	60.07
$L_6$	131.15	6.73	39.96	54.39	91.22	41.21
$T_1$	70.5	6.85	36.68	47.18	105.37	60.22
$T_2$	107.25	6.83	37.32	51.72	110.17	65.53
$T_3$	93.15	7.10	37.33	48.89	104.34	56.74
$T_4$	213.37	7.78	49.20	67.48	121.00	45.25
$H_1$	74.08	7.20	40.40	55.57	102.28	62.17
$H_2$	236.38	8.50	51.20	66.40	115.18	75.17
H <sub>3</sub>	205.18	11.00	52.30	68.30	120.57	72.02
$H_4$	270.15	8.81	55.24	64.28	123.40	68.25
$H_5$	35.22	5.80	30.30	43.25	90.28	16.03
$H_6$	37.20	4.90	32.55	44.24	100.20	17.05
$H_7$	40.02	4.52	35.20	46.35	96.33	15.05
$H_8$	47.20	5.60	40.51	50.05	108.27	17.05
H <sub>9</sub>	61.27	6.10	33.24	46.30	94.35	39.40
$H_{10}$	65.20	8.21	30.16	44.29	105.34	67.16
$H_{11}$	66.28	7.92	40.35	52.38	102.39	65.31
$H_{12}$	172.10	8.13	42.20	55.25	110.39	64.25
H <sub>13</sub>	208.22	8.20	50.38	68.64	112.29	52.12
$H_{14}$	235.11	9.57	52.38	71.50	124.30	71.27
H <sub>15</sub>	196.30	7.53	49.63	68.49	120.38	61.13
H <sub>16</sub>	250.26	8.12	53.35	73.65	130.28	62.00
H <sub>17</sub>	71.20	7.51	44.10	56.28	106.12	54.19
H <sub>18</sub>	240.33	8.20	54.21	68.48	130.10	62.22
H <sub>19</sub>	250.24	9.75	58.19	70.18	131.33	71.03
$H_{20}$	268.40	10.50	60.65	72.20	140.49	72.21
$H_{21}$	70.385	6.50	38.17	45.32	96.45	28.02
H <sub>22</sub>	102.18	7.53	32.17	43.11	92.21	36.35
$H_{23}$	98.17	7.21	40.20	52.25	108.33	32.22
H <sub>24</sub>	200.21	9.28	56.38	68.35	130.17	52.19

Table 6b. Mean performance of parents and hybrids for different traits (contd)

Genotypes	Length of pod (cm)	Pod weight (g)	Seeds / pod	Test weight (g)	Grain yield/ plant (g)	Protein content (%)
$L_1$	52.49	25.03	17.85	22.60	135.73	26.07
$L_2$	15.45	4.05	14.03	9.93	10.77	28.18
$L_3$	32.38	16.06	18.03	15.20	117.72	27.6
$L_4$	53.37	24.07	20.13	20.51	145.49	27.05
$L_5$	53.83	27.04	22.28	22.86	154.94	27.75
$L_6$	18.01	10.03	18.04	12.03	100.86	25.38
$T_1$	24.50	19.08	20.08	21.84	166.34	25.34
T <sub>2</sub>	23.40	21.07	20.10	21.90	175.40	28.5
T <sub>3</sub>	22.03	16.10	17.04	23.04	138.64	28.49
T <sub>4</sub>	40.76	18.06	18.79	18.95	100.24	27.10
$H_1$	50.32	25.46	18.02	24.63	151.38	24.45
H <sub>2</sub>	55.19	28.52	19.21	25.33	178.33	30.03
$H_3$	62.29	30.27	21.09	27.36	170.18	25.33
H <sub>4</sub>	58.15	31.12	22.12	24.00	165.45	25.00
H <sub>5</sub>	16.51	5.33	14.36	20.28	20.04	29.23
$H_6$	15.69	6.15	13.28	10.59	19.29	28.75
H <sub>7</sub>	17.13	5.01	14.13	9.85	18.43	28.83
$H_8$	19.25	7.20	16.12	13.14	20.44	27.65
H <sub>9</sub>	25.19	12.55	15.00	12.52	90.39	29.83
H <sub>10</sub>	31.28	18.20	19.57	23.57	155.55	30.03
H <sub>11</sub>	29.12	17.60	20.05	21.20	146.20	30.06
H <sub>12</sub>	38.18	19.46	19.55	23.26	170.27	28.88
H <sub>13</sub>	55.08	25.21	19.43	19.55	175.11	25.59
H <sub>14</sub>	54.18	26.37	20.15	20.22	180.18	26.35
H <sub>15</sub>	53.22	23.28	18.07	18.05	178.17	29.83
H <sub>16</sub>	55.55	24.33	19.18	20.25	165.50	24.79
H <sub>17</sub>	54.05	25.50	22.14	22.32	135.30	24.61
H <sub>18</sub>	53.17	24.12	21.00	22.19	165.22	31.00
H <sub>19</sub>	52.18	22.23	22.50	21.35	178.18	28.27
H <sub>20</sub>	54.18	25.50	22.17	19.80	180.25	23.43
H <sub>21</sub>	16.54	8.53	15.04	11.25	75.24	28.45
H <sub>22</sub>	18.05	10.22	16.13	12.23	125.30	30.03
H <sub>23</sub>	17.07	10.17	15.47	11.62	115.18	31.10
H <sub>24</sub>	18.25	10.55	18.28	13.56	160.21	28.95

Table 7. Variability and genetic parameters for various character

Chanastan	Ra	nge	Mean		cient of on (%)	Heritabilit y	Genetic	Genetic gain as
Character	Minimu m	Maximu m	Mean	PCV	GCV	(Broad sence)	advance	% of mean
Plant height	30.53	254.48	95.71	83.28	75.37	81.89	134.49	140.51
No.ofbranches	4.5	9.3	6.48	23.17	15.86	46.89	1.45	22.38
Days to first flowering	27.19	55.08	44.23	18.89	12.99	47.29	8.14	18.40
Days to first harvest	38.14	70.2	57.96	16.39	12.20	55.43	10.85	18.72
Days to last harvest	65.85	127.38	104.14	16.89	10.03	35.32	12.80	12.29
No. of pod / plant	10.79	60.07	24.32	69.08	50.96	54.41	18.83	77.43
Length.of pod	12.26	53.83	26.58	56.60	46.07	66.23	20.53	77.24
Pod weight	2.65	27.04	12.88	68.29	38.14	31.18	5.65	43.88
Seeds /pod	7.92	22.28	14.62	31.94	26.77	70.22	6.75	46.22
Test weight	8.81	23.04	14.86	41.14	24.87	36.53	4.60	30.97
Grain yield/ plant	9.30	200.35	75.11	96.35	84.06	76.12	113.49	151.09
Protein content	18.15	28.50	23.41	16.67	14.69	77.69	6.24	26.68

Table 8a.Analysis of variance for LxT analysis for various characters

Genotypes	df			Mean su	m of squares		
				Days to1 st harvest			
Hybrids	23	974.138*	11.21	565.17**	1052.31**	1374.21**	600.11**
Line	5	7150.15*	1.86	3281.23**	4450.14**	5314.14**	3210.24**
Tester	3	315.46	17.05	105.26	190.14	224.16	60.20
Linex tester	15	196.45	9.05	55.37	95.14	106.27	468.30**
Error	33	96.55	5.76	62.21	85.11	100.31	53.15
μ GCA		259.38	-0.18	150.31	310.11	425.26	67.31
SCA		10.76	1.96	15.22	25.56	27.13	140.11
GCA/ SCA		24.10	-0.10	9.8	12.13	15.67	0.48

Table 8b.Analysis of variance for LxT analysis for various characters

Genotypes	df			Mean sum of	squares		
Genotypes	ui	Length.of pod	Pod weight	Seeds / pod	Test weight	Grain yield/ plant	Protein content
Hybrids	23	16.56**	9.24	10.22**	38.25**	85.21**	7.34**
Line	5	3.91	1.17	72.21**	78.61	189.79**	34.31**
Tester	3	1.42	8.12	1.01	22.51	50.76	3.98
Line x tester *	15	27.01**	12.01**	2.72**	35.23**	81.53**	3.83**
Error	33	5.76	5.05	0.45	4.42	15.50	0.11
μ GCA		-1.91	1.02	2.88	1.01	3.54	0.89
SCA		8.02	3.07	0.91	11.33	24.11	1.33
GCA/ SCA		-0.23	0.33	3.14	0.08	0.12	0.67

## 4.3.2.1.2 Number of branches per plant

The gca effect among lines ranged from -2.57 (L2) to 1.21 (L5) and all were recorded significance. For testers gca effect varied from -0.89 (T1) to 0.63 (T4). Two testers T1 (-0.89) and T4 (0.63) registered significant gca effects. The sca effect of hybrids varied from -1.04 (H15) to 1.91 (H3). Sixteen hybrids recorded significant sca effect.

## 4.3.2.1.3 Days to flowering

Among parents, gca effect for lines was minimum for L2 (-10.09) and maximum for L5 (9.56) and four lines registered significant gca effect. It varied between -5.57 (T1) and 6.66 (T4) for testers. T1 (-5.57) and T4 (6.66) registered significant gca effects. The sca effect of hybrids varied from -6.94 (H22) to 7.99 (H24). Four hybrids registered significant sca effect.

# 4.3.2.1.4 Days to first harvest

The gca effect for days to first harvest ranged from -12.17 (L2) to 12.44 (L4), among lines with all the lines showing significant gca effect. Among testers it varied between -5.57 (T1) to 5.83 (T4). Two testers T1 (-5.57) and T4 (5.83) registered significant gca effect. Among hybrids the sca effect varied between -7.36 (H22) to 10.26 (H24). Two hybrids H22 (-7.36) and H24 (10.26) recorded significant sca effect.

# 4.3.2.1.5 Days to last harvest

Among the parents, the gca effect for lines varied between -13.37 (L2) and 14.87 (L5), with all of them registering significance. In testers, it varied between -11.85 (T1) and 11.69 (T4). Testers T1 (-11.85) and T4 (11.69) recorded significant gca effect. The sca effect among hybrids ranged from between -13.66 (H22) and 11.69 (H24). Three hybrids, H17 (-9.04), H22 (-13.66) and H24 (11.69) recorded significant sca effect for days to last harvest.

# 4.3.2.1.6 Number of pods per plant

The gca effect for pods per plant for all lines and testers were significant. In lines it ranged from -35.12 (L2) to 17.99 (L1) and in testers, it ranged from -9.42 (T1) to 4.58 (T2). Among hybrids the sca effect varied between -10.21 (H9) and 10.42 (H22). Nineteen among twenty four hybrids recorded significance for sca effect.

## **4.3.2.1.7** Length of pods

Among lines, gca effects ranged from -21.18 (L2) to 18.16 (L1), with all of them exhibiting significance. In testers it ranged from -2.05 (T1) to 2.27 (T4). Two testers T1 (-2.05) and T4 (2.27) registered significance for gca effect. Among hybrids, the sca effects varied between -4.12 (H1) to 5.62 (H3). Four among twenty four hybrids recorded significance for sca effect.

# **4.3.2.8 Pod weight**

The gca effect of line varied from -12.53 (L2) to 10.39 (L1), with all of them exhibiting significance. In testers it ranged from -1.36 (T1) to 1.24 (T4), with two of them registering T1 (-1.36) and T4 (1.24) significant gca effect. The sca effect for hybrids ranged from -3.04 (H9) to 2.52 (H17). Eight hybrids recorded significant sca effect.

## 4.3.2.9 Number of seeds per pod

Among the lines, the gca effect ranged from -3.95 (L2) to 3.53 (L5), with all of them exhibiting significance. In testers, it ranged from -1.09 (T1) to 1.15 (T4). Out of four testers, two testers T1(-1.09) and T4 (1.15) recorded significance for gca effect. Among hybrids, sca effect varied between -2.46 (H9) and 1.38 (H11). Seven hybrids recorded significance for sca effect.

## **4.3.2.10** Test weight

The gca effect for test weight was significant in all lines and testers. In lines it varied from -10.34 (L6) to 13.96 (L2). In testers it ranged from -3.50 (T4) to 11.25 (T1). Among hybrids sca effect ranged from -22.39 (H6) to 64.56 (H5). Twelve hybrids recorded significant sca effect.

# 4.3.2.11 Grain yield per plant

The gca effect for grain yield per plant was significant in all the lines and testers. Among lines, gca effect of this trait was ranged from -111.28 (L2) to 43.91 (T4) and in testers, it ranged between -22.91 (T1) to 12.86 (T4). Among hybrids sca effect ranged from -27.30 (T9) to 28.36 (T24). Fifteen hybrids recorded significant sca effect.

## 4.3.2.12 Protein content

The gca effect for protein content was significant in all the lines and testers. In lines it varied from -1.73 (L1) to 1.76 (L3) and in testers it ranged between -1.49 (T4) to 1.43 (T2). Among hybrids, sca effect ranged from -1.91 (H20) to 2.74 (H18). Twelve among twenty four hybrids recorded significant sca effect.

Table 9a.Estimation of gca effect of line and testers for different characters

Genotypes	Plant height	No .of branches	Days to first flowering	Days to first harvest	Days to last harvest	Pods / plant
			Lines			
V.Jyothika	-50.56**	1.10**	5.06**	5.51**	3.21*	17.99**
Bhagyalakshmi	-105.98**	-2.57**	-10.09**	-12.17**	-13.37**	-35.12**
Anaswara	-54.67**	-0.18	-8.24**	-8.57**	-9.03**	7.62**
Vyjayanthi	76.69**	0.58**	6.71**	12.44**	9.67**	10.22**
Lola	61.65**	1.21**	9.56**	8.66**	14.87**	13.50**
Kanakamony	-28.15**	-0.15	-2.99	-5.87**	-5.35**	-14.21**
			Testers			
AV-5	-59.16**	-0.89**	-5.30**	-5.57**	-11.85**	-9.42**
PKB-3	6.85**	0.04	-2.62	-1.79	-0.92	3.46**
PKB-4	-3.19	0.21	1.25	1.53	1.08	1.38**
Sharika	55.50**	0.63**	6.66**	5.83**	11.69**	4.58**

<sup>\*</sup> significant at 5% level

<sup>\*\*</sup> significant at 1% level

Table 9b. Estimation of gca effect of line and testers of different characters

Genotypes	Length of pod	Pod weight	Seed/ pod	Test weight	Grain yield/ plant	Protein content
			Lines			
V.Jyothika	18.16**	10.39**	1.69**	2.83**	35.31**	-1.73**
Bhagyalakshmi	-21.18**	-12.53**	-3.95**	13.96**	- 111.28**	0.68*
Anaswara	-7.38**	-1.50**	0.12**	-2.37**	9.78**	1.76**
Vyjayanthi	16.18**	6.34**	0.79*	-2.99**	43.91**	-1.30**
Lola	15.07**	5.88**	3.53**	-1.09*	33.91**	-1.11**
Kanakamony	-20.85**	-8.59**	-2.19**	-10.34**	-11.84**	1.69**
			Testers			
AV-5	-2.05**	-1.36**	-1.09**	11.25**	-22.91**	-0.91**
PKB-3	-0.40	0.48	-0.20	-3.48**	6.49**	1.43**
PKB-4	0.18	-0.36	0.13	-4.27**	3.57**	0.97**
Sharika	2.27**	1.24**	1.15**	-3.50**	12.86**	-1.49**

Table 10 a. Estimation of sca effect of hybrids for different characters

Sl. no	Hybrids	Plant height	No. of branches	Days to first flowering	Days to first harvest	Days to last harvest	Pods / plant
1	$H_1$	-63.21**	-0.79*	-4.09	-2.50	-1.23	2.19*
2	$H_2$	33.09**	-0.42	4.03	4.55	0.74	2.31*
3	H <sub>3</sub>	11.92**	1.91**	1.26	3.13	4.14	1.24
4	$H_4$	18.20**	-0.70*	-1.21	-5.18	-3.65	-5.74**
5	H <sub>5</sub>	54.47**	1.48**	0.95	2.86	3.36	9.15**
6	$H_6$	-9.56*	-0.35	0.53	0.07	2.35	-2.71*
7	H <sub>7</sub>	3.30	-0.90**	-0.69	-1.14	-3.52	-2.62*
8	$H_8$	-48.21**	-0.24	-0.79	-1.79	-2.19	-3.82**
9	H <sub>9</sub>	29.22**	-0.60*	2.05	2.31	3.08	-10.21**
10	$H_{10}$	-32.86**	0.58*	-3.71	-3.47	3.15	4.67**
11	H <sub>11</sub>	-21.74**	0.12	2.61	1.30	-1.81	4.90**
12	$H_{12}$	25.39**	-0.10	-0.95	-0.14	-4.42	0.64
13	$H_{13}$	44.91**	0.74	4.24	3.64	2.33	-0.08
14	$H_{14}$	5.79	1.17**	3.56	2.72	3.41	6.18**
15	$H_{15}$	-22.99**	-1.04**	-3.06	-3.61	-2.51	-1.88
16	$H_{16}$	-27.71**	-0.87**	-4.74*	-2.75	-3.22	-4.21**
17	$H_{17}$	-77.19**	-0.59*	-4.89*	-4.94	-9.04**	-1.30
18	$H_{18}$	25.94**	-0.84**	2.54	3.49	4.01	-6.15**
19	H <sub>19</sub>	45.89**	0.54*	2.65	1.86	3.24	4.73**
20	H <sub>20</sub>	5.36	0.88**	-0.30	-0.41	1.79	2.72*
21	$H_{21}$	11.80**	-0.24	1.74	-1.37	1.51	0.25*
22	$H_{22}$	-22.40**	-0.15	-6.94**	-7.36*	-13.66**	-4.30**
23	$H_{23}$	-16.38**	-0.63*	-2.78	-1.54	0.46	-6.36**
24	$H_{24}$	26.98**	1.02**	7.99**	10.26**	11.69**	10.42**

Table 10 a. Estimation of sca effect of hybrids for different characters

Sl.						Grain	
no	Hybrids	Length.of	Pod	Seeds	Test	yield/	Protein
		pod	weight	/pod	weight	plant	content
1	$H_1$	-4.12*	-2.03**	-1.00	-11.96**	7.96**	-0.84
2	$H_2$	-0.90	-0.80	-0.71	3.49**	5.51*	2.410**
3	H <sub>3</sub>	5.62**	1.79*	0.85	6.3**	0.28	-1.84**
4	H <sub>4</sub>	-0.61	1.04	0.86	2.17	-13.75**	0.28
5	H <sub>5</sub>	1.41	0.76	0.98	64.56**	23.40**	1.52**
6	$H_6$	-1.05	-0.25	-1.00	-22.39**	-6.75	-1.29*
7	H <sub>7</sub>	-0.19	0.55	-0.47	22.35**	-4.68	-0.75
8	$H_8$	-0.16	0.04	0.50	-19.32**	-11.97**	0.52
9	H <sub>9</sub>	-3.71*	-3.04**	-2.46**	-18.87**	-27.30**	1.04*
10	$H_{10}$	0.73	0.77	1.23*	6.92	8.48	-1.10*
11	$H_{11}$	-2.00	1.01	1.38*	5.33	2.03	-0.61
12	$H_{12}$	4.97**	1.27*	-0.14	6.62	16.81**	0.67
13	$H_{13}$	2.62	1.77*	1.31*	-11.92**	23.28**	-0.14
14	$H_{14}$	0.07	1.10	1.14	4.19	-1.04	-1.72**
15	$H_{15}$	-1.46	-1.16	-1.27*	2.80	-0.14	2.22**
16	H <sub>16</sub>	-1.23	-1.71*	-1.18*	4.24**	-22.10**	-0.36
17	$H_{17}$	2.70	2.52**	1.27*	-10.35**	-6.52*	-1.31*
18	$H_{18}$	0.17	-0.69	-0.76	4.26	-6.00*	2.74**
19	$H_{19}$	-1.39	-1.75*	0.41	4.20	9.88**	0.48
20	$H_{20}$	-1.48	-0.08	-0.93	1.89	2.65	-1.91**
21	$H_{21}$	1.10	0.02	-0.10	-12.97**	-20.83**	-0.27
22	$H_{22}$	0.97	-0.13	0.10	3.55	-0.17	-1.03*
23	$H_{23}$	-0.58	0.67	-0.89	3.72	-7.37**	0.50
24	$H_{24}$	-1.49	-0.56	0.90	4.90	28.36**	0.80

<sup>\*</sup> significant at 5% level

<sup>\*\*</sup> significant at 1% leve

#### 4.4 Studies on heterosis

Hybridization was done in LxT model and 24 hybrids were evaluated for heterosis in comparison with mid parent, better parent and standard parent. The result of estimates of different type of heterosis is presented in Table 11. Standard parent was selected from bush, semi trailing and trailing based on the cross combination.

# 4.4.1 Plant height

The relative heterosis for this trait ranged between -62.43 (H8) to 46.56 (H19). Sixteen hybrids recorded significant relative heterosis of which ten hybrids registered significant negative values. Heterobeltiosis varied from -166.18 (H8) to 52.66 (H24). Fourteen hybrids registered significant heterobeltiosis in which H24 registered positive significance. Twelve hybrids registered significant standard heterosis which varied from -53.27 (H9) to 24.60 (H8). In ten hybrids all three types of heterosis were significant.

## 4.4.2 Number of branches per plant

All hybrids except H5 and H18 registered significant relative heterosis which varied from -23.37 (H7) to 45.65 (H3). Fourteen hybrids showed positive relative heterosis. Heterobeltiosis ranged from -36.27 (H7) to 37.41 (H3). Twenty two hybrids registered significant heterobeltiosis in which twelve hybrids recorded positive heterobeltiosis. All the hybrids except H5 exhibited significant standard heterosis which varied from -26.15 (H10) to 48.12 (H3). Eleven hybrids recorded positive significance for standard heterosis for this trait.

## 4.4.3 Days to flowering

Lowest relative heterosis of this trait among hybrids was recorded for H10 (-22.68) and highest for H24 (26.48). Fourteen hybrids recorded significant relative heterosis among which, 10 hybrids recorded positive significance. Heterobeltiosis varied from -25.87 (H10) to 41.10 (H24). Nine hybrids recorded significant

heterobeltiosis among which only H24 recorded positive significant value. Eight hybrids recorded significance for standard heterosis which varied from -24.52 (H10) to 19.60 (H8). Four hybrids had significance for three types of heterosis.

# 4.4.4 Days to first harvest

The relative heterosis for this trait ranged between -18.74 of H22 to 18.95 of H19. Eight hybrids exhibited significant relative heterosis of which six hybrids registered positive heterosis. Nine hybrids recorded significant negative heterobeltiosis which ranged from -25.90 (H8) to 25.68 (H24). Four hybrids showed significant standard heterosis which varied from -28.69 (H17) to 21.25 (H11). Only one hybrid exhibited positive standard heterosis. None of the hybrids recorded significance for all the three types of heterosis.

## 4.4.5 Days to last harvest

Hybrid H19 registered positive significance for all the three type of heterosis. Only four hybrids recorded significant relative heterosis which ranged from -14.28 (H9) to 22.67 (H24). Seven hybrids recorded significant heterobeltiosis. While fourteen hybrids registered significant standard heterosis. Lowest heterobeltiosis was observed for H1 (-15.55) and highest for H19 (26.99). Standard heterosis varied from -9.66 (H12) to 18.00 (H8).

## 4.4.6 Number of pods per plant

All the hybrids except H6 and H8 exhibited significant relative heterosis. The hybrids H5 (-9.79) and H7 (-12.66) recorded significant negative relative heterosis. Twenty one hybrids recorded significant heterobeltiosis which ranged from -32.14 (H7) to 145.22 (H24). Nineteen hybrids exhibited significant standard heterosis for this trait which ranged from -31.99 (H21) to 62.78 (H10). Only four hybrids recorded negative standard heterosis. Fifteen hybrids exhibited significance for all the three types of heterosis.

# 4.4.7 Length of the pods

All hybrids exhibited significant relative heterosis for this trait which varied from -37.88 (H24) to 67.18 (H2). Sixteen hybrids registered significant positive relative heterosis. Heterobeltiosis value ranged between -55.21 (H24) to 18.67 (H3) while, standard heterosis varied from -66.09 (H24) to 196.65 (H17). Twelve hybrids exhibited significant heterobeltiosis while nineteen hybrids exhibited significant standard heterosis. Five hybrids registered significance for all the three types of heterosis.

# 4.4.8 Pod weight

Twenty two among twenty four hybrids showed significant relative heterosis for pod weight, which ranged from -53.92 (H5) to 47.22 (H3). Thirteen hybrids exhibited positive significant relative heterosis. Heterobeltiosis ranged from -72.07 (H5) to 24.35 (H4) in which seven hybrids recorded significant positive heterobeltiosis. All the hybrids except H24 registered significant standard heterosis which ranged from -10.58 (H21) to 210.26 (H4). Nineteen hybrids had significance for all the three types of heterosis.

# 4.4.9 Seeds per pod

The relative heterosis of this trait ranged from -22.18 of H6 to 20.89 of H3. Sixteen hybrids exihibited significant relative heterosis of which seven hybrids showed significant positive relative heterosis. Eighteen hybrids registered significant heterobeltiosis which is ranged from -33.93 (H6) to 18.15 (H3). Only four hybrids recorded significant positive heterobeltiosis. Standard heterosis ranged between 19.09 (H9) to 19.60 (H20). Eighteen hybrids registered significant standard heterosis in which four hybrids had positive standard heterosis. Twelve hybrids exihibited significance for all the three types of heterosis.

## **4.4.10** Test weight

Lowest relative heterosis of this trait among hybrids was recorded for H7 with value of -40.27 and highest for H12 with a value of 36.25. Twenty one hybrids exhibited significant relative heterosis for this trait of these hybrids eight registered significant positive relative heterosis. Heterobeltiosis value ranged from -57.26 (H7) to 22.77(H12). Only seven hybrids registered significant positive heterobeltiosis. All the hybrids except H21 (-0.48) and H23 (2.78) exhibited significant standard heterosis. Two hybrids H6 (-6.36) and H7 (-12.90) recorded significant negative value for standard heterosis. Nineteen hybrids exhibited significance for all the three types of heterosis.

# 4.4.11 Grain yield per plant

The relative heterosis for this trait ranged from -79.28 (H6) to 59.33 (H24). Seventeen hybrids recorded significant positive relative heterosis of which ten hybrids showed significant positive relative heterosis. The value ranged from -89.00 (H6) to 58.84 (H24) and -26.95 (H21) to 89.69 (H7) for heterobeltiosis and standard heterosis respectively. Fifteen hybrids recorded significant heterobeltiosis while eleven hybrids exhibited significant standard heterosis. Seven hybrids exhibited significance for all the three types of heterosis.

#### **4.4.12 Protein content**

Sixteen hybrids recorded significance for all the three type of heterosis for protein content. Twenty hybrids exhibited significance for relative heterosis, similarly twenty hybrids registered significant heterobeltiosis in which twelve hybrids registered significant positive heterobeltiosis. Twenty hybrids were significant for standard heterosis. The value ranged from -14.57 (H20) to 15.45 (H23) and -15.47 (H20) to 12.10 (H21) for relative heterosis and heterobeltiosis. Standard heterosis varied from -7.68 (H20) to 22.53 (H23).

Table 11a. Relative heterosis, heterobeltiosis and standard heterosis for different characters

Hybrids		Plant height			No. of branch	nes	1	Days to flowering	g	Days to first harvest		
Hybrids	di	dii	diii	di	dii	diii	di	dii	diii	di	dii	diii
H1	-54.41**	-70.89**	- 43.51**	-3.06**	-10.06**	4.04**	-7.29	-19.95**	0.94	-2.4	-16.67**	-1.55
H2	30.69**	-7.11	-5.05**	14.62**	6.25**	-9.40**	16.64**	1.45	-6.8	12.16	-0.43	-3.92
Н3	18.04	-19.37	-18.25	45.65**	37.41**	17.14**	19.13**	3.63	-4.8	18.19**	2.42	-1.17
H4	15.48	6.16	9.23	11.65**	10.12**	-6.12**	10.85**	9.45	0.54	-4.17	-3.6	-6.98
H5	-35.00**	-35.28**	-7	0.35	-15.33**	-23.14**	-14.12**	-17.40**	-10.54**	-7.32	-8.34	-6.28
Н6	-48.74**	-70.05**	-1.79	-15.03**	-28.24**	4.14**	-8.55	-12.78**	-3.88	-9.58	-14.45**	-4.13
H7	-38.91**	-53.12**	5.66	-23.37**	-36.27**	-3.92**	-1.12	-5.71	3.94	-2.46	-5.2	0.43
Н8	-62.43**	-166.18**	24.60**	-10.36**	-28.07**	18.89**	-2.47	-17.66**	19.60**	-11.99	-25.90**	8.35
Н9	-36.23**	-49.64**	-53.27**	-11.20**	-11.52**	-21.96**	-14.06**	-18.29**	-16.853**	-9.69	-16.35**	6.5
H10	-43.04**	-46.42**	-50.28**	19.62**	19.06**	-26.15**	-22.68**	-25.87**	-24.52**	-17.27**	-19.38**	13.87
H11	-38.29**	-45.53**	-49.45**	13.21**	11.62**	-23.41**	3.44	-0.82	0.82	0.51	-5.36	21.25**
H12	2.73	-41.27**	-32.24**	10.73**	4.43**	-13.41**	-6.1	-14.23**	-23.18**	-10.04	-18.12**	-20.05**
H13	40.68**	-7.67	-16.96	10.21**	2.05**	-12.61**	12.57**	-4.63	-8.29	16.96**	-2.22	-0.68
H14	41.30**	4.25	-5.59	28.74**	19.09**	1.97**	16.20**	-0.85	-4.65	17.29**	1.85	3.45
H15	23.20**	-12.96	-22.01**	-0.46	-6.28**	-19.75**	10.09**	-6.06	-9.66	15.02**	-2.44	-0.89
H16	14.04	10.97	0.81	2.69**	1.06	-13.47**	4.59	0.99	-2.88	6.99	4.92	6.56
H17	-55.35**	-71.33**	-45.71**	-7.45**	-19.97**	15.75**	-3.74	-19.74**	10.14**	-3.21	-18.56**	-28.69**
H18	35.17**	-3.22	-3.38	1.08	-12.67**	-12.67**	17.50**	-1.34	-1.32	13.35**	-0.91	-0.91
H19	46.56**	0.77	0.8	18.25**	3.83**	3.83	26.12**	5.91	5.9	18.95**	1.55	1.54
H20	16.26	8.08	8.49	22.27**	11.82**	11.82**	16.47**	10.38	10.39**	5.72	4.47	4.47
H21	-30.19**	-46.33**	-46.33**	-4.27**	-5.11**	15.89**	-0.38	-4.47	-4.58	-10.76	-16.67**	-14.52**
H22	-14.28	-22.09**	-22.08**	11.02**	10.17**	24.27**	-16.74**	-19.38**	-19.51**	-18.74**	-20.74**	-11.41
H23	-12.47	-25.15**	-25.14**	4.34**	1.62	48.12**	4.03	0.61	0.46	1.19	-3.93	-8.3
H24	16.23	52.66**	-20.35**	27.94**	19.27**	-1.11	-1.11	41.10**	2.63	12.18	25.68**	-1.09

Table 11b.Relative heterosis, heterobeltiosis and standard heterosis for different characters

Hybride	Day	ys to last har	vest		No. of pods		L	ength of poo	ls		Pod weight	
Hybrids	di	dii	diii	di	dii	diii	di	dii	diii	di	dii	diii
H1	-9.68	-15.55**	10.81	52.60**	6.76	50.87**	30.73**	-4.12	176.20**	15.43**	1.72	166.87**
H2	-0.4	-4.9	-5.75	86.45**	29.07**	25.13**	45.46**	5.15	2.52	23.75**	13.96**	184.34**
Н3	6.96	-0.45	-1.33	79.11**	23.67**	19.90**	67.18**	18.67**	15.71**	47.22**	20.95**	20179**
H4	1.93	1.88	0.97	71.64**	17.19**	13.61**	24.72**	10.78**	8.02	44.45**	24.35**	210.26**
Н5	-8.4	-15.09**	-1.6	-9.79**	-31.05**	30.43**	-17.35**	-32.61**	6.86	-53.92**	-72.07**	31.60**
Н6	-0.75	-9.97	9.21	-1.69	-23.87**	38.73**	-19.20**	-32.93**	1.55	-51.04**	-70.81**	51.85**
Н7	-1.75	-8.01	4.99	-12.66**	-32.14**	22.49*	-8.59**	-22.24**	10.87	-50.22**	-68.85**	23.70**
Н8	1.78	-12.73	18.00**	1.59	-19.87**	38.77**	-31.49**	-52.76**	24.59	-34.89**	-60.14**	77.78**
Н9	-14.28**	-11.03	2.22	15.20**	-12.74**	-4.39	-11.44**	-22.22**	38.25**	-28.56**	-34.22**	31.60**
H10	-6.34	-4.83	14.13	98.87**	48.76**	62.98**	12.14**	-3.41	71.67**	-1.95	-13.60**	90.82**
H11	-6.54	-1.96	10.93	94.00**	44.66**	58.49**	7.04**	-10.07**	59.83**	9.47**	9.35**	84.53**
H12	-6.35	-8.77	-9.66	93.42**	42.30**	6.95	4.41**	-6.32	-29.07**	14.06**	7.75**	94.01**
H13	-1.74	6.92	-8.11	39.70**	1.46	-13.22**	41.46**	3.19	2.32	16.82**	4.71**	151.34**
H14	6.53	14.12	1.71	93.24**	38.73**	18.65**	41.14**	1.51	0.65	16.85**	9.55**	162.91**
H15	5.82	16.04**	-1.49	66.20**	18.99**	1.76	41.17**	-0.28	-1.13	15.89**	-3.3	132.10**
H16	6.71	9.28	6.6	70.66**	20.68**	3.21	18.02**	4.07	3.19	15.47**	1.06	142.57**
H17	-6.74	0.75	14.97	30.07**	-9.80**	31.49**	38.00**	0.4	196.65**	10.56**	-5.71**	167.29**
H18	11.97	19.93**	6.45	50.89**	3.57	3.57	37.68**	-1.24	-1.22	0.28	-10.8**	140.47**
H19	15.93**	26.99**	7.46	72.70**	18.24**	18.24**	37.56**	-3.07	-3.06	3.05**	-17.8**	121.63**
H20	15.53**	19.49**	14.96	77.52**	20.21**	20.21**	14.55**	0.64	0.65	13.06**	-5.71**	154.23**
H21	-1.88	-8.92	4.5	31.11**	20.54**	-31.99**	-22.19**	-32.49**	-9.22**	-41.40**	-55.31**	-10.58**
H22	-8.43	1.08	-0.09	73.55**	62.34**	-11.78**	.12.19**	-22.84**	-0.9	-34.28**	-51.50**	7.12**
H23	10.78	18.75**	17.36**	54.59**	45.53**	-21.81**	-14.72**	-22.49**	-6.28	-22.12**	-36.80**	6.65**
H24	22.67**	7.57	6.51	155.95**	145.22**	13.10**	-37.88**	-55.21**	-66.09**	-24.90**	-41.60**	5.18

Table 11c. Relative heterosis, heterobeltiosis and standard heterosis for different

Hybrids		Seeds per pod			Test weight	t	Grai	n yield per	Grain yield per plant			nt
•	di	dii	diii	di	dii	diii	di	dii	diii	di	dii	diii
H1	-4.96**	-10.23**	-2.77	10.83**	8.96**	117.77**	0.23	-8.99	46.96**	-4.87**	-6.19**	-3.64**
H2	1.24	-4.43**	-13.77**	13.84**	12.08**	124.00**	14.63**	1.67	15.09	10.06**	5.37**	18.32**
Н3	20.89**	18.15**	-5.34**	19.89**	18.75**	141.95**	24.06**	22.75**	9.83	-7.14**	-11.09**	-0.17
H4	20.77**	17.75**	-0.69	15.53**	6.19**	112.24**	40.23**	21.90**	6.77	-5.96**	-7.75**	-1.49
H5	-15.77**	-28.46**	2.38	606.72**	414.10**	892.74**	-77.37**	-87.55**	85.98**	9.22**	3.73**	15.16**
Н6	-22.18**	-33.93**	-5.34**	-33.48**	-51.65**	-6.36**	-79.28**	-89.00**	79.02**	1.46	0.89	13.29**
H7	-9.01**	-17.05**	0.74	-40.27**	-57.26**	-12.90**	-75.32**	-86.70**	71.09**	1.74	1.18	13.59**
Н8	-1.74	-14.18**	14.93**	-8.98**	-30.63**	16.22**	-63.18**	-79.61**	89.69**	0.05	-1.86	8.96**
Н9	-21.28**	-25.30**	-19.09**	-32.37**	-42.65**	10.74**	-36.36**	-45.66**	-12.25	12.70**	8.10**	17.55**
H10	2.68	-2.61	5.58**	27.07**	7.62**	108.44**	6.13	-11.32	51.00**	7.06**	5.37**	18.32**
H11	14.37**	11.23**	8.17**	10.89**	-7.98**	87.48**	14.06**	5.45	41.92**	7.18**	5.49**	18.43**
H12	6.22**	4.07**	-12.23**	36.25**	22.77**	105.70**	56.24**	44.64**	9.89	5.59**	4.64**	13.79**
H13	-3.36**	-3.48**	-12.79**	-7.69**	-10.49**	72.85**	12.31	5.27	13.01	-2.32**	-5.40**	0.82
H14	0.17	0.1	-9.56**	-4.64**	-7.67**	78.82**	12.3	2.73	16.28	-5.13**	-7.54**	3.82**
H15	-2.74	-10.21**	-18.87**	-17.10**	-21.65**	59.63**	25.41**	22.46**	14.98	7.41**	4.69**	17.53**
H16	-1.41	-4.69**	-13.89**	2.65	-1.27	79.08**	34.70**	13.75	6.81	-8.44**	-8.35**	-2.32
H17	4.53**	-0.63	19.41**	-0.15	-2.38	97.34**	-15.77**	-18.66**	31.35**	-7.30**	-11.32**	-3.033**
H18	-0.9	-5.75**	-5.74**	-0.87	-2.95	96.19**	0.03	-5.8	6.63	10.22**	8.77**	22.14**
H19	14.45**	0.99	-0.47	-6.97**	-7.33**	88.81**	21.39**	15	14.99	0.54	-0.77	11.40**
H20	7.99**	-0.47	19.60**	-5.27**	-13.38**	75.11**	41.27**	16.33**	16.33**	-14.57**	-15.57**	-7.68**
H21	-21.10**	-25.10**	-18.87**	-33.54**	-48.47**	-0.48	-43.68**	-54.77**	-26.95**	12.17**	12.10**	12.09**
H22	-15.40**	-19.73**	-12.97**	-27.92**	-44.17**	8.13**	-9.29	-28.77**	21.63**	11.47**	5.37**	18.32**
H23	-11.81**	-14.27**	-16.55**	-33.71**	-49.56**	2.78	-3.81	-16.92**	11.81	15.45**	9.14**	22.53**
H24	-0.75	1.3	-17.95	-12.43**	-28.42**	19.93**	59.33**	58.84**	3.39	10.33**	6.83**	14.06**

# Discussion

#### 5. DISCUSSION

Cowpea (*Vigna unguiculata* L. Walp) is one of the most important legume crops in the world and grown in many parts of India and elsewhere. It is the versatile pulse crop because of its nutritional value, weed smothering nature, drought tolerant characters, soil restoring properties and multi-purpose uses. It is gaining popularity in developing and under developed countries due to its nutritional value. The low yield of cowpea is attributed to lack of superior genotypes with high productivity. One of the important constraints limiting the productivity of the crop is the autogamous nature of flower, which restrict the induction of variation genetic variability by recombination that can be exploited for the crop improvement.

Variability is the basis for any crop improvement programme. Success of plant breeding depends on the identification of superior genotypes which can produce superior offspring. An understanding of variability of the genetic control of quantitative characters and knowledge on the combining ability of the parents and hybrids are of paramount importance for choosing the superior combinations with high heterotic response.

Considering the context, in the present study twenty two cowpea genotypes were evaluated and ten cowpea genotypes with high protein content were hybridized in line x tester mating design. The results of the study are discussed in this chapter.

## 5.1 EVALUATION OF COWPEA GENOTYPES

## **5.1.1** Mean performance of cowpea genotypes

The success of most crop improvement programs largely depends upon the genetic variability and the heritability of desirable traits. The magnitude and type of genetic variability help the breeder to determine the selection criteria and breeding schemes to be used for improvement purposes. In the present study, the twenty two

genotypes evaluated possessed sufficient variability for most of the traits including seed protein content and grain yield per plant. The cowpea genotypes were grouped in to three groups based on the height by Patel *et al.* (2007). Plants having more than 180 cm height was classified as trailing types, semitrailing type were with 80-180 cm height where as bushy type were with less than 80 cm height. Hence, the results are discussed based on plant habit for all the traits except protein content. The result obtained for mean performance of cowpea genotypes are discussed hereunder

# **5.1.1.1 Plant** height

The cowpea genotypes showed high degree of variability in plant height. Longest plants were observed for Vellayani Jyothika (254.48 cm) in trailing type and shortest plants were in Hridya (30.53 cm) of bushy type. Sobha and Vahab, (2000) and Chaudhary and Naik, (2010) also noted high variability of plant height in cowpea. The Fig 1 demonstrates the variability in plant height observed in the tested genotypes. Among the 22 genotypes four were falling under trailing, six were under semi trailing and 15 under bushy type. Sivakumar *et al.* (2013) reported high variability in plant height in bushy cowpea. However, in the present study bushy, semi trailing and trailing types exhibited comparable variability in plant height.

# **5.1.1.2** Days to flowering

The variability exhibited by the genotypes for days to flowering is represented in the figure 2. From the graph it is evident that in bushy type variation was higher for days to flowering. Difference in trailing type for days to flowering was low. This can be due to lesser number of genotypes studied in trailing type. In semi trailing type except CP-1 all other genotypes started flowering in 35-40 days. Bushy cowpea appears to be flower early due to its early vegetative growth followed by semi trailing. Trailing types were generally late to flower. In bushy type, Hridya (27.19 days) recorded minimum days to flowering and it was maximum for Co-6 with 51.14 days. Mishra *et al.* (2009) reported variation in days to flowering in bushy type

cowpea and Sharma *et al.* (2013) reported variation in semi trailing cowpea. Karpe *et al.* (2006) grouped cowpea genotypes based on the days to flowering. Genotypes which take less than 40 days to flowering are considered as early flowering type, between 40-50 days as medium and more than 50 days considered as late to flowering. Among the 22 cowpea genotypes evaluated six genotypes were early to flower which is a desirable trait in cowpea. Among the early genotypes two were bushy and three were semi trailing and none of them were trailing indicates dwarfness is associated with early flowering.

# **5.1.1.3** Days to first harvest

Similar to days to first flowering, days to first harvest also showed sufficient variability. Among the bushy type CP-1 (70.20) took maximum days to initiate harvest .The pods took 15 days from flowering to mature . While Hridya which flowered in 27 days pods could harvest in 11 days. This shows the presence of variability in maturation time between genotypes. Kumar and Sagwan, (2005) and Patel *et al.*, (2007) also reported high variability in days to first harvest in cowpea. In the semi trailing genotype AV-5 and PKB-3 flowered in 37 days and pods could harvest in 11 days, while in Anaswara pods took 15 days to mature. In case of trailing type, pods took more than 15 days to mature from the flowering date. Variability for days taken to pod maturity is comparable between three type of genotypes. The trailing types were having an extended vegetative phase they enter in to reproductive phase later compared to bushy and semi trailing type.

#### **5.1.1.4 Days to last harvest**

CP-1 which flowered late among bushy types registered maximum value for days to last harvest (124.37 days) also. Similarly in early flowered Hridya life cycle completed early and lowest value exhibited by Hridya (65.85 days). Similar to the observation by Guptha, (2010) variability for days to last harvest in cowpea was between 70 to 125 days. Among the bushy type, Kashi kanchan exhibited a growth

duration of 115 days which is comparable to that of semi trailing type. Kanakamony which is semi trailing type completed its lifecycle in 91 days. Trailing type cowpea exhibited maximum days to harvest due to its indeterminate growth habit.

# **5.1.1.5 Pods per plant**

Variability in number of pods per plant is presented in Fig 3. The genotypes Vellayani Jyothika (58.24), Vyjayanthi (51.37), Lola (60.07) of trailing type AV-5 (60.31), PKB-3 (63.63) and PKB-4 (55.60) of semi trailing type had more than fifty number of pods. Bushy types with more number of pods can result in more yield per unit area as more number of plants can be accommodated. However, none of the bushy genotypes recorded more than 20 pods per plant. AV-5, PKB-3 and PKB-4 of semi trailing type recorded higher number of pods which is comparable to the trailing type. Variability in pods per plant was earlier noted by Singh *et al.* (2009) and Dalsaniya *et al.* (2013).

# 5.1.1.6 Length of pod

Lola had longest pod of 53.83 cm and Hridya had shortest pod of 12.26 cm. Earlier findings of Chaudhary and Naik, (2010) and Indarsingh *et al.* (2007) about variability in pod length are in concurrent with the present study. Chaudhari *et al.* (2013) classified cowpea genotypes in to 3 groups based on length of pods namely short pods of less than 20 cm, medium with 20 - 40 cm and long with more than 40 cm. Ten genotypes had short pods of less than 20cm. Medium sized pods of 20- 40cm were observed in seven genotypes. Longer pods of more than 40 cm were observed in five genotypes of these four were trailing and only one (CP-1) was semi trailing type. Generally trailing type possess longer pods and short pods are possessed by bushy type. In bushy type Co-6 (22.74 cm) had medium sized pods.

## **5.1.1.7 Pod weight**

Variability in pod weight in cowpea as reported by Karpe *et al.* (2006) and Sharma *et al.* (2013) was at a range of 4.83g to 12.44g. In the present study, highest

pod weight was recorded in Lola (27.04g) a trailing type which also registered high pod length. Minimum pod weight was registered by Hridya (2.65g) belonging to bushy type having shortest pods. Tyagi *et al.* (2000) classified cowpea genotypes in to three groups namely low pod weight (< 10g), medium pod weight (10 - 20g) and high pod weight (< 20g). Among the 22 genotypes evaluated four genotypes were having high pod weight of which three were trailing and one (PKB-3) was semi trailing. Ten genotypes were having low pod weight and all of them were bushy types.

# **5.1.1.8 Seeds per pod**

Kukar and Sagwan, (2005) classified cowpea based on the seeds per pod in to three groups, low seeded cowpea (< 10 seeds per pod, medium seeded (10 - 20 seeds per pod) and high seeded cowpea (> 20 seeds per pod). Seeds per pod is dire <sup>80</sup> related to the length of pod (Santos *et al.*, 2012) as length increases seeds per pod also increases which was not true with CP-1. Out of the 22 genotypes evaluated four genotypes belonged to high seeded cowpea of which two were trailing and two were having semi trailing habit (Fig 4). This clearly indicates growth habit is influencing the seeds per pod. Among the bushy type four were belonging to the low seeded cowpea, all other eight genotypes were medium seeded. In semi trailing type even though CP-1 was having longer pods, number of seeds per pod was only thirteen. Genotypes AV-5, PKB-3 of semi trailing and Vyjayanthi, Lola of trailing type can be grouped as high seeded cowpea genotypes.

# **5.1.1.9** Test weight

Variability in test weight of cowpea was reported by Sivakumar *et al.* (2013). Test weight for bushy type ranged from 6.81g to 13.53g. In the case of trailing type test weight was more than 12g, while three genotypes had more than 20g. The highest test weight of the group was shown by the trailing type where all the genotype had more than 18g for test weight.

## 5.1.1.10 Grain yield per plant (g)

Bhavesh *et al.* (2012) classified cowpea genotypes in to 3 catagories based on yield per plant. High yielding genotypes ( > 100g per plant), medium (50 - 100g per plant) and low yielding ( < 50g per plant) genotypes. In the present study among the 22 genotypes nine genotypes (PKB-3 (175.40g), AV-5 (166.34g), Lola (154.94g), Vyjayanthi(145.49g), PKB-4 (138.64g), Vellayani Jyothika (135.73g), Anaswara (117.72g), Sharika (100.24g) and Kanakamony (100.86) recorded high grain yield per plant among which five were trailing type and four were semi trailing type (Fig 5). Due to its determinate growth habit per plant grain yield was very low in bushy type. However, the genotype CP-2 and CP-3 were having grain yield of more than 30g per plant. These genotypes can be used for high grain yield per unit area.

#### **5.1.1.11 Protein content**

The cowpea genotypes showed high degree of variability in protein content. The seed protein content of the 22 genotypes ranged from 17.56 to 28.74 per cent with a mean value of 23.41 per cent. Among the 22 genotypes screened for seed protein content eight genotypes (PKB-3 (28.5%), PKB-4 (28.49%), Bhagyalaksmi (28.18%), Lola (27.75%), Anaswara (27.6%), Sharika (27.10%), Vyjayanthi (27.05), Vellayani Jyothika (26.07) had high seed protein content. Out of the eight genotypes, five were trailing type, three were semi trailing and only one (Bhagyalakshmi) was bushy type with early flowering and harvest (Fig. 6) Even though, in Bhagyalakshmi per plant grain yield was low it can maintain a large population due to its bushy nature. Kumar and Sagwan, (2005), Usha Kumari *et al.* (2010) and Chaudhari *et al.* (2013) too observed similar results.

Among the high yielding genotypes PKB-3, PKB-4, Lola, Anaswara, Vyjayanthi, Vellayani Jyothika and Sharika recorded high yield and protein content. The genotypes more than 25 per cent protein content were selected for hybridization programme

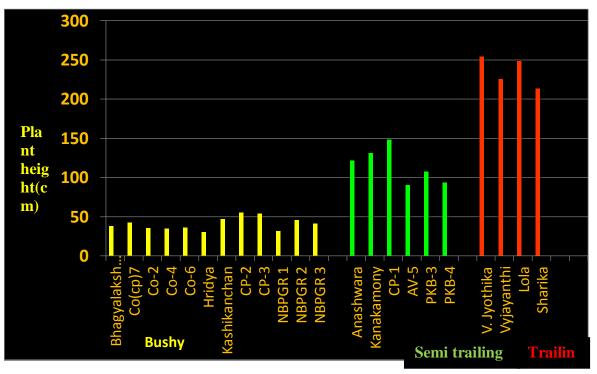


Fig 1. Variability in plant height of cowpea genotypes

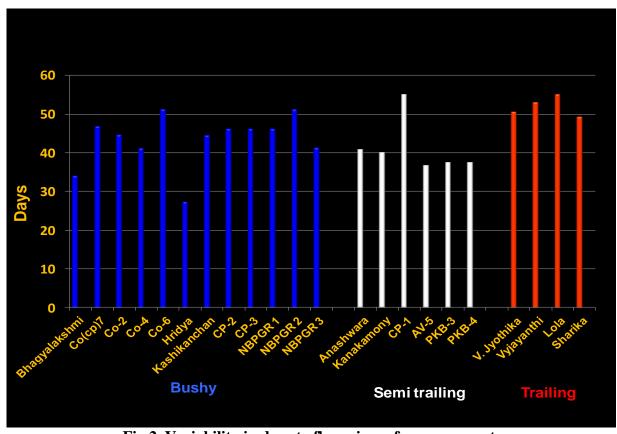


Fig 2. Variability in days to flowering of cowpea genotypes

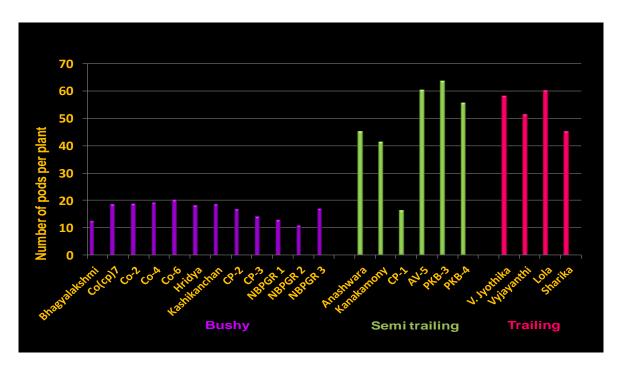


Fig 3. Variability in pods per plant of cowpea genotypes

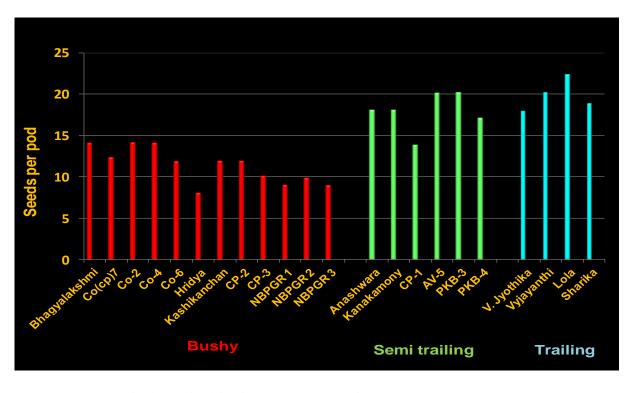


Fig 4. Variability in sees per pod of cowpea genotypes

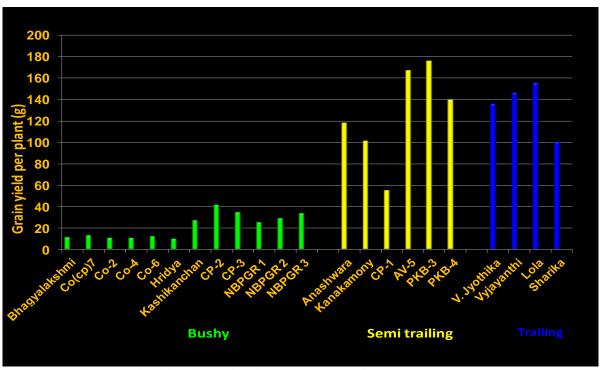


Fig 5. Variability in grain yield per plant of cowpea genotypes

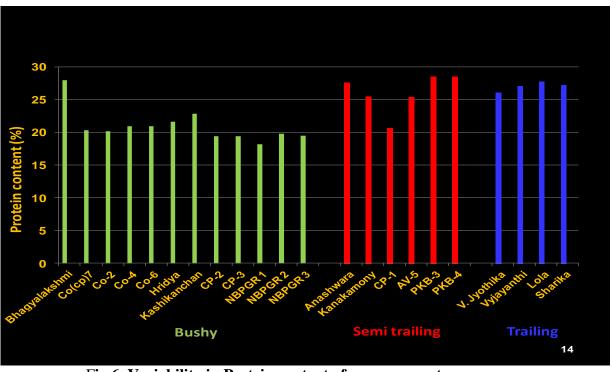


Fig 6. Variability in Protein content of cowpea genotypes

## **5.2 Evaluation of hybrids**

# 5.2.1 Mean performance of hybrids

Mean performance of hybrids for various traits are discussed.

# **5.2.1.1 Plant** height

Hybrids H2, H3, H4, H13, H16, H18, H19, H20 and H24 showed high mean value for plant height. Three hybrids H5,H6 and H8 registered low value for plant height. So these can be useful to develop dwarf F1 plants. Mean value of hybrid for plant height ranged from 35.22 - 270.15cm. Variability in cowpea hybrids for plant height earlier reported by Selvakumar *et al.* (2014).

# **5.2.1.2** Number of branches per plant

Number of branches per plant ranged from 4.5 to 11.01. Chauhan, (2008) reported variability for this trait among cowpea hybrids. Dwarf hybrids possessed less number of branches per plant where as trailing type hybrids exhibited more number of branches per plant.

## **5.2.1.3 Days to flowering**

Six hybrids were early to flower namely H5, H6, H7, H9, H10 and H22 while 10 hybrids H2, H3, H4, H13, H14, H16, H18, H19, H20 and H24 were late to flowering. So the hybrids involving Bhagyalakshmi as the female parent flowered early. Boukar *et al.* (2011) reported variability among cowpea hybrids for days to flowering.

## **5.2.1.4** Days to first harvest

Hybrids H5, H6, H7, H8, H9, H10, H21, H22 were early to first harvest where as hybrids H3, H13, H14, H15, H16, H18, H19, H20 and H24 were late to first harvest. Days to first harvest in cowpea hybrid ranged between 30.16 to 60.65 days. Low value of days to harvest means the hybrids attain harvesting within a short time,

these early maturing hybrids expected to be early in flowering also. Chaudhari *et al.* (2013) reported significant variability for days to first harvest among cowpea hybrids.

## **5.2.1.5** Days to last harvest

Twelve hybrids namely H2, H3, H4, H12, H13, H14, H15, H16, H18, H19, H20 and H24 registered high mean value for days to last harvest. Five hybrids H5, H7, H9, H21 and H22 exhibited low mean value for days to last harvest. In contrast to days to first harvest where low value is desirable, in this trait high value of days to last harvest is desirable. High value of days to harvest prolong the harvesting period of cowpea there by substantially increases the yield per plant.

## **5.2.1.6 Pods per plant**

Wide variability was noticed among cowpea hybrids for pods per plant. Sharma *et al.* (2013) noticed wide variability for pods per plant among cowpea hybrids. Four hybrids H5, H6, H7 and H8 showed low mean value for pods per plant. But hybrids namely H2, H3, H4, H10, H14, H19 and H20 registered high mean value for number of pods. Those hybrids in which parents include either bhagyalakshmi or AV-5 one of the parent possessed less pods per plant. Hybrids registering high pods per plant exhibiting high grain yield per plant, so these hybrids in which high numbers of pods were used for developing high yielding varieties through appropriate breeding programme.

# 5.2.1.7 Length of pods

Among cowpea hybrids pod length ranged from 15.69 - 62.29 cm. Bhavesh *et al.* (2012) reported wide variability for pod length in cowpea hybrids.

High pod length was registered by 11 hybrids H2, H3, H4, H13, H14, H15, H16, H17, H18, H19 and H20. Eight hybrids H5, H6, H7, H8, H21, H22, H23 and H24 were showed low pod length. As the pod length increases number of seeds per pod

also increases. So the eleven hybrids having high pod length registering high yield per plant there by these hybrids can be used for further crop improvement programmes.

# **5.2.1.8 Pod weight**

Wide variability for pod weight in cowpea hybrids was earlier reported by Yadav *et al.* (2005). Pod weight was higher in hybrids H1, H2, H3, H4, H13, H14, H17 and H20. But pod weight was less in eight hybrids H5, H6, H7, H8, H21, H22, H23 and H24. Pod weight is directly related to the length of the pods, grain as well as pod yield of the plant. So these seven hybrids registering high pod weight can used for future breeding programmes.

# **5.2.1.9** Seeds per pod

Seeds per pod in cowpea hybrid ranged between 13.28 to 22.50. Variability for seeds per pod among cowpea hybrids was noted by Indarsingh *et al.* (2007). 13 hybrids H2, H3, H4, H12, H10,H11, H12, H13, H14, H16, H17, H18, H19 and H20 had more seeds per pod while eight hybrids H5, H6, H7, H8, H9,H21, H22 and H23 had less seeds per pod. Seeds per pod is positively correlated with grain yield of the plant, so hybrids showing more seeds per pod would be used for developing high yielding varieties.

# **5.2.1.10** Test weight

Variability for test weight in cowpea hybrids was earlier reported by Valarmathi *et al.*,(2007) which is concurrent with present study. Test weight was more for hybrids H1, H2, H3, H4, H10 and H12. But in five hybrids H5, H6, H7, H21 and H23 possess less test weight. These hybrids showing high test weight values also registering high grain yield per plant. So these hybrids offer promise for the selection of superior cowpea high yielding varieties.

## 5.2.1.11 Grain yield per plant

Existence of wide variability for grain yield per plant in cowpea hybrids was earlier suggested by Mishra *et al.* (2009) and Gupta, (2010). Yield was higher in hybrids H2, H3, H4, H12, H13, H14, H15, H19 and H20. But four hybrids like H5, H6, H7 and H8 recorded low yield per plant. Hybrids H19 and H15 and H13 exhibiting moderate protein content and could be used for simultaneous improvement of these traits. These can also serve as the source to develop breeding materials in which selection can be exercised in succeeding generation

## **5.2.1.12 Protein content**

Sivakumar *et al.* (2013) reported variability for seed protein content among cowpea hybrids. In the present study seed protein content ranged between 23.43 to 31.10 per cent. Response to selection could be expected from progenies H2, H10, H11 H18, H23 and H22 which exhibited high mean value for high seed protein content. Hybrids H5, H6, H9, H12, H15 and H24 exhibited moderate mean value for high seed protein content. Hence, these could be exploited further in breeding programmes aimed at imparting protein rich cowpea. Hybrids H14 and H20 with high mean grain yield per plant but moderate protein content holds promise but attempt need to be made to improve their seed protein content.

# 5.3 Phenotypic and genotypic coefficient of variation

Coefficient of variation provides a relative measure of variance among different traits. The total variation present in a population arises due to genotypic and environmental effects. Hence, it is necessary to split the overall variability into its heritable and non heritable components resorting to estimation of genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV).

In the present study estimates of PCV were higher than GCV for all the traits. The PCV and GCV were classified as suggested by Sivasubramanian and Madhavamenon, (1973) into low (0-10%), moderate (10.1-20%) and high (>20%). As per the classification PCV were high for all the traits except days to first flowering, days to first harvest and days to last harvest. These characters were having moderate PCV. High GCV was observed for traits plant height, number of pods per plant, length of pod, pod weight, seeds per pod, test weight and yield per plant. All the other traits exhibited moderate GCV. High variability associated with the major characters indicates that there is possibility of improvement through selection. However, the most important traits for the present study, that is protein content variability was moderate.

Malarvizhi, (2004), Chaudhary and Naik, (2010) reported high PCV and GCV in case of grain yield per plant. High PCV and GCV estimates in plant height were reported by Borah and Khan, (2003), Patel *et al.* (2007), and Chauhan, (2008). Indarsingh *et al.* (2007) and Sharma *et al.* (2013) observed high PCV and GCV for pod length. High PCV and GCV estimates in pods per plant reported by Sobha and Vahab, (2000). According to Tyagi *et al.* (2000), days to flowering exhibit moderate GCV and PCV, while finding of Sharma *et al.* (2013) reported moderate PCV and GCV for protein content, which is concurrent with present study.

## **5.4** Heritability

The amount of genetic variation considered alone will not be of much use to the breeder unless supplemented with the information on heritability estimates which is a measure of heritable portion of the total variation. Heritability plays an important role in deciding the suitability and strategy for selection of a character. High heritability indicates high scope of genetic improvement of these characters through selection. Plant height, length of pod, seeds per pod, yield per plant and protein content recorded high heritability estimates indicating that selection would be effective in improving these traits. Findings of Kumar and Sagwan, (2005), Karpe *et al.* (2006) and Chaudhari *et al.* (2013) also reported high heritability in case of protein content. In case of grain yield per plant, high heritability was reported by Rangaiah and Manadevu, (2001). High heritability for seeds per pod was also reported by Satish, (2010) and Guptha, (2010). The findings of Chauhan, (2008) and Mishra *et al.* (2009) and also suggested high heritability value for pod length similar to the findings in the present study.

Moderate heritability estimates were observed for number of branches per plant, days to first flowering, first and last harvest. Similarly, number of pods per plant, pod weight and test weight registered moderate heritability reflecting possibility of moderate progress in these traits through selection. Borah and Khan, (2003) and Kukar and Sagwan, (2005) had also reported moderate heritability for branches per plant. The findings of Singh *et al.* (2009) also suggested moderate heritability value for test weight.

## 5.5 Genetic advance

Genetic advance is a measure of genetic gain under selection. It is the difference between the mean genotypic value of the selected lines and mean genotypic value of the population. Genetic advance as per cent of mean was categorized as suggested by Johnson *et al.*, (1955) as low (0-10%), moderate (10.1-20%) and high (>20%).

High genetic advance as per cent of mean was observed for all the traits except days to flowering and crop duration. For those traits genetic gain was moderate. High genetic advance for most of the traits in cowpea indicate that improvement of these traits are possible by selection. Tyagi *et al.* (2000), Rangaiah and Manadevu, (2001) and Gupta, (2010) observed high genetic advance for seeds per

pod. High genetic advance as per cent of mean for length of pods was reported by Yadav *et al.* (2005) and Selvakumar *et al.* (2014). Grain yield per plant and plant height had registered high genetic advance as per cent of mean, indicating that gain in grain yield per plant and plant height could be expected if judicious selection is exercised. Chaudhari *et al.* (2013) also reported high genetic advance for grain yield per plant.

High estimates of heritability along with genetic advance as per cent of mean was evident for the traits plant height, length of pods, seeds per pod, yield per plant and seed protein content. This indicate that selection will be effective for improving these traits. Similar findings in case of plant height was reported by Chaudhary and Naik, (2010) and Sharma *et al.* (2013). High heritability in conjunction with high genetic advance in case of seed protein content reported by Karpe *et al.* (2006), Raju *et al.* (2008) and Ushakumari *et al.* (2010). High heritability along with high genetic advance for grain yield per plant was reported by Rangaiah and Manadevu, (2001). This implies that grain yield per plant can be improved through selection.

Moderate heritability estimates with high genetic advance as per cent of mean was observed for number of branches per plant, number of pods per plant, pod weight and test weight, implying influence of both additive and non-additive gene action on expression of these traits. Hence, improvement of these traits could be attained by recurrent or reciprocal recurrent selection.

## 5.6 Combining ability analysis

The essential idea of the combining ability is to consider a systematic set of crosses between a number of parents and to enquire to what extent of variation among the crosses can be interpreted as due to statistically additive features of the parents and what must be attributed to residual interaction. Being based on first degree statistics, they are statistically robust and being genetically so to speak neutral, they are equally applicable to both inbreeders and outbreeders. (Simmonds, 1979).

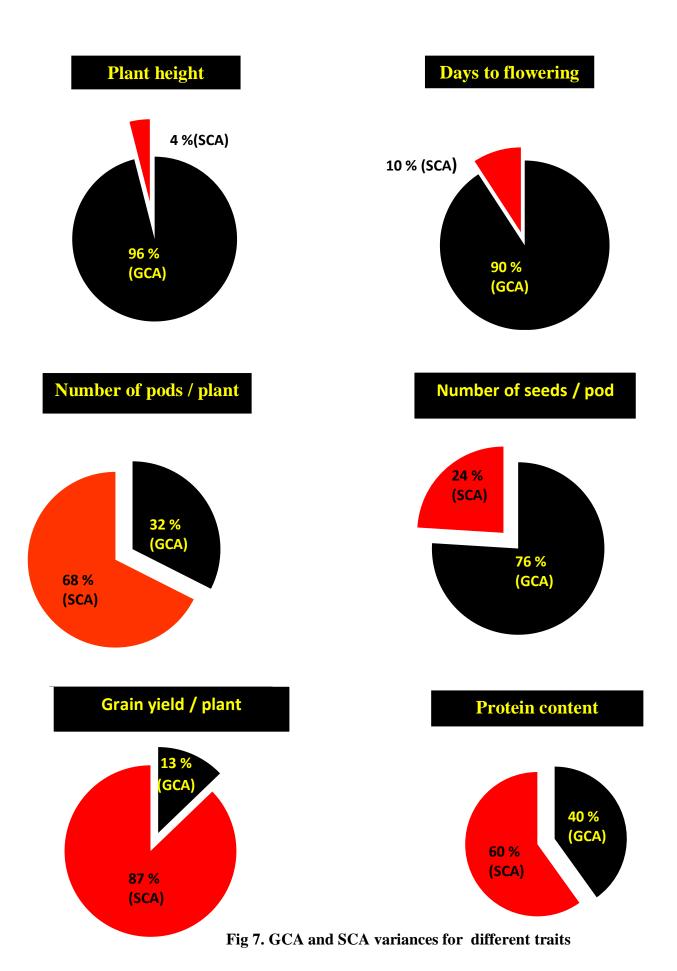
The analysis of variance for combining ability revealed that the hybrids differed significantly from each other except number of branches and pod weight. Lines vary for plant height, days to flowering, days to first harvest, days to last harvest, number of pods per plant, seeds per pod, grain yield per plant and protein content. Testers did not vary for these traits. Presence of significant variability among line x tester for number of pods per plant, length of pods, pod weight, seeds per pod, test weight, yield per plant and protein content. Partitioning of combining ability variance in to fixable and non-fixable variances indicates that both additive and non-additive gene action played a major role in controlling the expression of the characters studied.

The magnitude of SCA variances was higher than the GCA variances for pods per plant, length of pod, test weight, grain yield per plant and seed protein content indicating preponderance of non-additive gene action that is dominance and epistatic gene action in the inheritance of these traits (Fig 7). Gupta, (2010) reported prepondance of non-additive gene action in expression of grain yield per plant.

Estimates of GCA variances was higher than SCA variances for plant height, days to flowering, days to first harvest, days to last harvest pod-weight and seeds per pod (Fig.7, Fig.8 and Fig.10) This indicate the preponderance of additive gene action in controlling these traits. Heritable and fixable portion of genetic variance contributed by the additive gene action which facilitate improvement of these traits by selection. These results are in agreement with findings of Mishra *et al.* (2009) and Bhavesh *et al.* (2012).

# 5.6.1 Combining ability effects of parents and hybrids

For developing high yielding varieties and hybrids through hybridization or any breeding programme, the basic step is the choice of parents. For choosing the parents, the combining ability is taken one of the important criterion from the inception of the breeding programme. Hence, the general combining ability (gca) of parents and specific combining ability (sca) of the hybrids is discussed below.



## **5.6.1.1 Plant height**

Significant positive GCA effect in Vyjayanthi (76.69) and Lola (61.65) shows that these genotypes are good general combiners for increased plant height. Significant negative GCA in Bhagyalakshmi (-21.18) indicates that this genotype can be used as a general combiner for dwarfness. Bhagyalakshmi x AV-5 (54.47) showe highest positive value for sca effect. Significant highest negative value for sca effect was observed in Vellayani Jyothika x AV-5 (-63.21). The GCA variance higher than SCA variance implies that plant height is governed by additive gene action. Anbuselvam *et al.* (2010) reported additive gene action in plant height confirm the present study

# 5.6.1.2 Branches per plant

For branches per plant GCA/ SCA variances was less than unity indicating the predominance of non-additive gene action. Earlier studies by Indarsingh *et al.* (2007) and Tarawali *et al.* (2010) also reported the same findings. Significant positive gca effect observed in Vellayani Jyothika, Vyjayanthi and Lola indicate that these genotypes were good general combiners for branches per plant. Two hybrids namely H14 (Vyjayanthi x PKB-4) and H24 (Kanakamony x Sharika) exhibited high *per se*, as well as sca effects for branches per plant. It indicates that these combinations can be use to exploit heterosis for more number of branches per plant. Also it can be suggested that population involving these parents in multiple crossing programme might be developed to isolate desirable lines.

## 5.6.1.3 Days to flowering and harvest

Bhagyalakshmi (-10.09), Anaswara (-8.24), AV-5 (-5.30) Kanakamony (-2.99) were good general combiner for earliness since they showed high negative GCA values. Additive gene action was predominant for this trait which show that characters can be improved by appropriate selection model. The same genotypes were good combiner for early harvesting also. Among hybrids Kanakamony x PKB-3 had

high sca effect was earliest to harvest in 43.11 days. Earliness for yield is a desirable character in any crop. The preponderance of additive genetic variance over non-additive implies that days to harvest can be improved through selection. Malarvizhi, (2004) and Dalsaniya *et al.* (2013) also reported additive gene action of days to flowering in cowpea.

## **5.6.1.4 Pods per plant**

Information on the inheritance of this trait of immence value to make high yielding crooses. The component of variance due to SCA was higher than GCA pointed out that once genotype with more number of pods were isolated further improvement would be achieved through hybridization. Kumar and Sagwan, (2005) Guptha, (2010) and Chaudhari *et al.* (2013) were of the opinion that pod number was determined by non-additive gene action alone.

## **5.6.1.5** Length of pod

Higher magnitude of SCA variance indicated the role of non-additive gene action. This was earlier noted by Raju *et al.* (2008) and Chaudhary and Naik, (2010). However, earlier reports by Santos *et al.* (2012) proposed additive gene action in controlling the trait. The hybrid H3 (Vellayani Jyothika x PKB-4) and H17 (Anaswara x Sharika) had high mean value and sca effect so these hybrids might serve as a source for realising superior segregants or can be used for heterosis breeding.

## **5.6.1.6 Pod weight**

Higher estimates of GCA variances than SCA variances for pod weight implies that genetic variance contributed by additive gene action and hence selection would be effective. Importance of both additive and non-additive gene action in determining this trait was earlier observed by Karpe *et al.* (2006), Hazra *et al.* (2007) and Patel *et al.* (2007). Hybrids H17 (Lola x AV-5), H13 (Vyjayanthi x AV-5) and

H3 (Vellayani Jyothika x PKB-4) exhibited remarkably high mean performance and sca effect. Hence these combinations could be utilised for exploiting hybrid vigour in F1 and the character further be improved by selection in advanced generations.

## **5.6.1.7** Seeds per pod

High value of GCA variance suggested that seeds per pod was determined by additive gene action. This supports the earlier report by Mannivannan and Sekhar, (2005) and Boukar *et al.* (2011). Among the parents Vellayani Jyothika and AV-5 had high mean values and high gca effects indicating these parents can be used for multiple crossing programme. Three hybrids namely H11 (Anaswara x PKB-4), H13 (Vyjayanthi x AV-5) and H17 (Lola x AV-5) registered high sca value and mean performance. These would produce transgressive segregants in later generation.

## **5.6.1.8** Test weight

Estimates of SCA was higher than GCA indicates test weight was governed by non-additive gene action. Non-additive gene action in test weight was proposed by Yadav *et al.* (2005) and Kadam *et al.* (2013) confirm the present study. Six hybrids H3, H10, H11, H12, H14 and H16 exhibited high mean and sca values. These would produce transgressive segregants in later generation for high test weight.

## 5.6.1.9 Yield per plant

Higher value of SCA variances than the GCA for grain yield per plant implies that genetic variance contributed by non-additive gene action. Valarmathi *et al.* (2007) and Satish, (2010) reported non-additive gene action of grain yield per plant in cowpea. Lines such as Vellayani Jyothika (35.31), Anaswara (9.78), Vyjayanthi (43.91), and Lola (33.91) testers like PKB-3 (6.49), PKB-4 (3.57) and Sharika (12.86) registered significant positive GCA effects proved to be good combiner for grain yield per plant. Hybrids H2 (Vellayani Jyothika x PKB-3), H13 (Vyjayanthi X AV5),) and H24 (Kanakamony x Sharika) recorded significant sca effect for grain

yield per plant and had high mean values. So these hybrids could produce desirable transgressive segregants in advanced generations. Two hybrids H12 (Anaswara x Sharika), and H19 (Lola x PKB 4) had high mean values gca and sca effects. This could be utilized through pedigree method to develop superior genotypes.

#### **5.6.1.10 Protein content**

Increase in protein content along with seed yield is an important objective in any pulse breeding programme. The role of non-additive gene action in protein content was proved from high value of SCA variance. The report by Mishra *et al.* (2009) and Dalsaniya *et al.* (2013) confirm the present study. The parental lines like Anaswara (1.76), Kanakamony (1.69) and tester namely PKB-3(1.43) exhibited positive GCA effects proved to be good combiner for protein content. Significant SCA in the desired direction for seed protein content was exhibited by H2 (Vellayani Jyothika X PKB3), H15 (Vyjayanthi x PKB 4) and H 18 (Lola X PKB 3). Five hybrids had high SCA effects for seed protein content. In these crosses population approach of breeding would enhance the variability.

Hybrids H17 (Lola x AV-5) and H22 (Kanakamony x PKB-3) possess high significant negative sca value for plant height, days to flowering, days to first harvest and days to last harvest. The hybrid H24 registered high positive sca value for pods per plant. Only one hybrid H2 (Vellayani Jyothika x PKB-3) recorded significant sca effect for both grain yield per plant and seed protein content.

#### **5.7 Heterosis**

Heterosis is the genetical phenomenon referred to denote the expression of increased vigour. Vigour of hybrids is estimated over mid parent, better parent and standard parent. Utilization of heterosis is important for maximization of yield as well as seed protein content in cowpea. Gene action and combining ability in relation to information on heterosis determine whether heterosis is fixable or predictable (Tiwari *et al.*, 2011).

## 5.7.1 Plant height

Significant heterobeltiosis, relative heterosis and standard heterosis was reported for plant height are presented in Fig 8. In the present study, ten hybrids recorded significant negative relative heterosis, thirteen hybrids registered significant negative heterobeltiosis and twelve hybrids exhibited significant negative standard heterosis. Hybrids in which Bhagyalakshmi was the female parent exhibited high magnitude of all the three type of heterosis in negative direction. Hybrid H8 (Bhagyalakshmi x Sharika) recorded highest negative standard heterosis. Nagl *et al.* (2013) and Chaudhari *et al.* (2013) reported three type of heterosis in plant height.

#### 5.7.2 Number of branches per plant

Decrese in plant height subsequently resulted in decrease in branch number. The hybrid H3 (Vellayani Jyothika x PKB-4) showed highest value for relative heterosis and heterobeltiosis. Where as maximum value for standard heterosis registered by H23 (Kanakamony x PKB-4). Hybrids in which Vellayani Jyothika as the female parent exhibited high significant positive heterosis irrespective of the testers used. Heterosis for branch number already reported by Rajkumar, (2005) and Karpe *et al.* (2006). Owing to their additive type of gene action in controlling this trait pedigree type of breeding could be utilised to get segregants with more number of branches.

## **5.7.3** Days to flowering

Negative heterosis will be useful for the breeder to develop vigorous early maturing genotypes. Among 24 hybrids only four hybrids H5 (Bhagyalakshmi x AV-5), H6 (Bhagyalakshmi x PKB-3), H9 (Anaswara x AV-5) and H10 (Anaswara x PKB-3) exhibited significant negative relative heterosis, heterobeltiosis and standard heterosis (Fig 9). Hybrids involving Bhagyalakshmi as female parent registered high magnitude of three types of heterosis in negative direction. The standard heterosis were highest in negative direction in H10 (Anaswara x PKB-3). This hybrid had good negative gca effect for parents and high value of negative standard heterosis (-24.52). Hence, this hybrid could be exploited through pedigree breeding for earliness. While the hybrid H10 (Anaswara x PKB-4) resulted from one good and one poor combiner with high negative sca effect needed cyclic type of breeding to obtain an array of segregants which would vary in maturity group.

## **5.7.4 Days to first harvest**

For days to first harvest also negative heterosis is more desirable to develop early harvesting genotypes. Similar to days to flowering, hybrids in which Bhagyalakshmi as female parent exhibited high negative value for all the three type of heterosis. Four hybrids reported significant relative heterosis. Seven hybrids recorded significant heterobeltiosis while four hybrids registered significant standard heterosis. This was in accordance with earlier reports of Boukar *et al.* (2011) and Sharma *et al.* (2013).

#### 5.7.5 Pods per plant

This pods per plant is of importance for the selection of superior genotypes Since it had a linear relationship with seed yield (Mishra *et al.*, 2009). Hybrids in which both the parents were trailing or semi trailing exhibited significant positive heterosis for pods per plant. The hybrids H1, H2, H5, H10, H11, H14, H19, H20 and H24 had high sca effects as well as standard heterosis (Fig 10). Among these 6

hybrids H2, H10, H11, H14, H19 and H20 involved parents of good combining ability. Hence, these hybrids might be expected to produce segregants with more number of pods. The other hybrids could be utilized effectively through population improvement approach. Patel *et al.* (2007) and Selvakumar *et al.* (2014) reported three type of heterosis in pods per plant.

## 5.7.6 Length of pods

The hybrid namely H3, and H11 registered significance for all the three type of heterosis. Hybrids which possess positive significant heterosis for all the three types of heterosis in which female parent can be trailing type. This was in accordance with earlier reports of Mannivannan and Sekhar, (2005) and Boukar *et al.* (2011) reported three type of heterosis in cowpea. Hybrid H3 (Vellayani Jyothika x PKB- 4) had high sca effects and standard heterosis. These would serve as a source for improving pod length through transgressive segregation.

## 5.7.7 Pod weight

Significant positive relative heterosis was shown by 13, heterobeltiosis by seven and positive standard heterosis by 19 hybrids. Presence of heterosis over mid parental and better parental values for this trait was earlier proposed by Thiyagarajan *et al.* (1995), Kumar and Sagwan, (2005) and Chaudhary and Naik, 2010). Hybrids involving Vellayani Jyothika, Lola and Vyjayanthi as female parents exhibited significant three types of heterosis for pod weight The hybrid H3 (Vellayani Jyothika x PKB-4), H12 (Anaswara x Sharika) H13 (Vyjayanthi x AV-5) and H17 (Lola x AV-5) had high sca effects and standard heterosis. These hybrids could be utilized effectively through population improvement methods for increased pod weight.

## 5.7.8 Seeds per pod

Relative heterosis as well as heterobeltiosis for seeds per pod was proposed by Raju *et al.* (2008) and Satish, (2010) in cowpea. In the present study 16 hybrids had

relative heterosis, 18 hybrids had heterobeltiosis and 18 hybrids had standard heterosis (Fig 11). Hybrids in which female parent was Lola and Vyjayanthi exhibited positive significant three type heterosis. The hybrids H4 (Vellayani Jyothika x Sharika) and H20 (Lola x Sharika) had both parents as good general combiners high sca effects and standard heterosis. Hence, these crosses might leads to genotypes with more number of seeds per pod through pedigree breeding.

## 5.7.9 Test weight

Twenty one hybrids exhibited significant relative heterosis, seven hybrids registered significant positive heterobeltiosis and 22 hybrids showed significant standard heterosis. Increase as well as decrease in test weight over mid parent and better parent were identified by Rajkumar, (2005) and Mannivannan and Sekhar, (2005) suggested heterobeltiosis in cowpea for test weight. Those hybrids in which female parent was Vellayani Jyothika exhibited positive significant three type of heterosis The hybrid H5 (Bhagyalakshmi x AV-5), H4 (Vellayani Jyothika x Sharika) had high positive value for gca as well as sca effects and standard heterosis. Other hybrids like H2 (Vellayani Jyothika x PKB-3) and H3 (Vellayani Jyothika x PKB-4) had high sca effect and standard heterosis and could give rise to better segregants.

#### 5.7.10 Grain yield per plant

Tyagi *et al.* (2000) and Yadav *et al.* (2005) reported three type of heterosis in grain yield per plant. In the present study seven hybrids registered significance for all the three type of heterosis. Hybrids H3 (Vellayni Jyothika x PKB-4), H4 (Vellayni Jyothika x Sarika), H12 (Anaswara x Sarika), H15 (Vyjayanthi x PKB4) exhibited significant heterosis, heterobeltiosis and standard heterosis for grain yield per plant (Fig 12). These could be exploited for its yield potential to obtain desirable segregants in future breeding programme.

#### **5.7.11 Protein content**

Sixteen hybrids recorded significance for all the three type of heterosis. Chauhan, (2008) and Inuwa et al. (2013) reported three type of heterosis in protein content concurrent with the present study. Hybrids in which female parents were Bhagyalakshmi, Anaswara and Kanakamony registered positive significant three type of heterosis for protein content (Fig 13). The hybrids H2 (Vellayni Jyothika x PKB-3) and H5 (Bhagyalakshmi x AV-5) had high gca and sca effects and standard heterosis. So these genotypes could be used to isolate genotypes with high protein content. Other crosses, H9 (Anaswara x AV-5), H15 (Vyjayanthi x PKB-4) and H18 (Lola x PKB- 3) could give rise to transgressive segregants in later generation as they had high sca effects and standard heterosis. The hybrid H13 (Vyjayanthi x AV-5) and H24 (Kanakamony x Sharika) only have high sca effect and standard heterosis and parents involved were good combiners. Pedigree type of breeding is appropriate to exploit the heterotic vigour of the hybrid For other crosses intermating among the selected segregant and selection in the later generation would result in genotypes with high yield. Hybrids H1 (Vellayani Jyothika x AV-5) and H17 (Lola x AV-5) exhibited significant negative value for all the three type of heterosis for plant height, days to first flowering, days to first harvest and days to last harvest. Only two hybrids H2 (Vellayani Jyothika x PKB-3) and H5 (Bhagyalakshmi x AV-5) possess significant positive value for three type of heterosis for grain yield per plant and protein content.

## **Ranking of hybrids**

Considering yield and major yield contributing traits the genotypes were ranked as suggested by Arunachalam and Bandyapadhyay (1984). The hybrids were ranked based on mean value, *sca* effects and estimates of heterosis for the traits like days to flowering, pods per plant, seeds per pod, test weight, grain yield per plant and protein content. Four hybrids with the lowest scores were selected. Hybrids H2 (Vellayani Jyothika x PKB-3), H10 (Anaswara x PKB-3), H11(Anaswara x PKB-4) and H12 (Anaswara xSharika) were found to be the most promising.

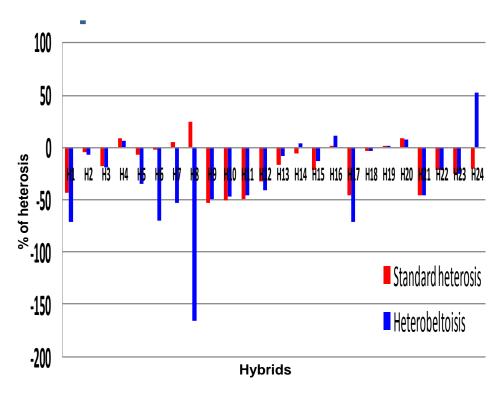
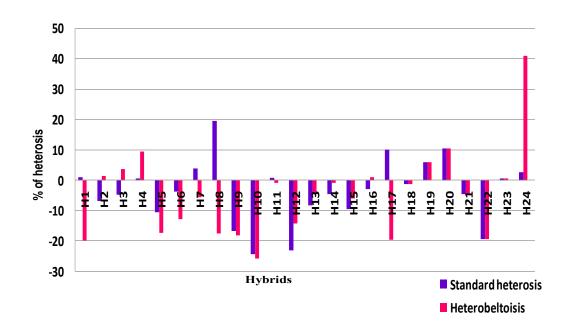


Fig 8. Standard heterosis and heterobeltiosis of hybrids for plant height



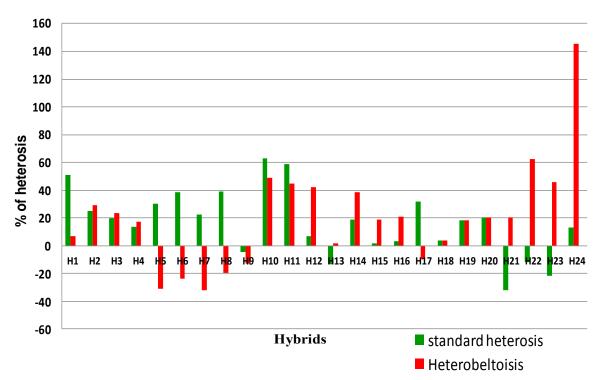


Fig 10. Standard heterosis and heterobeltiosis of hybrids for number of pods per plant

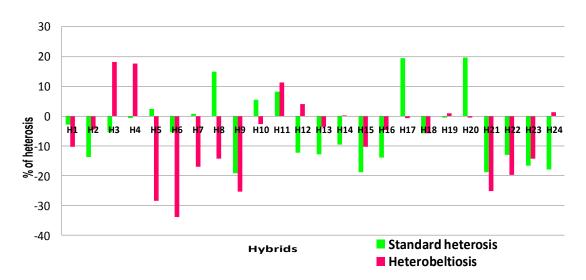


Fig 11. Standard heterosis and heterobeltiosis of hybrids for seeds per pod

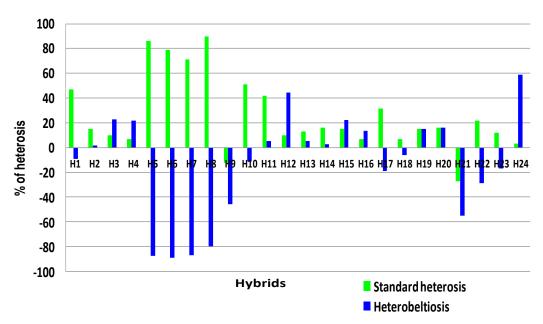


Fig 12. Standard heterosis and heterobeltiosis of hybrids for grain yield per plant

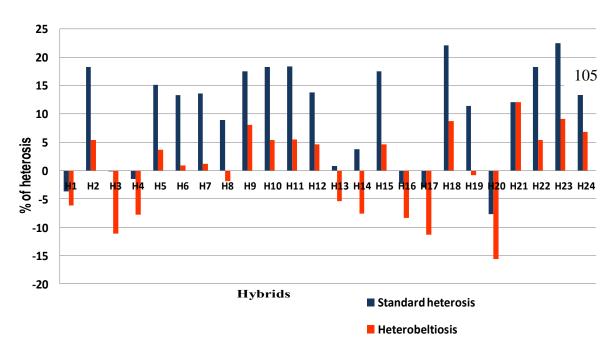


Fig 13. Standard heterosis and heterobeltiosis of hybrids for protein content

Table 12. Ranking of genotypes

Hybrids	Days to	Pods /	Seeds /	Test	Grain	Protein	Total
	flowering	plant	pod	weight	yield /	content	
					plant		
H1	40	54	79	38	55	99	365
H2	86	31	77	27	44	26	291
Н3	84	40	27	13	47	104	315
H4	84	67	25	35	60	91	362
H5	31	78	78	40	72	42	341
Н6	43	88	104	114	92	74	515
H7	58	97	92	98	87	66	498
Н8	60	85	72	92	84	72	465
Н9	35	101	115	98	104	35	488
H10	9	19	36	31	52	46	193
H11	74	22	20	46	41	37	240
H12	38	46	49	19	32	52	236
H13	75	86	56	77	45	82	421
H14	83	31	43	59	50	84	350
H15	52	73	91	80	41	38	375
H16	68	71	80	50	64	100	433
H17	48	72	24	51	76	110	381
H18	78	82	62	45	76	14	357
H19	109	47	29	53	37	70	345
H20	102	39	35	72	29	120	397
H21	59	85	98	108	106	45	501
H22	13	70	86	91	74	43	377
H23	61	103	94	99	85	14	456
H24	100	23	58	74	37	36	338

Table 13. Performance of promising hybrids

Hybrids	Plant height	No. of Branches	Days to first flowering	Days to first harvest	Days to last harvest	Pods per plant
Н2	236.38	8.50	51.20	66.40	115.18	75.17
H10	65.2	8.2	30.16	44.29	105.34	67.16
H11	66.28	7.92	40.35	52.38	102.39	65.31
H12	172.10	8.13	42.2	55.25	110.39	64.25
Hybrids	Length of pods (cm)	Pod weight (g)	Seeds / pod	Test weight (g)	Grain yield / Plant (g)	Protein content (%)
Н2	55.19	28.52	19.21	25.33	178.33	30.03
H10	31.28	18.20	19.57	23.57	155.55	30.03
H11	29.12	17.60	20.05	21.20	146.20	30.06
H12	38.18	19.46	19.55	23.26	170.27	28.88





Vellayani Jyothika x PKB-3

Anaswara x PKB-4







Anaswara x Sharika

Plate 9. Promising F1 hybrids

# Summary

#### 6. SUMMARY

The present study of Combination breeding for high protein cowpea (*Vigna unguiculata* L. Walp) was conducted in the Department of Plant Breeding and Genetics, College of Horticulture, Kerala Agricultural University Vellanikkara during 2014-2015. The salient findings are summarized below.

## **Evaluation of the cowpea genotypes**

## Variability studies

- Wide variability for most of the traits was found to exist among bushy and semi trailing types of cowpea genotypes indicating ample scope for improvement of the traits through selection.
- In trailing type sufficient variability was observed for plant height, number of pods per plant, pod weight and grain yield per plant.
- The cowpea genotypes showed high degree of variability in protein content indicating substantial genetic variability among the genotypes for the trait.

## **Evaluation of parents and Hybrids**

- The analysis of variance revealed that there exisisted significant difference among the genotypes for most of the characters studied with exception being number of branches.
- High significant differences between genotypes were observed with respect to plant height, days to flowering ,days to first and last harvest, length of pods, pod weight and number of pods per plant. grain yield per plant and protein content.
- Higher magnitude of phenotypic and genotypic coefficient of variation along with high heritability and high genetic advance was observed for plant height, grain yield per plant and length of pods suggesting scope for genetic improvement of these traits through selection.

• Seeds per pod and protein content showed low PCV and GCV but high heritability and low genetic gain, indicating that these traits are governed by non-additive gene action therefore selection is not appropriate.

## Studies on combining ability

- ANOVA for combining ability showed that hybrids vary for plant height, days to flowering, days to first harvest, days to last harvest, number of pods per plant, length of pod, test weight, seeds per pod, grain yield per plant and protein content. The line x tester interaction was significant for number of pods per plant, length of pods, pod weight, seeds per pod, test weight, grain yield per plant and protein content.
  - The magnitude of SCA variances was higher than the GCA variances for pods per plant, length of pod, test weight, grain yield per plant and seed protein content indicating preponderance of non-additive gene action that is dominance and epistatic gene action in the inheritance of these traits.
  - Higher estimates of GCA variances over SCA variances for plant height, days to flowering, days to first harvest, days to last harvest pod-weight and seeds per pod implies the preponderance of additive gene action in controlling these traits

#### **Studies on heterosis**

- All three types of negative heterosis for plant height and days to flowering was observed in hybrids H5 (Bhagyalakshmi x AV-5), H6 (Bhagyalakshmi x PKB-3), H7 (Bhagyalakshmi x PKB-4), H8 (Bhagyalakshmi x Sharika), H9 (Anaswara x AV-5) and H10 (Anaswara x PKB-3).
- Hybrids H3 (Vellayni Jyothika x PKB-4), H4 (Vellayni Jyothika x Sharika), H12 (Anaswara x Sharika), H15 (Vyjayanthi x PKB4) exhibited significant heterosis, heterobeltiosis and standard heterosis for grain yield per plant where as hybrids H2 (Vellayani Jyothika x PKB-3), H5 (Bhagyalakshmi x AV-5), H9 (Anaswara x AV-5), H10 (Anaswara x PKB-3), H11 (Anaswara x PKB-4), H12

(Anaswara x Sharika), H15 (Vyjayanthi x PKB-4), H18 (Lola x PKB-3), H21 (Kanakamony x AV-5), H22 (Kanakamony x PKB-3), H23 ((Kanakamony x PKB-4) and H24 (Kanakamony x Sharika) recorded significance for protein content in all the three type of heterosis. Two hybrids H2 (Vellayani Jyothika x PKB-3) and H5 (Bhagyalakshmi x AV-5) possess significant positive value for three type of heterosis for grain yield per plant and protein content.

- The hybrids were ranked based on mean value, *sca* effects and estimates of heterosis for the traits like days to flowering, pods per plant, seeds per pod, test weight, grain yield per plant and protein content.
- Four hybrids with the lowest scores were selected. Hybrids H2 (Vellayani Jyothika x PKB-3), H10 (Anaswara x PKB-3), H11(Anaswara x PKB-4) and H12 (Anaswara xSharika) were found to be the most promising.

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## Combination breeding for high protein cowpea

(Vigna unguiculata L.Walp)

by

Sarath P.S

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## **ABSTRACT OF THE THESIS**

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Department of Plant Breeding and Genetics COLLEGE OF HORTICULTURE VELLANIKKARA, THRISSUR -680 656 KERALA, INDIA 2015

#### **ABSTRACT**

Cowpea (*Vigna unguiculata* L. Walp) is one of the most important legume crops grown in India. It is a versatile pulse crop owing to its nutritional value, weed smothering nature, drought tolerant characters, soil restoring properties and multipurpose uses. Protein deficiency has been reported to be one of the main nutritional problems in the developing world. About one billion people are reported to be suffering from protein deficiency and malnutrition worldwide.

Studies have revealed that protein content in cowpea grain ranges between 18 to 40 per cent depending on the genotypes. Identifying high yielding varieties of cowpea with high protein content will not only contribute to food security and alleviate poverty but could also contribute to the alleviation of protein deficiencies. Review on the earlier research pointed to poor emphasis on the genetic improvement of cowpea for improved protein content. Hence, the present study was envisaged to combine the high protein trait with high yielding genotypes.

The study was grouped under three experiments, i) Evaluation of cowpea genotypes, ii) Hybridisation of the selected genotypes in line x tester design, iii) Evaluation of F1 hybrids. The experiments were conducted at College of Horticulture, Kerala Agricultural University, Vellanikkara during 2014-2015. All the crop management practices were followed as per KAU (2011).

Evaluation of cowpea genotypes revealed that there was wide variability for all the traits studied except branches per plant among bushy and semi trailing types of cowpea. In trailing type, variability was observed for plant height, number of pods per plant, pod weight grain yield per plant and seed protein content. Among the twenty two genotypes evaluated, ten genotypes that exhibited a protein content of above 25 per cent were selected for hybridization programme. The selected genotypes

(Vellayani Jyothika, Bhagyalakshmi, Anaswara, Kanakamony, Lola, Vyjayanthi, AV-5, PKB-3, PKB-4 and Sharika) were hybridized in line x tester (6 x 4) design.

High magnitude of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance was observed for plant height, grain yield per plant and length of pods were observed in parents and hybrids suggesting scope for genetic improvement of these traits through selection. Seeds per pod and protein content exhibited low PCV and GCV but high heritability and low genetic gain, indicating that these traits were governed by non-additive gene action and therefore breeding method other than simple selection is required.

Combining ability analysis revealed that higher magnitude of specific combining ability (SCA) variances than the general combining ability (GCA) variances for the traits like pods per plant, length of pod, test weight, grain yield per plant and seed protein content indicating preponderance of non-additive gene action in the inheritance of these traits. Higher estimates of GCA variances over SCA variances for plant height, days to flowering, days to first harvest, days to last harvest, pod-weight and seeds per pod implies the preponderance of additive gene action in controlling these traits.

The hybrids were ranked based on mean value, *sca* effects and estimates of heterosis for the traits like days to flowering, pods per plant, seeds per pod, test weight, grain yield per plant and protein content. Four hybrids with the lowest scores were selected. Hybrids H2 (Vellayani Jyothika x PKB-3), H10 (Anaswara x PKB-3), H11(Anaswara x PKB-4) and H12 (Anaswara xSharika) were found to be the most promising. The transgressive segregants with high yield and protein content can be identified on further evaluation of the segregating population from the above hybrids.