GENOTYPE x ENVIRONMENT INTERACTION IN ADVANCED BREEDING LINES OF COWPEA

(*Vigna unguiculata* (L.) Walp)

By

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(2019-11-135)

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VELLANIKKARA, THRISSUR- 680 656

KERALA, INDIA

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THESIS

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DEPARTMENT OF PLANT BREEDING AND GENETICS

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2021

DECLARATION

I, hereby declare that this thesis entitled "**Genotype x environment interaction in advanced breeding lines of cowpea (*Vigna unguiculata* (L.) Walp)**" is a bonafide record of research work done by me during the course of research and that it has not been previously formed the basis for the ward of any degree, diploma, fellowship or other similar title, of other University or Society.

Vellanikkara
02.12.2021

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CERTIFICATE

Certified that this thesis, titled **"Genotype x environment interaction in advanced breeding lines of cowpea (*Vigna unguiculata* (L.) Walp)"** is a bonafide record of research work done independently by **Ms. Swathi S.** 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 her.

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02.12.2021

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We, the undersigned members of the advisory committee of **Ms. Swathi S. (2019-11-135)**, a candidate for the degree of **Master of Science in Agriculture** with major field in **Plant Breeding and Genetics** agree that the thesis, titled **"Genotype x environment interaction in advanced breeding lines of cowpea (*Vigna unguiculata* (L.) Walp)"** may be submitted by her in partial fulfilment of the requirement for the degree.

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"Preparations produce opportunities"

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ABBREVIATIONS

AMMI: Additive main effects and multiplicative interaction effects

Env 1 : Environment 1

Env 2 : Environment 2

Env 3 : Environment 3

Fig : Figure

F_7 : Seventh filial generation

G : Genotype

GA : Genetic advance

G x E : Genotype x environment

GCV : Genotypic Coefficient of Variation

GGE : Genotype main effects plus Genotype-by-Environment

H^2 : Heritability

IPCA1: Interactive Principal Component Analysis 1

IPCA2: Interactive Principal Component Analysis 2

PCV : Phenotypic Coefficient of Variation

Introduction

1. INTRODUCTION

Cowpea (*Vigna unguiculata* (L.) Walp., 2n = 22) being a widely adopted crop is accepted as a high quality plant protein source, globally. It is one of the most ancient legume crop to be known and is often referred to as "poor man's meat". Cowpea is cultivated for human as well as livestock consumption of which, seeds are used as pulse, green pods as vegetable and leaves as forage. Because of its ability to tolerate drought and fix atmospheric nitrogen in soil, it forms an integral part of all major cropping systems. Cowpea provides cheap source of protein, vitamins and minerals to both rural and urban dwellers and act as a supplement for the carbohydrate rich diet obtained from cereals (Timko *et al*., 2008). The protein content in cowpea is about 25 per cent and the digestibility of protein is much higher than that of other legumes (Ologhobo and Fetuga, 1983).

The crop was introduced in India thousands of years ago and the country forms one of the main centres of genetic diversity for cowpea (Smart, 1976). Grown since ancient times it finds utmost significance culturally, by forming one of the components in navadhanya used during auspicious ceremonies (Baldev *et al*., 1988). It has a wide range of distribution across the country extending from sub-Himalayan regions and the fertile Indo-Gangetic plains in the north to the hot and humid tropical climate in the south (Singh *et al*., 1988). Under Kerala conditions, cowpea can be grown throughout the year as a floor crop in coconut garden and as an intercrop in Tapioca. During rabi and summer season it can be grown as a pure crop in rice fallows (KAU, 2016).

The cultivated cowpea consists of three main cultivar groups namely, cv. *biflora* (catiang), cv. *unguiculata*, (common cowpea) and cv. *sesquipedalis* (yard long or asparagus bean) (Menendez *et al*., 1997). In India, cultivar groups *biflora* and *unguiculata* types are the predominant ones while *sesquipedalis* type is very rare (Singh *et al.*, 1988).Yield potential of cowpea is high, averaging 1.5 to 6 tonnes per hectare depending on genotype, though actual yields are low with total annual production ranking 8th among the pulse crops (FAO, 2007).

Among the Kharif season (July to October) grain legumes, cowpea is considered to have the highest productivity potential (Singh and Sharma 1996). Over the world,

cowpea is cultivated covering an area of 12.6 million hectares with production and productivity of 5.6 million tonnes and 443 Kg/ha, respectively (FAOSTAT, 2014). The poor yield may be due to unavailability of high yielding and stable genotypes along with appropriate agronomic management practices (Ali *et al*., 2004).

The yielding ability of a genotype corresponds to the interaction of genotype with its environment. The main limitation preventing genetic enhancement of the crop lies in the poor knowledge regarding genetic diversity of available germplasm and the crop being chosen on varietal basis depending on combination of traits for specific regions (Ajayi, 2019). The specific response of a genotype can be visualized only in a particular environment that, its stable performance over different environments is a desirable characteristic. This mainly depends upon the extent of genotype x environment interaction (Ahmad *et al*., 1996).

In cowpea, the relative magnitude of genotype, environment and their interaction effects are a bigger challenge constraining its production below the requirement (Hall *et al*., 2003). A stable genotype is the one that makes the smallest contribution to the genotype x environment interaction (Eberhart and Russell, 1966). Though several previous studies on cowpea have shown high genetic divergence that have been proven through correlations and path analysis, studies regarding the adaptability and stability of cowpea genotypes are few (Santos *et al*., 2015).

Hence, the present study is an attempt to evaluate the genotype x environment interaction in cowpea cultures that have been developed through pedigree selection from segregating generations of inter varietal crosses.

Review of literature

2. REVIEW OF LITERATURE

Cowpea (*Vigna unguiculata* (L.) Walp.) occupies a unique position among all other cultivated legume crops because of its wide adaptable nature and stress tolerance. Despite its role in providing protein rich food, Cowpea plays a prominent socioeconomic role by generating employment and income in the tropical and sub-tropical regions of Asia (Santos *et al*., 2015). In developing countries, it is of utmost significance as it feeds millions of people with an annual production of 4.5 million metric tonnes on 12 to 14 million hectare (Diouf, 2011). Being a self-pollinated crop, variability existing in cowpea is limited. Development of cultivars with early maturity, superior grain quality, biotic and abiotic stress resistance has considerably increased the yield and cultivated area in cowpea (Ehlers and Hall, 1997).

The research programme entitled "Genotype x environment interaction in advanced breeding lines of cowpea (*Vigna unguiculata* (L.) Walp.)" was conducted at the Department of Plant Breeding and Genetics, College of Agriculture, Vellanikkara during the period of February 2021 to May 2021 and the relevant literature on various aspects of research in cowpea is reviewed in this chapter.

2.1. Genetic variability in cowpea

Genetic variability is a pre-requisite for every crop improvement programme. For an effective selection programme, quantification of fixable and non-fixable components of variation are essential. Phenotypic variation contributed in terms of Genotype x environment interaction has an immense role in the evolution and development of plant cultivars. A thorough knowledge regarding the magnitude and nature of genetic variability available within the species for various characters are required for the initiation of cowpea improvement programme (Gerrano *et al*., 2015).

Selection is effective for a population with broad genetic variability and high heritability in characters, thus a better understanding is required regarding the genetic factors controlling these characters (Manggoel *et al*., 2012). More reliable data on the obtainable genetic variability available within the gene pool can exploit heterosis and desirable traits (Mneney *et al*., 2011).

In a research conducted by Ramachandran *et al*. in 1982, the major part of total variation in yield for pods per plant and internode length in cowpea was largely contributed by genetic causes and he reported high genetic variance for days to flower and harvest. Considerable variations were observed among cultivars in the duration of reproductive period, growth rate and partitioning of photosynthates in an experiment conducted by Ntare (1992) while studying the variation in reproductive period and grain yield of cowpea under high temperature.

In an experiment conducted by Omoigui *et al*. in 2006, considerable variations were observed among cultivars in duration of reproductive phase and the rate of photosynthate partitioning. The Genotypic Coefficient of Variation (GCV) was high for days to first flowering, test weight, plant height and harvest index.

Field experiments were conducted during 2006 and 2007 regarding the effects of reproductive characters on grain yield of 10 cowpea accessions and significant variability was shown by the accessions for days to 50 per cent flowering, number of peduncles per plant, flowers per plant, pods per plant, seeds per pod, pod length, test weight and grain yield. Except for the traits of pod length and seeds per pod, the Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) were also high for all the traits studied (Manggoel *et al*., 2012).

In an experiment conducted for assessing the variability and correlation studies in cowpea, performance of 30 genotypes for 14 characters were recorded and all the characters exhibited significant variation. High GCV observed for leaf area index (45.17%) followed by days to 50 per cent flowering (40.04%), plant height (34.71%), number of branches per plant (27.99%), number of pods per plant (24.84%), number of clusters per plant (24.73%) and days to maturity (18.01%) (Thorat and Gadewar. 2013).

In a field experiment to study genetic variability in 20 genotypes of cowpea, significant differences were observed among the genotypes evaluated for all the characters. The PCV and GCV were higher for plant height, pod length, average pod weight, pod yield per plot, number of seeds per pod and number of pods per plant (Kharde *et al*., 2014). High degree of genetic variability was estimated for seed yield per plant (g), test weight (g), pod length (cm), number of seeds per pod, number of pods

per plant, number of pods per cluster, number of branches per plant, number of cluster per plant, plant height (cm), number of days to 50 per cent flowering and number of days to maturity in 33 indigenous and exotic accessions of cowpea during summer and kharif seasons of Rajasthan (Vir and Singh, 2014).

In a study conducted on twenty one genotypes of vegetable cowpea, high and significant variation was observed for all the characters, excluding pod width. The GCV value was higher for plant height and pod yield per plant (Chandrakar *et al*., 2016).

A study was conducted in the F_3 generation, derived from a cross between C-152 and V-16 for six quantitative traits and moderate PCV and GCV were recorded for plant height (15.75 % and 12.91%) and number of pods per plant (16.29% and 11.42%). Whereas, moderate PCV and low GCV was recorded for number of branches (15.01% and 6.66%), number seeds per pod (12.60% and 4.77%) and seed yield per plant (10.86% and 4.51%) (Dinesh *et al*., 2017).

Genetic variability for growth and yield in cowpea varieties were studied and significant difference was observed for plant height, number of days to fifty per cent flowering, number of days to maturity, number of pods per plant, pod length, number of seeds per plant, test weight and protein content (Magashi *et al*., 2017).

Twenty two genotypes of cowpea were assessed by field evaluation for twelve characters at Vellanikkara and a high degree of variability was reported for all the characters. High magnitude of the PCV and GCV was observed for plant height, grain yield per plant and length of the pods and the difference between the phenotypic coefficient of variation and genotypic coefficient of variation were found to be maximum in pod weight (30.15%), followed by number of pods per plant (18.12%) and test weight (16.27%) (Sarath and Reshma, 2017).

Thirty cowpea genotypes were studied for their genetic parameters considering ten characters. High estimate of GCV and PCV were observed for plant height (52.62%, 52.62%), primary branches per plant (26.26%, 26.26%), seed yield per plant (24.10%, 24.75%) and harvest index (18.1%, 19.4%) (Sharma *et al*., 2017).

High genotypic and phenotypic coefficient of variation was recorded for characters like number of pods per plant, grain yield per plant, biological yield per plant,

100-seed weight and plant height in an experiment conducted by Surpura and Sharma in 2017 on twenty five diverse genotypes of cowpea for sixteen characters.

One hundred and eighty genotypes of cowpea (*Vigna unguiculata* (L.) Walp) were evaluated for genetic variability in thirteen biometrical traits. Analysis of variance revealed significant differences among the genotypes for all the traits studied and PCV was higher than GCV for all the traits. The high estimates of GCV was obtained in traits of number of pods per plant (31.01 %), number of clusters per plant (34.51 %), hundred seed weight (22.29 %) and single plant yield (42.15 %) (Devi and Jayamani, 2018).

The maximum phenotypic and genotypic variance was observed for average yield per plot and the highest PCV and GCV was recorded in number of primary branches (23.54%, 22.81%) in an experiment consisting sixteen genotypes of cowpea (Kumar *et al*., 2018).

In a study conducted to assess the genetic variability, heritability and genetic advance in 20 genotypes of cowpea in F_5 generation on fifteen characters, significant differences among the genotypes for different morphological characters was observed and high values of GCV and PCV was observed for pod yield per plot, pod length, number of seeds per pod, number of pods per plant, average pod weight, and number of cluster per plant (Palve *et al*., 2018).

Twenty three F_2 generation genotypes of cowpea were assessed for their variability and the estimates revealed that phenotypic variances for all the characters studied were higher than genotypic variances. High PCV and GCV were observed for seed yield per plant (37.16%, 36.25%), number of pods per plant (29.73%, 28.86%), number of clusters per plant (26.17%, 24.83%) and number of primary branches per plant (20.76%, 19.63%) while low GCV and PCV was observed for days to first flowering (2.60%, 4.74%) and days to maturity (2.40%, 3.75%) (Sabale *et al*., 2018).

Twenty seven genotypes of cowpea were considered for studying the genetic variability. Analysis of variance showed significant difference among genotypes for all the eighteen quantitative characters recorded. High PCV and GCV were estimated for number of pods per plant (50.8%, 49.59%), pod weight (29.05%, 28.46%), pod length (20.19%, 19.77%) and number of seeds per pod (18.07%, 16.7%) (Gupta *et al*., 2019).

Investigation on genetic variability parameters for yield and yield attributing traits consisting of F_2 generation of nine crosses of cowpea recorded high PCV and GCV for number of branches per plant, number of clusters per plant, number of pods per plant and single plant yield (g) (Meenatchi *et al*., 2019).

In a study conducted by Nguyen *et al*. in 2019, the magnitude of PCV and GCV were high for biological yield per plant, plant height, harvest index, number of clusters per plant, pod yield per plant, seed yield per plant, number of pods per plant, number of branches per plant, pod weight and days to 50 per cent flowering. The prominence of environmental variation in the total variance as explained by the high PCV than the GCV for all the eleven characters studied among 22 genotypes of cowpea was observed by Sharma *et al*., 2019.

Forty cowpea genotypes collected from different locations of Tamil Nadu were evaluated for their genetic variability in eight biometrical characters. High PCV was observed for the character plant yield (28.78%) followed by number of cluster per plant (26.87%) and number of pods per plant (23.68 %), while high GCV percentage was for the characters plant yield (15.40%) and number of pods per plant (11.76%) followed by number of cluster per plant (8.28%) (Pandiyan *et al*., 2020).

In an experiment carried out to assess the genetic variability, heritability and genetic advance with a set of forty two genotypes of cowpea, a high PCV and GCV estimates were recorded for number of pods per plant (41.34%, 40.48%), seed yield per plant (35.14%, 34.15%), test weight (29.46%, 29.31%), plant height (28.28%, 27.45%) and number of clusters per plant (27.25%, 26.97%) (Rukhsar *et al*., 2020).

In a study conducted to evaluate the genetic variability and heritability of twelve genotypes in cowpea, data on fourteen characters revealed high magnitude of GCV and PCV for economic yield (kg/plot) (71.97 % and 81.76 %) followed by biological yield (kg per plot) (61.59 % and 79.96 %) (Shrivas *et al*., 2020).

In a field experiment conducted for evaluating genetic variability and genetic divergence in cowpea to identify divergent parents to be used in hybridisation programmes, thirty one genotypes were analysed for twelve characters. Analysis of variance confirmed significant differences among all the genotypes for all the

characters. GCV and PCV were high for the characters pod yield per hectare (37.14%, 39.42%), plant height (31.04%, 32.52%), number of primary branches per plant (21.74%, 27.03%) and pod length (21.20%, 24.93%) (Ugale *et al*., 2020).

An experiment conducted with Forty one genotypes of cowpea on fourteen characters revealed wide range of variation for yield and yield attributing traits. In general, PCV was found to be higher in magnitude than GCV. The highest phenotypic coefficient of variability was recorded for iron content (36.18%), plant height at maturity (24.72%) and number of primary branches per plant (23.14%). Highest genotypic coefficient of variability was recorded for iron content (36.17 %), plant height at maturity (24.57 %), number of branches per plant (19.83 %) and seed yield per plant (16.22 %) (Tambitkar *et al*., 2021).

2.2. Heritability and Genetic advance in cowpea

Heritability estimation enables plant breeders to select superior genotypes from countless gene combinations (Neji *et al*., 2019).High genetic variation coupled with high heritability provides scope for effective selection of phenotypic traits in cowpea which can be further improved through hybridisation (Panchta *et al*., 2021).

In an experiment carried out by Borah and Khan in 2000, the extent of genetic variability, heritability and genetic advance in 60 cowpea genotypes were studied and it was observed that all the 13 characters under study showed high heritability estimates, indicating low environmental effect. Fifty varieties of cowpea were evaluated for yield and few related characters. Heritability in broad sense and genetic advance were estimated for the characters of yield and associated traits. High estimates for heritability and genetic advance were observed for pods per plant, number of pods per plant and pod weight (Vidya *et al*, 2002).

Eighteen forage cowpea genotypes were studied for their genetic parameters by Chauhan *et al*. (2003). High broad sense heritability and genetic advance of yield components were obtained for days to maturity, plant height, pods per plant, pod length, seeds per pod, test weight, plant stand, seed yield per plant and seed yield per plot.

Forty diverse genotypes of cowpea were evaluated at IIVR, Varanasi and high heritability with moderate to high genetic advance was observed for plant height,

peduncle length, number of primary branches per plant, number of peduncles per plant and green pod yield per plant while high heritability coupled with low genetic advance was observed in days to 50 per cent flowering, first green pod picking, pod diameter, number of seeds per plant and test weight (Pal *et al*., 2003).

In an experiment conducted for evaluating variability, heritability and genetic advance for seven traits in thirty two genotypes of cowpea, high heritability coupled with high genetic gain were observed for plant height (96.39% and 90.78%), number of pods per plant (67.84% and 38.39%), seed yield per plot (175.02% and 122.83%) and 100-seed weight (37.40% and 39.34%) indicating the predominance of additive gene effects for these traits (Ahmed *et al*., 2005).

Lesly (2005) carried out evaluation of 169 cowpea genotypes and all the characters under study except the traits: seeds per pod, pod length and number of branches per plant showed significant variation. Highest heritability was observed in test weight and high genetic advance was observed for germination percentage, plant height, number of clusters per plant, number of pods per plant, test weight, harvest index and seed yield per plant. Sixty genotypes of cowpea were evaluated for genetic variability, heritability and genetic advance for thirteen characters. High heritability coupled with high genetic advance was reported for the traits: number of branches per plant, number of leaves per plant, dry weight of leaves, dry weight of stem, dry matter yield and plant height (Malarvizhi *et al*., 2005).

In a genetic variability study carried out with thirty genotypes of cowpea in sixteen characters, high estimates of heritability and genetic advance were observed for plant height at the time of first flowering (91.89%, 53.96%), plant height at the time of 50 per cent flowering (89.99%, 53.537%) and plant height at the time of 50 per cent maturity (84.61%, 28.41%) (Eswaran *et al*., 2007).

Thirty genotypes of cowpea were evaluated for ten metric traits and high heritability values were observed for test weight, seed yield per plant, seeds per pod, clusters per plant, pod length, pods per plant, days to first flower and plant height (Suganthi and Murugan, 2008). Twenty genotypes of vegetable cowpea were evaluated for fourteen quantitative characters and highest heritability values were observed for

seed yield per plant (99.6%) followed by pod length (99.1%), test weight (98.8%), number of seed per plot (97.9%), days to fifty per cent flowering (96.2%), green pod yield per plant (95.8%), diameter of pod (94.5%), days taken for first flowering (93.5%) and leaf area per plant (93.0%) (Tamgadge *et al*., 2008).

In an experiment conducted in seventy two diverse genotypes of cowpea to examine the genetic variability, heritability and genetic advance on nine characters, moderate to high heritability accompanied by high genetic advance was recorded for plant height (97.60%, 71.81), 100 seed weight (96.78%, 70.95), yield per plant (75.22%, 54.03), pod length (95.76%, 45.29), number of pods per plant (72.83%, 41.98) and number of branches per plant (69.94%, 35.89) (Kumar *et al*., 2009).

A cross was made between two genetically diverse parents V-1188 and Goa local and superior progenies were advanced to F_2 and F_3 generations. It was observed that the extent of variability observed in F_2 was more than that in F_3 and similar trend of declination was found in F_3 for heritability and genetic advance as per cent mean indicating selection will be less effective in further advanced generations (Kurer *et al*., 2010).

Crosses were made between five cultivated cowpea varieties and var. *pubescens* (as pollen parent) to study the inheritance of hairiness, pod shattering, heritability and correlation between them. F_1 plants exhibited dominance for both hairiness as well as pod shattering traits and high heritability was observed for days to pod maturity (77.93 %), test weight (68.45 %), seeds per pod (69.76 %) and number of branches per plant (62.54 %) (Mohammed *et al*., 2010).

Nwosu *et al*. in 2013 while investigating cross compatibility and F_1 reproductive potential in cultivated and wild relatives of cowpea could observe that additive gene action dominated the expression of traits because of high heritability in the broad sense. They also observed higher heritability values for most of the phenotypic traits in cultivated as well as wild relatives of cowpea.

Twenty four crosses were made by Line x Tester analysis and among these, elite crosses were advanced to F_2 and F_3 generations. It was observed that the cross L_5T_1 exhibited high heritability and genetic advance for number of pods (97.03%, 53.95%),

pod yield (98.13%, 191.35%), pod length (72.88%, 59.83%) and crude fibre content (80.08%, 14.83%) in both F_2 and F_3 generations (Subbiah *et al*., 2013). Ajayi *et al*. in 2014 conducted a study on ten genotypes of cowpea for the interrelationship among twenty quantitative traits. High broad sense heritability values were obtained for all the traits studied except for plant height.

Chattopadhyay *et al*. in 2014 estimated higher broad sense heritability coupled with higher genetic advance for number of pods per plant, pod yield per plant, pod weight, number of seeds per pod and pod length in a study conducted in seventeen genotypes of vegetable cowpea for eight characters. Forty genotypes of Cowpea were evaluated for twelve traits and it was found that high heritability along with high genetic advance expressed as percentage of mean was observed for number of pods per plant, 100 fresh seeds weight, 10 pods weight, green pod yield per plant and plant height (Sapara *et al*., 2014).

In an experiment conducted on twenty two genotypes of cowpea, the highest heritability was observed for the characters days to 50 per cent flowering (99.89%) followed by hydration capacity (99.74%), days to maturity (99.63%), 100 seed weight (99.34%), seed volume (99.19%), swelling capacity (98.15%), swelling index (96.09%), seed density (94.02%), seed yield per plot (93.54%), hydration index (82.48%) and pod length (76.94%). Genetic advance was estimated as high for days to maturity, seed volume, swelling capacity, swelling index and seed yield per plot (Tigga *et al*., 2014).

In a study conducted by Khanpara *et al*. (2015), high heritability combined with high genetic advance was observed for green pod yield per plant, plant height, pod length, pod width, number of seeds per pod, number of pods per plant, ten pod weight, number of pods per cluster and hundred fresh seed weight. It was further concluded that further improvement of these traits can be rewarding as these traits are controlled by additive gene action.

A field experiment was conducted for evaluating 72 genotypes of cowpea to estimate genetic variability, heritability and genetic advance in 10 biometric characters. High estimates of heritability along with high genetic advance as per cent of mean was

recorded for test weight (95.95%, 51.81%) and plant height (94.78%, 77.52%) which indicated the prevalence for additive gene action in the expression of these characters while high heritability along with moderate genetic advance as per cent of mean was recorded for pod wall proportion, seed yield per plant and pod length which indicated that these characters were mainly under the action of non-additive genes (Meena *et al*., 2015).

Investigation carried out on fifteen genotypes of bush cowpea for ten quantitative characters reported high estimate of broad sense heritability and genetic advance for the characters of plant height, number of pods per plant, edible pod yield per plant and edible pod yield per hectare (Tudu *et al*., 2015).

Sixty diverse genotypes of cowpea were evaluated for genetic parameters for twelve characters and high heritability along with high genetic advance were observed for green pod yield per plant, plant height, pod length, pod width, number of seeds per pod, number of pods per plant, pod weight, number of pods per cluster and hundred fresh seed weight (Khanpara *et al*., 2015). In an experiment conducted by Omoigui *et al*., in 2006, broad sense heritability estimate (h^2) was 98.9 per cent for 100 seed weight, 94 per cent for duration of reproductive phase, 84.5 per cent for days to first flower, 83.9 per cent for days to maturity and 77.3 per cent for harvest index.

Khandait *et al*. in 2016 reported high estimate of heritability for characters of pod length, number of pods per plant, pod weight, number of flower clusters per plant and pod width. The estimate of genetic advance as percentage of mean was observed high in number of flower cluster per plant followed by number of pods per plant, pod length, number of pods per cluster, pod weight, pod width, number of flowers per cluster, number of branches at 30 days after sowing, pod yield per plot, pod yield per ha and pod yield per plant. Sixty six advanced bush type vegetable cowpea were evaluated and high values of heritability (broad sense) and genetic advance were reported in pod yield per plant, number of peduncles, pods per plant, peduncle length, number of primary branches per plant, pod length, pod weight and number of seeds per pod (Lal *et al.,* 2017).

In a study conducted by Dinesh *et al*. in 2017, six quantitative traits were estimated for F_3 generation derived from the cross between C-152 × V-16. High heritability coupled with high genetic advance as per cent of mean (GAM) was observed for plant height (67.13% and 21.78%) and moderate heritability and GAM was observed for number pods per plant (49.14% and 16.49 %).

Fifty diverse genotypes of cowpea were evaluated by Lovely and Radhadevi (2017) for fourteen characters. The characters: clusters per plant (82.49%, 71.23%), pods per cluster (78.60%, 84.83%), pods per plant (76.31%, 80.88%), primary branches per plant (84.66%, 24.39%), pod yield per plant (77.00%, 76.44%), pod weight (95.86%, 88.43%), pod length (98.21%, 66.76%), seeds per pod (88.42%, 20.70%) and main stem length (82.30%, 39.89%) had high heritability coupled with high genetic advance.

One hundred and sixty nine cowpea genotypes were evaluated for ten quantitative characters and high heritability and genetic advance were obtained for days to 50 per cent flowering (94.41%, 87.94%), number of branches per plant (83.96%, 54.31%), number of pods per plant (75.87%, 58.59%) and seed yield per plant (97.19%, 63.76%) (Viswanatha and Yogeesh, 2017).

Thirty genotypes of cowpea were evaluated to assess genetic variation and inter relationship among seventeen characters. High heritability coupled with high genetic advance was observed for the traits: biological yield per plant, followed by plant height, harvest index, number of clusters per plant, seed yield per plant, pod yield per plant, number of branches per plant, pod weight, days to 50% flowering, 100 seed weight, number of seeds per pod, days to maturity and pod length (Nguyen *et al*., 2019).Twenty-eight cowpea accessions including the local cultivar Glenda were used in a study and the highest broad-sense heritability was recorded for grain yield per plant (98.57%) and the lowest heritability was observed for number of seeds per pod (84.24 %) (Nkoana *et al*., 2019).

Twenty two genotypes of cowpea were evaluated for their variability in 11 characters and heritability estimates were found to be high for seed yield per plant (98.75%), plant height (96.47%), primary branches per plant (91.37%), days to 50 per

cent flowering (88.28%), number of seeds per pod (87.68%), days to 80% maturity (85.91%), no. of cluster per plant (81.54%), pods per plant (77.36%), green pod weight (77.27%) and test weight (75.33%) (Sharma *et al*., 2019).

2.3. G x E interaction in cowpea

The apparent variation exhibited by a plant is not only due to the genotype but also due to the influence of the environment on the expression of characters (Nehru *et al*., 2019). The Genotype x Environment (G x E) interaction is an important limiting factor in testing the efficiency of breeding programmes since the occurrence of a large G x E interaction affects the recommendations of breeders in selecting genotypes for specific environments (Adewale *et al*., 2010).

Genotype x Environment analysis provides an unbiased estimate of yield and other agronomic traits and in determining the ability of a genotype to withstand both predictable and unpredictable environmental variation (Kamdi, 2001). In cowpea, larger contribution on yield variation is by Genotype x Environment interaction than genotypic effect as reported by Stanley *et al*. (2005). It is necessary to evaluate genotypes in contrasting environments while developing cowpea varieties for desirable traits (Hall *et al*., 2003).

Seven elite genotypes of cowpea were grown at five different locations and the forage production potential of the genotypes among the group of characters was studied. The data was subjected to Principal Component Analysis (PCA) for genotype x environment interactions. The genotypes IFC-9802 and UPC-5286 exhibited superiority over the other genotypes and UPC-606 falling close to the origin was identified as the most stable genotype (Kohli *et al*., 2001).

Twenty six cowpea cultivars were tested for genotype x environment analysis so as to select disease resistant and stable high yielding cultivars. According to three parameters of high mean seed yield, regression coefficient and standard deviation to regression the genotypes with significant and highest seed yield, NIAB cowpea mutant-1 (880 kg/ha) was selected followed by Elite (729 kg/ha). These genotypes showed excellent and stable performance for seed yield over different environments (Ali *et al*., 2004).

The genotypes SARI-6-2-6 and IT07K-303-1 were adapted to Damongo, Nyankpala, and Tumu, whereas the genotype SARI-2-50-80 was adapted to Yendi and Manga. The best ranking location was Damongo followed by Tumu and Nyankpala. The high-yielding genotypes of IT86D-610, IT10K-837-1, IT07K-303-1 and SARI-2-50-80 were recommended for release as cultivars since they had significantly higher grain yield than the check (Owusu *et al*., 2020).

Six improved cowpea genotypes were evaluated for three seasons at four locations with an objective of comparing their yield performance and assessing their adaptability. The data obtained was analysed using the AMMI model to determine the stability of the genotypes. Among the six genotypes MU-93 was recognised as the best genotype in all environments (Asio *et al*., 2005).

Twenty two genotypes of cowpea were evaluated for fodder yield potential. The mean fodder yield of cowpea genotypes across different environments were used to assess the stability. Significant differences were recorded for genotypic effects, environment and genotype x environment interaction. Eight group of stability parameters were identified and an enlarged rank sum method identified cowpea genotype with the best fodder yield. Genotypes IT 98K-1111-1, IT 86D-1010, IT 86D-719, IT 93K-452 and IT 97K-503-1 were identified to be of stable and of higher fodder yield across environments (Taiwo, 2007).

The grain yield components of eleven cowpea genotypes were studied so as to understand the sensitivity of quantitative traits to different environments. It was reported that out of the total characters studied, days to fifty per cent flowering, days to ninety five per cent maturity, test weight and pod yield were significantly influenced by the effect of genotype, year and their interactions (Adewale *et al*., 2010).

In a study conducted by Cholin *et al*. 2010, twenty diverse genotypes of cowpea including one local check (C-152) was evaluated to assess the stability parameters over three seasons. It was found that variances due to genotype, environment, genotype x environment, environment + (genotype x environment), environment (linear) were significant for pods per plant and seed yield per plant. Genotype IL3 was found to be

stable across the seasons for test weight and genotypes M17, Goa local and Bailhongal local were stable and superior for seed yield over all environments.

Forty one genotypes of cowpea were field evaluated to identify grain cowpea possessing low pod wall proportion (PWP) and high pod filling index (PFI) with least environment interaction. The Additive Main effects and Multiplicative Interactions (AMMI) model was used to identify stable genotypes. It was found that the genotype EC 394767 was promising for most of the pod characters except PWP while C 440 showed the least number of unfilled locules (Dhanasekhar *et al*., 2010).

Stability analysis so as to identify phenotypically stable genotypes for yield and yield related component traits was carried out by Patel and Jain (2012) with eleven genotypes of cowpea over four different environments for six characters. Pooled analysis of variance revealed significant differences for all the characters. Except for days to fifty per cent flowering and seeds per pod, G x E interaction was significant for all the characters. The genotype GC-0121 was found to be stable and 20 per cent superior over the check variety GC-5.

In a stability analysis experiment conducted by Chaudhari *et al*. (2013), analysis of variance indicated highly significant Genotype x Environment interaction for the majority of traits indicating the differential response of genotypes to varied environments. Seed yield per plant and its related traits showed significant Genotype x Environment (linear) and pooled deviation suggesting the importance of both linear and non-linear components in G X E interaction. The parents GC-4 and V-240 with high gca effects for seed yield per plant and its other attributes were found to be stable. DCP-10 x GC-5, DCP-2 x V-240 and GC-3 x GC-5 were identified as the best stable hybrids.

Stability analysis of component characters in cowpea was assessed using nineteen genotypes of cowpea over twelve environments. Significant interaction between genotype and environment was observed for all the characters except pod length, hundred seed weight and weight of pods per plant. Dokii331 and Cream12 were identified as the best and stable genotypes (El-shaieny *et al*., 2015).

Grain yield data was analysed using the AMMI and the genotype main effects plus genotype-by-environment interaction (GGE) biplot methods to determine the

effects of genotype by environment (G x E) interaction and stability among superior cowpea selections derived by gamma irradiation. Thirty four newly developed mutant genotypes were evaluated and the AMMI and GGE-Biplot models could explain 77.49 per cent and 75.57 per cent of total observed genotypic variation (Horn *et al*., 2017).

Sixteen cowpea genotypes were tested at seven environments and the combined analysis of variance revealed significant difference among genotypes and environments along with significant effect of Genotype x Environment interactions on grain yield, days to flowering, days to maturity, plant height and pods per plant. ANOVA for grain yield from AMMI model indicated the contribution of genotype and environment and GEI contribution of about 63.3 per cent, 5.3 per cent and 29.7 per cent of the total sum of squares (Simion *et al*., 2018).

In a study to evaluate the genotype by environment (G x E) interaction, the grain yield of 40 cowpea genotypes, 30 lines and 10 cultivars were evaluated and the data was subjected to GGE-Biplot analysis. The graphical results showed variation in the performance of the genotypes in the location evaluated over years. The performance of the genotypes MNC02-675F-4-9 and MNC02-675F-4-10 with maximum yield and good stability were considered as ideal. The lines MNC02-675F-4-9, MNC02-675F-9-3 and MNC02-701F-2 had the best performance within each mega-environment (Sousa *et al*., 2018).

Fourteen genotypes of cowpea were evaluated to study the G x E interaction for seed yield along with three checks over two seasons in two years. Variation due to genotype, genotype x environment, environment + (genotype x environment), environment (linear) and pooled deviation were significant for seed yield. Based on Eberhart and Russell model for stability, the genotypes VCP 12006, VCP 13001 and VCP 15006 with a unity regression coefficient and deviation from regression equal to zero were found to be stable across the environments for seed yield (Manivannan *et al*., 2019).

In a study undertaken to assess the yield stability performance of cowpea genotypes, nine improved genotypes of cowpea were assessed across six environments. The GGE-Biplot method was used to determine the yield stability. Highly significant

genotype x environment interaction effect was detected for seed yield. IT90K-277-2 had the highest grain yield while ACC004 reported the lowest. Palotaka was observed as a highly discriminating environment. While IT07K-211-1-8 and Mading Bor II were the most responsive genotypes, IT90K-277-2 was recognised as the most stable and high yielding genotype (Ngalamu *et al*., 2019).

In an attempt to select strains of cowpea for high productivity, adaptability and stability, 27 genotypes, 23 strains and four cultivars were assessed in six environments using the GGE-Biplot method. It was found that the interaction between the environment and genotypes was complex and the general average for the productivity of the grains was 1231.98 kg/ha. The method could also identify best strains to be suggested for cultivation and the strains Pingo-de-ouro 1-5-8, Bico-de-ouro 1-5-19 and Pingo-de-ouro 1-5-4 were classified as ideotypes because of their superior performance over the control cultivars BRS Tumucumaque, BRS Imponente, BRS Itaim e CB-27 and because of their stability (da Cruz *et al*., 2020).

Fifteen cowpea genotypes were evaluated for yield performance and stability across three different locations. The AMMI analysis of variance revealed genotypes (G), environments (E) and their interaction were significant for grain yield. The G and GE effects accounted for about 10 per cent of the total variation in grain yield whereas the environment accounted for 66 per cent of the total variation (Gerrano *et al*., 2020).

In an experiment conducted by Owusu *et al*. (2020) to assess the yield stability of eight advanced breeding lines of cowpea and to identify mega-environments for cowpea production in Ghana, the genotypes were evaluated across five environments and analysed using the GGE-Biplot method. ANOVA detected significant variation for G x E interaction and the principal component 1 (PC1) and 2 (PC2) accounted for 46.75 of the total variation and 22.84 of the total variation of GGE sum of squares.

In an experiment conducted to identify cowpea genotypes suitable for summer season, thirty eight accessions of cowpea along with three check varieties (V-585, FTC-27 and GC-3) were evaluated for nine quantitative traits for five consecutive seasons. It was observed that the G X E interaction variance was significant for all the characters except peduncle length and plant height and the accession C-863 was reported to be the

most suitable one for the characters seed yield per plant and number of clusters per plant (Singh *et al*., 2020).

G x E interaction was estimated in thirty cowpea genotypes during the kharif season of 2019 and 2020 across six environments and all the genotypes under study showed significant interaction with the environment. The analysis of GGE-Biplot revealed FD-2258 genotype as the ideal genotype and E_1 environment as ideal environment for the character, days to 50 per cent flowering. The genotype FD-2229 was equally good in environment E_3 and E_6 and the genotype FD-2258 was good in E_1, E_2, E_4 and E_5 for selecting superior stable fodder cowpea genotypes (Banik *et al*., 2021).

Materials and methods

3. MATERIALS AND METHODS

The study entitled as "Genotype x Environment interaction in advanced breeding lines of cowpea (*Vigna unguiculata* (L.) Walp)" was carried out at the Department of Plant Breeding and Genetics, College of Agriculture, Thrissur during September 2019 to May 2021. The objective of the study was to assess the genotype x environment interaction in advanced breeding lines of cowpea (*Vigna unguiculata* (L.) Walp). The study was undertaken at three different locations: Pattambi, Vellanikkara and Vyttila (Plate 1), belonging to Central midland, Malayoram and CoAstal sandy agro-ecological zones of Kerala, during February to May 2021. The study emphasised on the development of stable genotypes with higher yield in cowpea to be used as a dual purpose type (both as vegetable and grain purpose type). The materials used and the methodologies followed in the study are presented in this chapter.

3.1 Materials

3.1.1 Experimental site

The field experiments were conducted at three locations namely, Pattambi, Vellanikkara and Vyttila. The area at G Block, Regional Agricultural Research Station, Pattambi is at 10º 48' 39" North latitude and 76º 11' 20" East longitudes at an altitude of 205 m above MSL. The location belongs to the central midland agro-ecological zone of Kerala and the soil of the experimental site is laterite. The area at Experimental field plot, Dept. of Plant Breeding and Genetics, College of Agriculture, Vellanikkara is at 10º 32' 53" North latitude and 76º 16' 42" East longitudes at an altitude of 195 m above MSL, belonging to the Malayoram agro-ecological zone of Kerala. The soil of the experimental site is laterite without B horizon. The area at Rice Research Station, Vyttila is at 9º 58' 27" North latitude and 76º 19' 22" East longitude at an altitude of 61 m above MSL, belonging to the CoAstal sandy zone regions of Kerala. The soil of this experimental site is sandy loam.

3.1.2 Experimental material

The material used for the study included five cowpea cultures in stabilised F_7 generation developed through pedigree selection from two crosses (H-11 and H-10) at the Department of Plant Breeding and Genetics, College Of Agriculture, Thrissur along

with two check varieties Anaswara and Kanakamony. The details regarding the cultures are presented in Table 1 and Table 2.

3.2 Methods

The crops were raised over three locations of Pattambi, Vellanikkara and Vyttila during the month of February to May, 2021. The field experiment was laid out in randomized block design with three replications. The details of the environments are presented in Table 3. The plot size was 12.5m x 5.2m and plants were raised adopting a spacing of 25 x 30 cm^2. Standard cultural and plant protection measures were followed according to the Package of Practices Recommendations Crops 2016 by Kerala Agricultural University (KAU, 2016). Gap filling was done one week after sowing, to maintain a minimum plant population of 25 plants per treatment in each replication. In all the locations, hand weeding was done 30 and 60 days after sowing (DAS) at all the three locations. The crop was harvested when 90 per cent of the pods in all the plants were dried. All the observations were recorded after harvest except for days to flowering.

Table 3. Details of the environments studied

Sl. No.	Environment	Season/ condition	Location
1.	Environment 1	Summer season (Feb - May, 2021)	RARS, Pattambi
2.	Environment 2	Summer season (Feb - May, 2021)	CoA, Vellanikkara
3.	Environment 3	Summer season (Feb – May, 2021)	RRS, Vyttila

Table 1. Cultures and check varieties used in the experiment

Sl. No	Cultures/ Lines	Renamed cultures	Original cross combination
1	H-11-3-9-1-7-13-17	L_1	Anaswara x PKB 4
2	H-11-49-7-1-8-10-15	L_2	Anaswara x PKB 4
3	H-11-3-9-1-1-18-13	L_3	Anaswara x PKB 4
4	H-11-2-20-3-14-16-12	L_4	Anaswara x PKB 4
5	H-10-71-16-1-9-15-12	L_5	Anaswara x PKB 3
6	Anaswara	C_1	
7	Kanakamony	C_2	

Table 2. Details of the cultures used in the experiment

Sl. No	Cultures/ Lines	Details of cultures									
		Plant height (cm)	Number of branches	Number of pods per plant	Length of pod (cm)	Pod weight (g)	Number of seeds per pod	Test weight (g)	Grain yield (g)	Protein content (%)	Pod husk crude fibre (g)
1	H-11-3-9-1-7-13-17	150	5	43	22	3.17	18	14.50	105.00	23.40	35.1
2	H-11-49-7-1-8-10-15	204	6	42	28	3.92	18	20.23	152.60	25.50	31.4
3	H-11-3-9-1-1-18-13	180	4	43	21	3.27	19	14.80	120.82	20.53	37.8
4	H-11-2-20-3-14-16-12	169	3	37	26	3.85	17	17.68	112.50	24.40	30.8
5	H-10-71-16-1-9-15-12	162	4	37	27	4.07	16	19.20	113.50	21.87	32.5

3.2.1 Observations

Observations were recorded from 25 plants per replication for each treatment.

3.2.1.1 Plant height (cm)

The height of each plant of all the treatments and three replications was recorded from ground level till its growing point and expressed in centimetres.

3.2.1.2 Number of branches

The number of branches per plant was recorded for each treatment from all the three replications.

3.2.1.3 Days to first flowering

The number of days taken for first flowering in each plot was recorded.

3.2.1.4 Days to first harvest

The number of days taken for first harvest was recorded for each treatment in each replication.

3.2.1.5 Days to last harvest

The number of days taken till last harvest was recorded for each treatment in each replication.

3.2.1.6 Number of pods per plant

The number of pods per plant were counted and recorded for each treatment in each replication.

3.2.1.7 Length of pod (cm)

The mean length of 10 randomly collected pods of each plant per treatment in each replication at the time of harvest was recorded and expressed in centimetres.

3.2.1.8 Pod weight (g)

The mean weight of 10 randomly collected pods of each plant per treatment in each replication was recorded at the time of harvest and expressed in grams.

3.2.1.9 Number of seeds per pod

The mean number of seeds per pod for 10 randomly collected pods of each plant per treatment in each replication were recorded at the time of harvest.

3.2.1.10 Test weight (g)

The weight of 100 grains for each treatment in each replication was taken at random and expressed in grams.

3.2.1.11 Grain yield per plant (g)

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

3.2.1.12 Protein content (%)

Lowry's method was adopted in estimating protein content and was expressed in percentage (Sadasivam and Manickam, 1996). 500 mg of cowpea grains were made into fine powder using mortar and pestle. It was then homogenized in 25 ml phosphate buffer (pH: 7.4) and centrifuged at 11,000 rpm (25 ºC) for 10 minutes. Supernatant was collected and used as test sample. Afterwards, 0.2 ml of test sample was pipetted out into a test tube and made up to 1.0 ml with distilled water. A test tube with 1ml distilled water served as the blank. Five ml of alkaline copper sulphate reagent (50 ml of 2% sodium carbonate in 0.1 N sodium hydroxide mixed with 1 ml of 0.5% copper sulphate in 1% potassium sodium tartrate) was added to each test tube and mixed well and incubated at room temperature for 10 minutes. Half ml of Folin-Ciocalteu reagent was then added and the test tubes were kept at dark for 30 minutes. Simultaneously, 0.2 ml to 1.0 ml standard protein solution (0.2 mg BSA ml^{-1}) was also pipetted out into a series of test tubes and the volume was made up to 1 ml with distilled water. Reagents added as in case of the test sample were also added to the standard solution and kept under dark for 30 minutes. Blue colour developed was read using a spectrophotometer at 660 nm. A standard curve was plotted using the standard protein absorbance against concentration and from this curve, protein content of the sample was calculated and expressed in percentage.

3.2.2 Statistical analysis

Data collected from all the three locations with respect to quantitative traits as mentioned above were tabulated and subjected to location wise analysis of variance and stability using the statistical software R version 3.4.1 (R Core Team, 2018).

3.2.2.1 Analysis of variance

The data collected from three locations (Pattambi, Vellanikkara and Vyttila) for all the twelve quantitative traits were subjected to individual, location wise analysis of variance suggested by Panse and Sukhatme in 1954. Least significant difference based on minimal critical difference was attempted to identify the actual differences among lines for each particular trait and for determining their ranking orders, respectively.

Table 4. Analysis of variance of Randomized Block Design

Source of variation	Degrees of freedom (df)	Sum of Squares (SS)	Mean Sum of Squares(MS)	Expected MS
Replications	r-1	-	-	-
Between genotypes	t-1	SS_1	MS_1	$\sigma^2_e + r\,\sigma^2_g$
Within genotypes or error	(r-1) (t-1)	SS_2	MS_2	σ^2_e
Total	(rt-1)	-	-	-

Where,

r = number of replications

t = number of genotypes

Phenotypic and genotypic components of variance can be estimated according to the formula suggested by Snedecor and Cochran (1994).

Environmental variance $= \sigma^2_e$

Genotypic variance $(\sigma^2_g) = \frac{MS_1 - MS_2}{r}$

Phenotypic variance $(\sigma^2_p) = \sigma^2_g + \sigma^2_e$

Phenotypic, genotypic and environmental coefficients of variation were estimated using the formula suggested by Burton and De Vane (1953).

Phenotypic coefficient of variation (PCV) $= (\sigma_p / \text{mean}) \times 100$

Genotypic coefficient of variation (GCV) $= (\sigma_g / \text{mean}) \times 100$

Environmental coefficient of variation (ECV) $= (\sigma_e / \text{mean}) \times 100$

Where σ_p, σ_g and σ_e are phenotypic, genotypic and environmental standard deviations. PCV and GCV are classified as low when less than 10 per cent, moderate when it is between 10 and 20 per cent and high if it is more than 20 per cent (Sivasubramanian and Madhavamenon, 1973).

3.2.2.2 Heritability

Heritability in a broad sense was computed for all the quantitative traits using the formula suggested by Lush in 1945.

$H = \sigma^2_g / \sigma^2_p$

Heritability can be classified as low when less than 30 per cent, as moderate when between 30 and 60 per cent and as high when it is more than 60 per cent (Robinson *et al.,* 1949).

3.2.2.3 Genetic advance

Genetic advance is a measure of genetic gain under selection. The expected genetic gain is estimated from the formula suggested by Johnson *et al.* (1955).

$GA = \sigma^2_g / \sigma^2_p \times k$

Where,

σ^2_g - Genotypic variance

σ^2_p - Phenotypic variance

k– Selection differential at particular level of selection intensity

(for 5% selection intensity, k= 2.06)

Genetic advance was expressed as percentage of mean as suggested by Allard in 1960:

$$\text{Genetic advance (per cent)} = \frac{\text{Genetic advance}}{\text{Mean}} \times 100$$

Genetic advance expressed as percentage of mean can be classified as low (0-10%), as moderate (10.1-20%) and as high (>20%) as suggested by Johnson *et al*. (1955).

3.2.3 Pooled analysis of variance

The data at environments where significant differences for genotypes were observed was used for pooled analysis of variance, forming a two way table. Pooled analysis was done as data pooled for all the characters over three locations.

Table 5. Pooled analysis of variance

Source of variation	**Degrees of freedom (dof)**	**Sum of Squares (SS)**	**Mean Sum of Squares (MS)**
Genotype (G)	g-1	-	$\sigma^2_e + r\,\sigma^2_{ge} + re\,\sigma^2_g$
Environment (E)	e-1	-	$\sigma^2_e + r\,\sigma^2_{ge} + rg\,\sigma^2_e$
G x E Interaction	(g-1) (e-1)	-	$\sigma^2_e + r\,\sigma^2_{ge}$
Pooled error	e (r-1) (g-1)	-	σ^2_e
Total	r (ge-1)	-	

MS due to pooled error = $\frac{\text{SS in E1 + SS in E2 +……...……+ SS in En}}{\text{Error dof in E1 + Error dof in E2 +….+ Error dof in En}}$

3.2.4 Stability analysis

3.2.4.1 Eberhart and Russell model

Analysis of variance for stability was done when the pooled analysis of variance was found to be significant for genotype x environment interaction. The three parameters of stability, namely mean, regression coefficient (bi) and mean squared deviation (S^2di) for each line were estimated following the Eberhart and Russell (1966) model. Using this model, stability parameters pooled over three environments for seven lines were estimated.

The linear model proposed by Eberhart and Russell (1966) is as follows:

$$Y_{ij} = \mu_i + b_iL_j + \sigma_{ij}$$

Where,

Y_{ij} – Mean performance of i^{th} line in j^{th} environment

μ_i - Average performance of j^{th} line over all environments

b_i - Regression coefficient that measures the response of the i^{th} line to varying environments

σ_{ij} – Deviation from regression of the i^{th} line at j^{th} environment

L_j - Environmental index as the deviation of the mean of all lines in j^{th} environment from grand mean

3.2.4.1.1 Analysis of variance for stability

Eberhart and Russell (1966) proposed analysis of variance for stability as follows:

Table 6. Analysis of variance for stability

Source of variation	Degrees of freedom	Sum of squares	Mean sum of squares (MS)
Total	(ge-1)	$\Sigma_i \Sigma_j Y_{ij}^2$- CF	
Genotypes [G]	(g-1)	1/e $\Sigma_i Y_i^2$- CF	MS_1
Environment [E] (linear)	1	I/g $(\Sigma_i Y_{ij} I_j)^2/ \Sigma_j I_j^2$	
Environments + (G x E)	g(e-1)	$g_i \Sigma_j Y_{ij}$- Y_i^2/e	
G x E (linear)	(g-1)	$\Sigma_j [(\Sigma_j \Sigma Y_{ij} I_j)^2/ \Sigma_j I_j] –$ $[I/g (\Sigma_j Y_j I_j)^2/ \Sigma_j I_j^2]$	MS_2
Pooled deviation	g(e-2)	$\Sigma_i \Sigma_j \sigma_{ij}^2$	MS_3
Deviation due to genotypes -1	(e-2)	$[\Sigma_j \Sigma Y_{ij}^2$-$(Y_i^2/e)]$- $[(\Sigma_j Y_{ij} I_j^2)/ \Sigma_j I_j^2] = \Sigma_j \sigma_{ij}^2$	MS_3 -1
Genotypes -g	e(r-2)	$[\Sigma_j Y^2$- $(Yg^2/e)]$ - $[(\Sigma_j Ygi I_j^2)/ \Sigma_j I_j^2] = \Sigma_j \sigma_{ij}^2$	MS_3 –g
Pooled error	e(r-1)(g-1)	-	σ^2_e

Where,

g : Genotype

r : Number of replications

e : Environment

CF: Correction Factor

3.2.4.1.2 Estimation of stability parameters

Estimation of the regression coefficient (bi) and mean square deviation from the linear regression (s^2di) are as follows:

3.2.4.1.3 Estimation of regression coefficient

Regression coefficient refers to the performance of each genotype over different environments on the environmental means over all the genotypes. It can be computed as follows:

$$bi = \frac{\Sigma ij\ Yij\ Ij}{\Sigma j\ Ij^2}$$

Where,

$\Sigma ij\ Yij\ Ij$ - the sum of products of environmental index (Ij) with corresponding mean of that genotype at each environment (Yij)

$\Sigma j\ Ij^2$ - the sum of squares of the environmental index (Ij)

- The factor, $\Sigma ij\ Yij\ Ij$ for each genotype is the sum of products of environmental index (Ij) and the corresponding mean (X) of the genotype in each environment, the values of which can be obtained as follows:

$$[Ij] \times [X] = [\Sigma ij\ Yij\ Ij]$$

Where, [Ij] – Vector for environmental index

[X] – Matrix of means

- The factor, $\Sigma j\ Ij^2$ is common for each value of regression coefficient and can be determined as follows:

$$\Sigma j\ Ij^2 = I_1^2 + I_2^2 + \ldots\ldots + I_i^2 + \ldots.. + I_n^2$$

- The regression coefficient for each genotype can then be estimated by dividing the factor $\Sigma ij\ Yij\ Ij$ of each genotype with the factor $\Sigma j\ Ij^2$. Environmental index of the jth environment (Ij) can be computed as follows:

3.2.4.1.4 Estimation of environmental index (Ij)

$$I_j = \frac{\Sigma i\ Yij}{g} - \frac{\Sigma i\ \Sigma j\ Yij}{ge} \quad (\text{with } \Sigma j\ Ij = 0)$$

$$= \frac{\text{Total of all the genotypes at the jth location}}{\text{Number of genotypes}}$$

Mean square deviation (S^2di) can be estimated from the linear regression as follows:

3.2.4.1.5 Computation of mean square deviation (S^2di)

$$S^2di = \frac{\Sigma j\ Sij^2}{e-2} - \frac{Se^2}{r}$$

$$\text{here, } \Sigma j\ Sij^2 = \Sigma j\ Y^2ij - \frac{Yi^2}{g} - \frac{(\Sigma jYij\ Ij)^2}{\Sigma j\ Ij^2}$$

where,

$\Sigma j\ Sij^2$ = Variance of a genotype due to deviation from the regression

$\Sigma j\ Y^2ij - \frac{Yi^2}{g}$ = Variance due to dependent variable

$$\frac{(\Sigma jYij\ Ij)^2}{\Sigma j\ Ij^2} = \frac{(\Sigma j\ Yij\ Ij)\ (\Sigma j\ Yij\ Ij)}{\Sigma j\ Ij^2} = bi\ (\Sigma j\ Yij\ Ij)$$

The stability parameter, mean square deviation (S^2di) for each genotype can be estimated from $\Sigma j\ Sij^2$ values as follows:

$$S^2di = \frac{\Sigma j\ Sij^2}{e - 2} - \frac{Se^2}{r}$$

$$S^2di = \frac{\text{Deviation from regression}}{\text{Degrees of freedom for each environment}} - \frac{\text{Pooled error}}{\text{Number of replications}}$$

S^2 - Estimated pooled error

e - Number of environments

g - Number of genotypes

r - Number of replications

3.2.4.1.6 Test of significance

The following test of significance were carried out:

- To test the significant difference among genotypes mean, the F test used was:

$$F = \frac{\text{Mean squares due to genotypes}}{\text{Mean square due to pooled deviation}} = \frac{MS_1}{MS_3}$$

- To test that genotypes did not differ due to environmental index, the F test used was:

$$F = \frac{\text{Mean square due to genotype x environment (linear)}}{\text{Mean square due to pooled deviation}} = \frac{MS_2}{MS_3}$$

- Individual deviation from linear regression is tested as follows

$$F = \frac{\Sigma j\ Sij^2}{e - 2} - \frac{\text{pooled error}}{rt}$$

F_{value} is tested against p = 0.05 at (g - 2) degrees of freedom

- The hypothesis that the regression coefficient does not differ from unity or from zero is tested using the t test

$$t = \frac{(1-b)\ 1-b}{SE_{(b)}}$$

It is tested against p=0.05 at (g-e) degrees of freedom

Mean standard error of b:

$$SE_{(b)} = \sqrt{\frac{\text{MS due to pooled deviation}}{\Sigma j\ Ij^2}}$$

Population mean (μ) and standard error can be calculated as:

$$\text{Population mean } (\mu) = \frac{\text{Grand total}}{\text{Number of observations}}$$

$$\text{SE (mean)} = \sqrt{\frac{\text{MS due to pooled deviation}}{\text{Number of environment} - 1}}$$

3.2.4.1.7 Genotypic stability

A genotype can be referred to as stable when it has a regression coefficient of unity (b_i=1) and the mean square deviation not significantly differing from zero (s^2di=0)

3.2.4.2 Additive Main effects and Multiplicative Interactive effects (AMMI) model

The AMMI model using ANOVA, calculates the genotype and environmental main effects and then analyses the residual (ie. the interaction extracted from the genotype x environment portion of the ANOVA) using the principal components analysis (PCA) ((Zobel *et al*., 1998). Being a combination of ANOVA and PCA, AMMI model is an additive as well as multiplicative model. In statistical hybrid model AMMI, the results in a least squares analysis which when further presented in a graphical way (Biplot analysis) allows a straightforward interpretation of the underlying causes of G x E.

In AMMI model analysis, the main effects of genotype and environment were first estimated through ANOVA using the linear equation (Sabaghnia *et al*., 2008):

$$Y_{ijk} = \mu + g_i + e_j + \theta_{ij} + \varepsilon_{ijk}$$

Where,

g – genotypes

e - environments

Yijk - yield of genotype i in environment j for replication k

μ – grand mean for yield

g_i – deviation between the mean and grand mean for genotype i

e_j – deviation between the mean and grand mean for environment j

θ_{ij} - residuals

ε_{ijk} – Error term

The residuals were then divided into the interaction effects of genotype and environment through principal component analysis (PCA) using the equation:

$\theta ij = \sum^{N}_{n=1} \lambda_n \gamma_{in} \delta_{jn} + \rho_{ij}$

Where,

N - number of interaction principal components (IPC) used in the model

λ_n - is the singular value of the N axis in the PCA

γin - IPC scores for axis N of genotype i

δjn - IPC scores for axis N of environment j

ρij - residuals

Table 7. Analysis of variance for stability for AMMI model

Source of variation	**Degrees of freedom**	**Sum of Squares**	**Mean Sum of Squares**	**F_{value}**
Treatment	(ge-1)			
Genotype	(g-1)			
Environment	(e-1)			
Interactions	(g-1)(e-1)			
IPCA 1				
IPCA 2				
Residual				
Replication	(r-1)			
Error	(r-1)(ge-1)			
Total	(ger-1)			

3.2.4.3 GGE Biplot (Genotype main effect plus Genotype-by-Environment Biplot)

The GGE biplot can be used for identifying better performing genotypes across environments, delineating the best genotypes for specific environments and for evaluating the yield and stability of genotypes (Yan and Tinker, 2006).

The GGE biplot methodology contains a set of biplot interpretation methods that can provide a better visual understanding of genotype and test-environment evaluation (Yan *et al*., 2000).To overcome the drawbacks of conventional methodologies in providing limited information regarding important patterns of the Genotype x

Environment interaction, methods involving GGE biplot are being used. In the first stage of analysis in a GGE Biplot, the effect of Genotype (G) +Genotype × Environment (Gx E) is analyzed following the formation of biplot graphs in the second stage (Sousa *et al*., 2018).

The GGE-Biplot model considers the terms G and G×E together in two multiplicative terms as in the following equation (Yan *et al*., 2000):

$$Y_{ij} - \mu - \beta_j = g_{1i}\, e_{1j} + g_{2ji}\, e_{2j} + \varepsilon_{ii}$$

Where,

Y_{ij} - expected yield of the genotype i in the environment j

μ - general mean of the observation

β_j - principal effect of the environment j

g_{1j} - principal scores of the genotype i

e_{1j} - principal scores of the environment j

g_{2j} - secondary scores for the genotype i

e_{2j} - secondary scores for the environment j

ε_{ij} - not explained residue of both effects

In the GGE-Biplot, main effect of environment is not considered while only the main effect of genotype and G×E are important and must be considered together for the selection of genotypes. Construction of GGE-Biplot is based on the first two major components of a principal component analysis (PCA) using Site Regression (SREG) model. Proportion of yield is considered to be contributed by a particular character of a genotype when the first component is highly correlated with the main effect of the genotype. The second component represents the part of the yield due to the G×E (Yan, 2011).

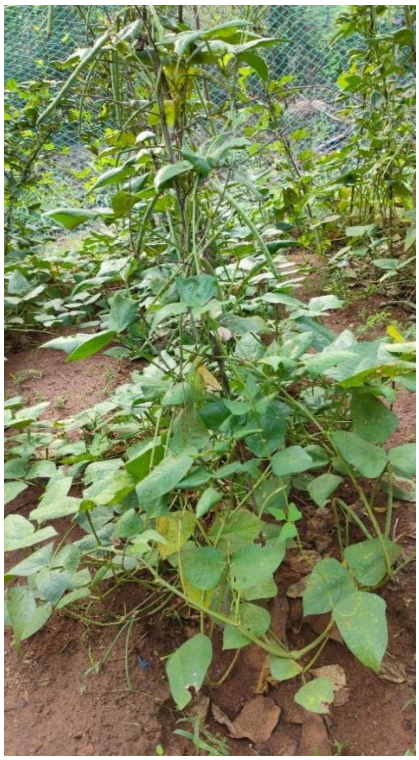
Plate 1. Field view of the experiment

a) Location 1: RARS, Pattambi

b) Location 2: COA, Vellanikkara

c) Location 3: RRS, Vyttila

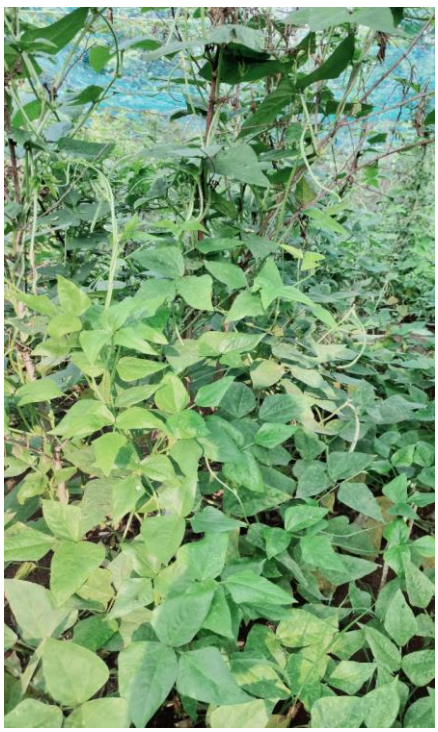
Plate 2. Plants at 60 days after sowing



Genotype L_1

Genotype L_2

Genotype L_3



Genotype L_4

Plate 2. Plants at 60 days after sowing

Genotype L_5

Anaswara

Kanakamony

Plate 3. Pods after harvest

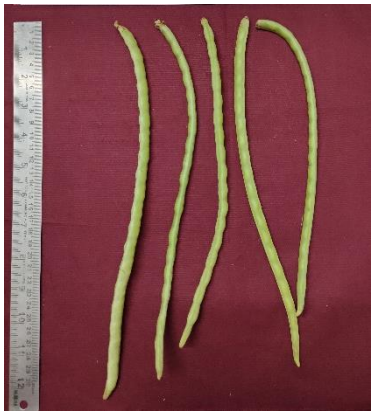
Genotype L_1

Genotype L_2

Genotype L_3

Genotype L_4

Genotype L_5



Anaswara

Kanakamony

Plate 4. Seeds after harvest

Genotype L_1

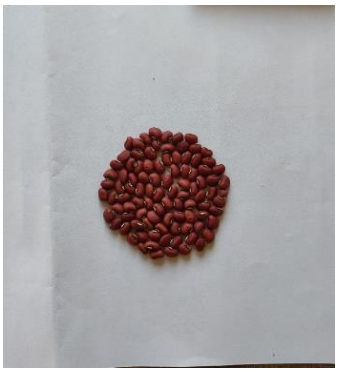
Genotype L_2

Genotype L_3

Genotype L_4

Genotype L_5

Anaswara



Kanakamony

Results

4. RESULTS

Five cultures of cowpea in the stabilised F_7 generation were evaluated for finding out Genotype x Environment interactions along with two check varieties. The results of the study are presented in this chapter.

4.1 Assessment of variability under different environments

4.1.1 Variability under environment 1

The mean values of different quantitative traits and their genetic parameters under environment 1 are presented in Table 8 and Table 9, respectively. The results showed a wide variability among the cultures for all the characters studied.

4.1.1.1 Plant height (cm)

The plant height for the cultures ranged from 169.38 cm in L_4 to 210.87 cm in C_2. PCV and GCV values were 11.92 and 5.43, respectively. The genetic advancement was 9.57 and the genetic advance calculated as per cent of mean was 5.09. The broad sense heritability was 0.21.

4.1.1.2 Number of branches

The number of branches for the cultures varied between 6.23 in L_4 and 8.44 in L_2. PCV and GCV values were 14.01 and 8.87, respectively. The genetic advancement was 0.88 and the genetic advance calculated as per cent of mean was 11.57. The broad sense heritability was 0.40.

4.1.1.3 Days to first flowering

The days to first flowering for the cultures varied between 38.33 in C_2 and 42.33 in L_3. PCV and GCV values were 3.67 and 3.07, respectively. The genetic advancement was 2.14 and the genetic advance calculated as per cent of mean was 5.27. The broad sense heritability was 0.69.

4.1.1.4 Days to first harvest

The days to first harvest for the cultures varied between 52 in C_2 and 63.29 in L_5. PCV and GCV values were 6.34 and 5.89, respectively. The genetic advancement

was 6.50 and the genetic advance calculated as per cent of mean was 11.29. The broad sense heritability was 0.86.

4.1.1.5 Days to last harvest

The days to last harvest for the cultures varied between 83.03 in C_1 and 92.07 in L_1. PCV and GCV values were 4.22 and 3.69, respectively. The genetic advancement was 5.82 and the genetic advance calculated as per cent of mean was 6.68. The broad sense heritability was 0.77.

4.1.1.6 Number of pods per plant

The number of pods per plant for the cultures varied between 32.56 in C_1 and 56.01 in C_2. PCV and GCV values were 16.99 and 16.57, respectively. The genetic advancement was 14.90 and the genetic advance calculated as per cent of mean was 33.27. The broad sense heritability was 0.95.

4.1.1.7 Length of pod (cm)

The length of pod for the cultures varied between 16.31 cm in C_2 and 30.61 cm in L_2. PCV and GCV values were 18.41 and 18.40, respectively. The genetic advancement was 10.33 and the genetic advance calculated as per cent of mean was 37.89. The broad sense heritability was 0.99.

4.1.1.8 Pod weight (g)

The pod weight for the cultures varied between 2.88 g in C_2 and 3.94 g in L_2. PCV and GCV values were 10.04 and 9.96, respectively. The genetic advancement was 0.73 and the genetic advance calculated as per cent of mean was 20.36. The broad sense heritability was 0.98.

Table 8. Mean performance of cowpea genotypes under environment 1

Genotypes	Plant height (cm)	Number of branches	Days to first flowering	Days to first harvest	Days to last harvest	Number of pods per plant	Length of pod (cm)	Pod weight (g)	Number of seeds per pod	Test weight (g)	Grain yield per plant (g)	Protein content (%)
L_1	179.56^{ab}	8.36^{a}	42.00^{a}	57.00^{c}	92.07^{a}	48.87^{b}	30.00^{b}	3.73^{b}	19.01^{a}	19.55^{ab}	181.45^{a}	23.55^{c}
L_2	185.56^{ab}	8.44^{a}	40.29^{b}	57.68^{bc}	90.03^{ab}	46.84^{b}	30.61^{a}	3.94^{a}	19.05^{a}	18.68^{b}	166.26^{b}	24.26^{b}
L_3	205.83^{a}	7.37^{ab}	42.33^{a}	60.00^{b}	84.01^{cd}	47.65^{b}	28.90^{c}	3.73^{b}	18.97^{a}	16.15^{c}	146.34^{c}	20.38^{g}
L_4	169.39^{b}	6.23^{b}	40.33^{b}	56.01^{c}	85.03^{cd}	40.73^{c}	30.04^{b}	3.69^{b}	16.97^{b}	19.85^{a}	137.84^{cd}	24.62^{a}
L_5	187.80^{ab}	7.43^{ab}	40.04^{b}	63.29^{a}	89.35^{ab}	40.89^{c}	28.49^{d}	3.71^{b}	16.97^{b}	19.36^{ab}	134.53^{d}	22.03^{e}
C_1	175.60^{ab}	7.04^{ab}	40.33^{b}	57.01^{c}	83.03^{d}	32.56^{d}	26.56^{e}	3.31^{c}	15.09^{c}	19.31^{ab}	94.93^{e}	20.70^{f}
C_2	210.87^{a}	8.32^{a}	38.33^{c}	52.00^{d}	87.00^{bc}	56.01^{a}	16.31^{f}	2.88^{d}	14.96^{c}	10.91^{d}	91.61^{e}	22.37^{d}

Table 9. Genetic parameters of cowpea genotypes under environment 1

Genotypes	Plant height (cm)	Number of branches	Days to first flowering	Days to first harvest	Days to last harvest	Number of pods per plant	Length of pod (cm)	Pod weight (g)	Number of seeds per pod	Test weight (g)	Grain yield per plant (g)	Protein content (%)
Phenotypic coefficient of variation	11.92	14.01	3.67	6.34	4.22	16.99	18.41	10.04	10.39	18.46	24.94	7.38
Genotypic coefficient of variation	5.43	8.87	3.07	5.89	3.69	16.57	18.40	9.96	10.37	18.24	24.49	7.38
Genetic advancement at 5%	9.57	0.88	2.14	6.50	5.82	14.90	10.33	0.73	3.69	6.57	67.42	3.43
Genetic advance as percentage of mean at 5%	5.09	11.57	5.27	11.29	6.68	33.27	37.89	20.36	21.35	37.12	49.52	15.21
Broad sense heritability	0.21	0.40	0.69	0.86	0.77	0.95	0.99	0.98	0.99	0.98	0.96	1.00

4.1.1.9 Number of seeds per pod

The number of seeds per pod for the cultures varied between 14.96 in C_2 and 19.05 in L_2. PCV and GCV values were 10.39 and 10.37, respectively. The genetic advancement was 3.69 and the genetic advance calculated as per cent of mean was 21.35. The broad sense heritability was 0.99.

4.1.1.10 Test weight (g)

The test weight for the cultures varied between 10.91 g in C_2 and 19.85 g in L_4. PCV and GCV values were 18.46 and 18.24, respectively. The genetic advancement was 6.57 and the genetic advance calculated as per cent of mean was 37.12. The broad sense heritability was 0.98.

4.1.1.11 Grain yield per plant (g)

The grain yield per plant varied between 91.61 g in C_2 and 181.45 g in L_1. Both the PCV and GCV values were 24.94. The genetic advancement was 67.42 and the genetic advance calculated as per cent of mean was 49.52. The broad sense heritability was 0.96.

4.1.1.12 Protein content (%)

The protein content varied between 20.38 per cent in L_3 and 24.62 per cent in L_4. Both the PCV and GCV values were 7.38. The genetic advancement was 3.43 and the genetic advance calculated as per cent of mean was 15.21. The broad sense heritability was 1.00.

4.1.2 Variability under environment 2

The mean values of different quantitative traits and their genetic parameters observed under environment 2 are presented in Table 10 and Table 11. The results showed a wide variability among the cultures for all the characters studied, except for plant height.

4.1.2.1 Plant height (cm)

The plant height for the cultures ranged from 180.96 cm in L_3 to 238.96 cm in L_5. However, no variability was observed for the trait.

4.1.2.2 Number of branches

The number of branches for the cultures varied between 3.31 in C_2 and 4.35 in L_3. PCV and GCV values were 12.28 and 7.39, respectively. The genetic advancement was 0.35 and the genetic advance calculated as per cent of mean was 9.17. The broad sense heritability was 0.36.

4.1.2.3 Days to first flowering

The days to first flowering for the cultures varied between 38.33 in C_2 and 41.24 in L_3. PCV and GCV values were 2.90 and 2.27, respectively. The genetic advancement was 1.45 and the genetic advance calculated as per cent of mean was 3.65. The broad sense heritability was 0.61.

4.1.2.4 Days to first harvest

The days to first harvest for the cultures varied between 51 in C_2 and 59.85 in L_5. PCV and GCV values were 5.82 and 5.63, respectively. The genetic advancement was 6.40 and the genetic advance calculated as per cent of mean was 11.21. The broad sense heritability was 0.94.

4.1.2.5 Days to last harvest

The days to last harvest for the cultures varied between 82.13 in L_3 and 89.04 in L_1. PCV and GCV values were 3.51 and 2.88, respectively. The genetic advancement was 4.16 and the genetic advance calculated as per cent of mean was 4.85. The broad sense heritability was 0.67.

4.1.2.6 Number of pods per plant

The number of pods per plant for the cultures varied between 30.12 in C_1 and 58.01 in C_2. PCV and GCV values were 20.24 and 19.89, respectively. The genetic advancement was 17.01 and the genetic advance calculated as per cent of mean was 40.28. The broad sense heritability was 0.97.

Table 10. Mean performance of cowpea genotypes under environment 2

Genotypes	Plant height (cm)	Number of branches	Days to first flowering	Days to first harvest	Days to last harvest	Number of pods per plant	Length of pod (cm)	Pod weight (g)	Number of seeds per pod	Test weight (g)	Grain yield per plant (g)	Protein content (%)
L_1	229.52^{a}	4.04^{ab}	40.37^{ab}	59.40^{a}	89.04^{a}	43.28^{b}	27.91^{b}	3.18^{e}	18.00^{b}	17.88^{b}	139.25^{a}	23.01^{c}
L_2	211.88^{a}	3.57^{bc}	39.25^{bc}	58.65^{ab}	87.05^{ab}	44.11^{b}	27.77^{c}	3.84^{b}	18.95^{a}	15.97^{c}	134.02^{a}	25.32^{a}
L_3	180.96^{a}	4.35^{a}	41.24^{a}	58.95^{a}	82.13^{c}	43.01^{b}	26.53^{d}	3.11^{f}	18.99^{a}	14.96^{d}	122.24^{b}	20.64^{g}
L_4	197.41^{a}	3.73^{abc}	40.33^{ab}	57.35^{b}	87.99^{a}	38.72^{c}	28.32^{a}	3.77^{c}	17.01^{c}	14.16^{e}	93.19^{c}	24.70^{b}
L_5	238.96^{a}	3.91^{abc}	39.01^{c}	59.85^{a}	84.61^{bc}	38.35^{c}	27.79^{c}	3.98^{a}	16.05^{d}	15.08^{d}	92.50^{c}	21.42^{e}
C_1	195.61^{a}	3.52^{bc}	39.33^{bc}	54.39^{c}	82.53^{c}	30.12^{d}	24.00^{e}	3.29^{d}	15.01^{e}	19.82^{a}	89.55^{c}	21.26^{f}
C_2	212.65^{a}	3.31^{c}	38.33^{c}	51.00^{d}	86.19^{ab}	58.01^{a}	17.32^{f}	2.41^{g}	14.03^{f}	10.74^{f}	87.49^{c}	22.24^{d}

Table 11. Genetic parameters of cowpea genotypes under environment 2

Genotypes	Plant height (cm)	Number of branches	Days to first flowering	Days to first harvest	Days to last harvest	Number of pods per plant	Length of pod (cm)	Pod weight (g)	Number of seeds per pod	Test weight (g)	Grain yield per plant (g)	Protein content (%)
Phenotypic coefficient of variation	19.31	12.28	2.90	5.82	3.51	20.24	15.44	16.17	11.43	18.57	21.17	7.88
Genotypic coefficient of variation	6.91	7.39	2.27	5.63	2.88	19.89	15.44	16.17	11.43	18.47	20.77	7.88
Genetic advancement at 5%	-10.67	0.35	1.45	6.40	4.16	17.01	8.16	1.12	3.97	5.87	45.45	3.68
Genetic advance as percentage of mean at 5%	-5.09	9.17	3.65	11.21	4.85	40.28	31.81	33.30	23.54	37.85	41.96	16.23
Broad sense heritability	0.13	0.36	0.61	0.94	0.67	0.97	0.99	0.99	0.99	0.98	0.96	1.00

4.1.2.7 Length of pod (cm)

The length of pod for the cultures varied between 17.32 cm in C_2 and 28.32 cm in L_4. Both the PCV and GCV values were 15.44. The genetic advancement was 8.16 and the genetic advance calculated as per cent of mean was 31.81. The broad sense heritability was 0.99.

4.1.2.8 Pod weight (g)

The pod weight for the cultures varied between 2.41 g in C_2 and 3.98 g in L_5. Both the PCV and GCV values were 16.17. The genetic advancement was 1.12 and the genetic advance calculated as per cent of mean was 33.30. The broad sense heritability was 0.99.

4.1.2.9 Number of seeds per pod

The number of seeds per pod for the cultures varied between 14.03 in C_2 and 18.99 in L_3. Both the PCV and GCV values were 11.43. The genetic advancement was 3.97 and the genetic advance calculated as per cent of mean was 23.54. The broad sense heritability was 0.99.

4.1.2.10 Test weight (g)

The test weight for the cultures varied between 10.74 g in C_2 and 19.82 g in C_1. PCV and GCV values were 18.57 and 18.47, respectively. The genetic advancement was 5.87 and the genetic advance calculated as per cent of mean was 37.85. The broad sense heritability was 0.98.

4.1.2.11 Grain yield per plant (g)

The grain yield per plant varied between 87.49 g in C_2 and 139.25 g in L_1. PCV and GCV values were 21.17 and 20.77, respectively. The genetic advancement was 45.45 and the genetic advance calculated as per cent of mean was 41.96. The broad sense heritability was 0.96.

4.1.2.12 Protein content (%)

The protein content varied between 21.26 per cent in C_1 and 25.32 per cent in L_2. Both the PCV and GCV values were 7.88. The genetic advancement was 3.68 and

the genetic advance calculated as per cent of mean was 16.23. The broad sense heritability was 1.00.

4.1.3 Variability under environment 3

The mean values of different quantitative traits and their genetic parameters observed under environment 3 are presented in Table 12 and Table 13. The results showed a wide variability among the cultures for most of the characters under study. There existed no variability for plant height and number of branches.

4.1.3.1 Plant height (cm)

The plant height for the cultures ranged from 81.07 cm in L_2 to 113.88 in C_1. However, no variability was observed for the trait.

4.1.3.2 Number of branches

The number of branches for the cultures varied between 3.39 in L_5 and 4.92 in L_2. However, there exist no variability for the trait.

4.1.3.3 Days to first flowering

The days to first flowering for the cultures varied between 35.01 in L_3 and 39.32 in C_2. PCV and GCV values were 5.23 and 4.20, respectively. The genetic advancement was 2.62 and the genetic advance calculated as per cent of mean was 6.96. The broad sense heritability was 0.65.

4.1.3.4 Days to first harvest

The days to first harvest for the cultures varied between 51.03 in C_2 and 61.00 in L_5. PCV and GCV values were 6.85 and 5.25, respectively. The genetic advancement was 4.69 and the genetic advance calculated as per cent of mean was 8.29. The broad sense heritability was 0.59.

Table 12. Mean performance of cowpea genotypes under environment 3

Genotypes	Plant height (cm)	Number of branches	Days to first flowering	Days to first harvest	Days to last harvest	Number of pods per plant	Length of pod (cm)	Pod weight (g)	Number of seeds per pod	Test weight (g)	Grain yield per plant (g)	Protein content (%)
L_1	92.32^{a}	4.03^{a}	35.67^{bc}	56.36^{bc}	84.00^{a}	38.09^{bc}	26.21^{d}	3.59^{d}	16.03^{b}	16.53^{b}	100.79^{a}	26.47^{a}
L_2	81.07^{a}	4.25^{a}	37.71^{ab}	60.04^{ab}	81.04^{abc}	38.27^{bc}	28.24^{a}	3.88^{b}	16.99^{a}	15.27^{c}	99.36^{a}	24.74^{b}
L_3	107.00^{a}	4.37^{a}	35.01^{c}	55.04^{cd}	71.01^{d}	40.11^{b}	27.17^{b}	3.44^{e}	16.08^{b}	14.95^{c}	95.90^{ab}	20.96^{c}
L_4	109.85^{a}	3.83^{a}	39.08^{a}	57.33^{abc}	80.03^{bc}	35.45^{d}	22.74^{e}	3.64^{c}	16.01^{b}	15.03^{c}	85.29^{c}	20.10^{d}
L_5	101.35^{a}	4.05^{a}	37.44^{ab}	61.00^{a}	83.04^{ab}	37.01^{cd}	26.50^{c}	3.91^{a}	15.05^{c}	16.13^{b}	89.56^{bc}	15.31^{g}
C_1	113.88^{a}	4.55^{a}	39.05^{a}	56.03^{bc}	78.12^{c}	29.39^{e}	28.39^{a}	3.27^{f}	16.08^{b}	18.97^{a}	89.44^{bc}	18.03^{f}
C_2	104.71^{a}	3.92^{a}	39.32^{a}	51.03^{d}	84.01^{a}	51.03^{a}	15.03^{f}	2.75^{g}	15.05^{c}	9.72^{d}	74.42^{d}	18.43^{e}

Table 13. Genetic parameters of cowpea genotypes under environment 3

Genotypes	Plant height (cm)	Number of branches	Days to first flowering	Days to first harvest	Days to last harvest	Number of pods per plant	Length of pod (cm)	Pod weight (g)	Number of seeds per pod	Test weight (g)	Grain yield per plant (g)	Protein content (%)
Phenotypic coefficient of variation	25.09	13.45	5.23	6.85	6.09	17.15	19.04	11.47	4.24	18.41	10.65	18.95
Genotypic coefficient of variation	11.35	5.69	4.20	5.25	5.54	16.80	19.03	11.47	4.22	18.34	9.78	18.95
Genetic advancement at 5%	-10.73	-0.20	2.62	4.69	8.32	13.05	9.76	0.83	1.38	5.73	16.78	8.03
Genetic advance as percentage of mean at 5%	-10.58	-4.95	6.96	8.29	10.37	33.91	39.20	23.62	8.65	37.63	18.50	39.04
Broad sense heritability	0.20	0.18	0.65	0.59	0.83	0.96	0.99	1.00	0.99	0.99	0.84	1.00

4.1.3.5 Days to last harvest

The days to last harvest for the cultures varied between 71.01 in L_3 and 84.01 in C_2. PCV and GCV values were 6.09 and 5.54, respectively. The genetic advancement was 8.32 and the genetic advance calculated as per cent of mean was 10.37. The broad sense heritability was 0.83.

4.1.3.6 Number of pods per plant

The number of pods per plant for the cultures varied between 29.39 in C_1 and 51.03 in C_2. PCV and GCV values were 17.15 and 16.80, respectively. The genetic advancement was 13.05 and the genetic advance calculated as per cent of mean was 33.91. The broad sense heritability was 0.96.

4.1.3.7 Length of pod (cm)

The length of pod for the cultures varied between 15.03 cm in C_2 and 28.39 cm in C_1. PCV and GCV values were 19.04 and 19.03, respectively. The genetic advancement was 9.76 and the genetic advance calculated as per cent of mean was 39.20. The broad sense heritability was 0.99.

4.1.3.8 Pod weight (g)

The pod weight for the cultures varied between 2.75 g in C_2 and 3.91 g in L_5. Both the PCV and GCV values were 11.47. The genetic advancement was 0.83 and the genetic advance calculated as per cent of mean was 23.62. The broad sense heritability was 1.00.

4.1.3.9 Number of seeds per pod

The number of seeds per pod for the cultures varied between 15.05 in L_5 and C_2 and 16.99 in L_2. The PCV and GCV values were 4.24 and 4.22, respectively. The genetic advancement was 1.38 and the genetic advance calculated as per cent of mean was 8.65. The broad sense heritability was 0.99.

4.1.3.10 Test weight (g)

The test weight for the cultures varied between 9.72 g in C_2 and 18.97 g in C_1. PCV and GCV values were 18.41 and 18.34, respectively. The genetic advancement

was 5.73 and the genetic advance calculated as per cent of mean was 37.63. The broad sense heritability was 0.99.

4.1.3.11 Grain yield per plant (g)

The grain yield per plant varied between 74.42 g in C_2 and 100.79 g in L_1. PCV and GCV values were 10.65 and 9.78, respectively. The genetic advancement was 16.78 and the genetic advance calculated as per cent of mean was 18.50. The broad sense heritability was 0.84.

4.1.3.12 Protein content (%)

The protein content varied between 15.31 per cent in L_5 and 26.47 per cent in L_1. Both the PCV and GCV values were 18.95. The genetic advancement was 8.03 and the genetic advance calculated as per cent of mean was 39.04. The broad sense heritability was 1.00.

Bartlett's test was performed to examine the homogeneity of error variances for doing pooled ANOVA. The test was significant for the characters days to first flowering, days to last harvest, number of pods per plant, number of seeds per pod, grain yield per plant and protein content and hence pooled ANOVA was performed for the above characters.

4.2 Pooled analysis of variance over three environments

Pooled analysis of variance was done for the observations recorded over three environments for the six characters days to first flowering, days to last harvest, number of pods per plant, number of seeds per pod, grain yield per plant (g) and protein content (%). The results are presented in Table 14. There was a significant difference between the environments for all the six characters studied. Significant differences were observed among the genotypes for all the six characters studied, except for days to first flowering. The genotype x environment (G x E) interaction was found significant for the six characters considered and hence, the analysis using stability models of Eberhart and Russel, Additive Main effects and Multiplicative Interactive effects (AMMI) and Genotype and Genotype by Environment (GGE) – Biplot were attempted. Further statistical analysis was performed by partitioning genotype- environment mean squares

into its components: variance due to genotype x environment (linear) and pooled deviation (non-linear).

4.3 Analysis of stability (Eberhart and Russell model)

To understand the suitability of a variety for general cultivation over wide range of environments, experiments were conducted over three different locations and stability was analysed over pooled data using linear regression model.

4.3.1 Analysis of variance for stability over three environments

The results of the analysis of variance for stability are presented in Table 15. Significant differences were observed among the genotypes for the characters days to last harvest, number of pods per plant, number of seeds per pod, grain yield per plant and protein content. Environment (linear) was not significant for the traits considered. G x E interaction (linear) was significant for the characters days to first flowering, number of seeds per pod, grain yield per plant and protein content.

4.3.2 Stability parameters of cowpea genotypes (Eberhart and Russell model)

The character wise estimate of stability parameters are presented in Table 16a and Table 16b.

4.3.2.1 Days to first flowering

The mean values for days to first flowering ranged between 38.66 in C_2 and 39.91 in L_4. None of the genotypes had significant bi and S^2di values.

4.3.2.2 Days to last harvest

The mean values for days to last harvest ranged between 79.05 in L_3 and 88.37 in L_1. Significant bi value was shown by genotypes L_3 and C_2. Genotypes L_3, C_1 and C_2 showed significant S^2di value.

Table 14. Pooled ANOVA over three environments

Source of variation	Degrees of freedom	Days to first flowering	Days to last harvest	Number of pods per plant	Number of seeds per pod	Grain yield per plant (g)	Protein content (%)
Total	20	3.29	21.43	58.01	2.58	884.1	7.31
Environment (E)	2	47.30*	286.59*	211.9*	10.65*	11029.7*	28.89*
Genotypes (G)	6	0.59	30.23*	163.56*	5.78*	1310.4*	13.53*
G x E	12	7.67*	14.02*	9.38*	2.41*	616.6*	11.47*
Pooled error	36	0.85	3.41	2.36	0.004	25.4	0.01

Table 15. ANOVA for stability for different traits over three environments

Source of variation	Degrees of freedom	Days to first flowering	Days to last harvest	Number of pods per plant	Number of seeds per pod	Grain yield per plant (g)	Protein content (%)
Total	20	3.29	21.43	58.01	2.58	884.1	7.31
Genotypes (G)	6	0.59	30.23*	163.56*	5.78*	1310.4*	13.53*
Environment-linear (E)	1	31.54	191.07	141.27	7.10	7353.2	19.26
G x E linear	6	29.58*	6.17	3.73	1.35*	347.2*	7.44*
Pooled deviation- non linear	7	0.16	2.72	2.16	0.22	54.7	0.18
Pooled error	42	0.24	0.97	0.67	0.001	7.3	0.01
Non linear: linear		0.0054:1	0.44:1	0.58:1	0.17:1	0.15:1	0.024:1

Table 16a. Estimates of stability parameter for different traits under three environments (Eberhart and Russel model)

Genotypes	Days to first flowering			Days to last harvest			Number of pods per plant		
	Mean	bi	S^2di	Mean	Bi	S^2di	Mean	Bi	S^2di
L_1	39.35	2.19	-0.26	88.37	1.09	-0.22	43.41	1.68 *	0.18 *
L_2	39.08	0.86	-0.22	86.04	1.23	-0.56	43.07	1.37	-0.42
L_3	39.53	2.60	0.32	79.05	1.89 *	-0.52 *	43.59	1.16	0.85
L_4	39.91	0.46	-0.20	84.35	0.90	8.89	38.3	0.84	-0.78
L_5	38.83	0.86	-0.23	85.67	0.74	5.57	38.75	0.59	-0.17
C_1	39.57	0.38	-0.02	81.23	0.72	-0.92 *	30.69	0.48	0.08 *
C_2	38.66	-0.36	-0.23	85.73	0.42 *	-1.12 *	55.02	0.87 *	9.89

Table 16b. Estimates of stability parameter for different traits under three environments (Eberhart and Russel model)

Genotypes	Number of seeds per pod			Grain yield per plant (g)			Protein content (%)		
	Mean	bi	S^2di	Mean	bi	S^2di	Mean	Bi	S^2di
L_1	17.68	2.12	0.003	140.49	1.75	25.09	24.34	-1.58	0.07
L_2	18.33	1.58	0.17	133.21	1.44	41.15	24.77	0.04	0.55
L_3	18.01	2.24	0.51	121.49	1.09	21.56	20.66	-0.22	0.04
L_4	16.66	0.75	0.07	105.44	1.19 *	93.72 *	23.14	2.24	0.01
L_5	16.02	1.32 *	0.68	105.53	1.04 *	129.65 *	19.59	3.14 *	0.42
C_1	15.39	-0.78	0.09 *	91.31	0.13 *	-5.79 *	19.99	1.46 *	0.09 *
C_2	14.68	-0.24 *	0.59 *	84.51	0.36 *	18.37	21.01	1.90 *	0.05 *

*significant at 0.05%

4.3.2.3 Number of pods per plant

The mean values for number of pods per plant ranged between 30.69 in C_1 and 55.02 in C_2. L_1 and C_2 had significant bi value while L_1 and C_1 had significant S^2di value.

4.3.2.4 Number of seeds per pod

The mean values for number of seeds per pod ranged between 14.68 in C_2 and 18.33 in L_2. Significant bi value was shown by L_5 and C_2 and S^2di values were found significant for genotypes C_1 and C_2.

4.3.2.5 Grain yield per plant (g)

The mean values for grain yield per plant ranged between 84.51 in C_2 and 140.49 in L_1. L_4, L_5, C_1 and C_2 had significant bi value while L_4, L_5 and C_1 had significant S^2di value.

4.3.2.6 Protein content (%)

The mean values for protein content ranged between 19.59 in L_5 and 24.77 in L_2. L_5, C_1 and C_2 had significant bi value. Genotype C_1 and C_2 had significant S^2di value.

4.4 Analysis of stability (AMMI model)

4.4.1 Analysis of variance for AMMI analysis

The results of the analysis of variance for AMMI is presented in Table 17. Genotypic effects were significant for the traits days to last harvest, number of pods per plant, number of seeds per pod, grain yield per plant and protein content. Environmental effects were significant for the traits namely, days to first flowering, days to last harvest, number of pods per plant, number of seeds per pod, grain yield per plant and protein content. Genotype x environment interaction was partitioned into IPCA 1 and IPCA 2 and was found significant for the traits days to first flowering, days to last harvest, number of pods per plant, number of seeds per pod, grain yield per plant and protein content.

4.4.2 Estimates of stability parameters (AMMI model)

Genotype x environment interactions were partitioned into IPCA 1 and IPCA 2. The results recorded for various stability parameters under AMMI model for the traits days to first flowering, days to last harvest, number of pods per plant, number of seeds per pod, grain yield per plant and protein content are presented in Table 18a and Table 18b.

4.4.2.1 Days to first flowering

Mean values for days to first flowering for the genotypes ranged between 38.66 in C_2 and 39.91 in L_4 (Table 18a). Environmental means for days to first flowering varied from 37.61 (E_3) to 40.52 (E_1). Positive values for IPCA 1 were observed for genotypes L_1 and L_3 and environments E_1 and E_2. IPCA 2 values were positive in genotypes L_3, L_4 and C_2 and environment E_2.

4.4.2.2 Days to last harvest

Mean values for days to last harvest for the genotypes ranged from 79.05 in L_3 and 88.37 in L_1 (Table 18a). Environmental means for days to last harvest varied from 80.18 in E_3 and 87.21 in E_1. Positive values for IPCA 1 were observed for the genotypes L_1, L_2, L_3 and L_4 and environments E_1 and E_2. IPCA 2 values were positive for the genotypes L_1, L_2, L_3 and L_5 and the environments E_1 and E_3.

4.4.2.3 Number of pods per plant

Mean values for number of pods per plant varied from 30.69 in C_1 to 55.02 in C_2 (Table 18a). Environmental mean for number of pods per plant ranged from 38.48 in E_3 to 44.79 in E_1. Positive values for IPCA 1 was observed for the genotypes L_1, L_2 and L_3 and for the environment E_1. IPCA 2 values were positive for the genotypes L_2 and C_2 and for the environment E_2.

4.4.2.4 Number of seeds per pod

Mean values for number of seeds per pod for the genotypes ranged between 14.68 in C_2 and 18.33 in L_2 (Table 18b). The environmental mean ranged from 15.89 in E_3 and 17.29 in E_1. Positive values of IPCA 1 were obtained for L_1, L_2, L_3 and L_5 and

for the environments E_1 and E_2. IPCA 2 values were positive for the genotypes L_1, L_5 and C_2 and for the environments E_1 and E_2.

4.4.2.5 Grain yield per plant

Mean values for grain yield per plant for the genotypes ranged between 84.51 in C_2 and 140.50 in L_1 (Table 18b). The environmental mean ranged from 90.68 in E_3 and 136.14 in E_1. Positive values for IPCA 1 were observed for the genotypes L_1, L_2, L_3, L_4 and L_5 and environment E_1. IPCA 2 values were positive for genotypes L_1, L_2, L_3, C_1 and C_2 and environment E_2.

4.4.2.6 Protein content

Mean values of protein content for the genotypes ranged between 19.59 in L_5 and 24.77 in L_2 (Table 18b). The environmental mean ranged from 20.58 in E_3 and 22.65 in E_2. Positive values for IPCA 1 were observed for the genotypes L_1, L_2 and L_3 and environment E_3. IPCA 2 values were positive for genotypes L_1, L_5 and C_2 and the environments E_1 and E_3.

Table 17. Analysis of variance for AMMI for different traits

Source of variation	Degrees of freedom	Days to first flowering	Days to last harvest	Number of pods per plant	Number of seeds per pod	Grain yield per plant (g)	Protein content (%)
Genotypes	6	1.77	90.69*	490.67*	17.35*	3931.2*	40.58*
Environments	2	47.30*	286.59 *	211.90*	10.65*	11029.7*	28.89*
G x E Interaction	12	7.68	14.02	9.38	2.41	616.6	11.47
IPCA1	7	12.9 *	16.23 *	9.69 *	26.68 *	896.35 *	134.50 *
IPCA2	5	0.32 *	10.93 *	8.95 *	2.19 *	224.92 *	3.08 *
Residuals	36	0.85	3.41	2.36	0.004	25.4	0.001

Table 18a. Mean and IPCA scores of different genotypes and environments

Genotypes	Days to first flowering			Days to last harvest			Number of pods per plant		
	Mean	IPCA1	IPCA2	Mean	IPCA1	IPCA2	Mean	IPCA1	IPCA2
L_1	39.35	1.07	-0.26	88.37	0.10	0.49	43.41	1.46	-0.22
L_2	39.08	-0.14	-0.23	86.04	0.41	0.48	43.07	0.70	0.45
L_3	39.53	1.49	0.34	79.05	1.91	0.09	43.59	0.44	-0.57
L_4	39.91	-0.46	0.51	84.35	0.07	-1.55	38.30	-0.34	-0.01
L_5	38.83	-0.13	-0.22	85.67	-0.76	1.08	38.75	-0.76	-0.56
C_1	39.57	-0.59	-0.37	81.23	-0.52	-0.36	30.69	-0.98	-0.68
C_2	38.66	-1.24	0.22	85.73	-1.21	-0.25	55.02	-0.53	1.58
E_1	40.52	1.17	-0.55	87.21	1.02	1.46	44.79	1.59	-0.70
E_2	39.69	0.72	0.65	85.65	1.005	-1.46	42.23	-0.12	1.60
E_3	37.61	-1.89	-0.09	80.18	-2.02	0.007	38.48	-1.48	-0.89

Table 18b. Mean and IPCA scores of different genotypes and environments

Genotypes	Number of seeds per pod			Grain yield per plant (g)			Protein content (%)		
	Mean	IPCA1	IPCA2	Mean	IPCA1	IPCA2	Mean	IPCA1	IPCA2
L_1	17.67	0.61	0.45	140.50	3.65	0.93	24.34	1.64	0.56
L_2	18.33	0.39	-0.24	133.21	2.19	1.37	24.77	0.63	-0.63
L_3	18.01	0.82	-0.32	121.49	0.47	1.19	20.66	0.78	-0.06
L_4	16.67	-0.09	-0.36	105.44	0.83	-2.39	23.14	-0.79	-0.04
L_5	16.03	0.13	0.38	105.53	0.05	-2.68	19.59	-1.39	0.39
C_1	15.39	-1.04	-0.29	91.31	-4.19	0.07	19.99	-0.29	-0.34
C_2	14.68	-0.82	0.37	84.51	-3.02	1.50	21.01	-0.58	0.12
E_1	17.29	0.69	0.66	136.14	4.94	-1.61	22.56	-1.11	0.70
E_2	16.86	0.72	-0.65	108.33	-0.33	3.59	22.65	-1.004	-0.72
E_3	15.89	-1.41	-0.009	90.68	-4.61	-1.98	20.58	2.11	0.02

4.5 Analysis of stability (GGE biplot Model)

Analysis of variance for the stability has identified that the genotypic effects are significant for the traits days to last harvest, number of pods per plant, number of seeds per pod, grain yield per plant and protein content (Table 17). Environmental effects were significant for the traits: days to first flowering, days to last harvest, number of pods per plant, number of seeds per pod, grain yield per plant and protein content. Genotype x environment interaction was partitioned into IPCA 1 and IPCA 2 and was found significant for all the traits considered. Performance and stability of genotypes were visualized graphically through GGE biplots.

4.5.1 Mean performance and stability of the genotypes across environments

For genotype evaluation 'mean versus stability' graph was drawn. Mean performance and stability of genotypes across environments were visualized graphically through GGE biplots. The environment centered genotype-metric biplots for days to first flowering, days to last harvest, number of pods per plant, number of seeds per pod, grain yield per plant and protein content are presented in Figure 1a to Figure 1f. The line with single arrowhead passing through the biplot origin and marker for average environment is referred to as the average-environment coordination (AEC) abscissa. It points towards the direction of higher mean value.

Genotypes were further ranked for each character in terms of 'ideal genotype' with regards to its high performance and high stability across environments, using Column Metric Preserving SVP and Tester-Centered G + GE with no scaling (Figure 2a to Figure 2f). An ideal genotype is the one that shows the highest mean performance and is highly stable across all the test environments. Based on the average-environment coordination (AEC) view comparison biplot, a desirable genotype is the one that is located closer to an ideal genotype, which is usually at the center of the concentric circles (Yan and Tinker, 2006).

4.5.1.1 Days to first flowering

The first two principal components (PC) explained 98.63 per cent of the total variation for days to first flowering. All the genotypes produced comparable length of

projection from the AEC abscissa (Figure 1a). All the genotypes were observed close to the ideal genotype while ranking of genotype (Figure 2a).

4.5.1.2 Days to last harvest

The first two principal components (PC) explained 93.39 per cent of total variation for days to last harvest. Genotype L_3 followed by C_2 had higher projection from the AEC abscissa while L_5 had the lowest (Figure 1b). While ranking genotypes, it was observed that genotypes L_1, L_2 and L_5 were very close to the ideal genotype with L_5 being the closest (Figure 2b).

4.5.1.3 Number of pods per plant

The first two principal components (PC) explained 99.65 per cent of the total variation for number of pods per plant. Genotypes L_1 and C_2 had higher projection from the AEC abscissa while it was low for L_2 and L_3 (Figure 1c). On ranking the genotypes, all the genotypes were closer towards the ideal genotype with L_2 and L_3 being the closest (Figure 2c).

4.5.1.4 Number of seeds per pod

The first two principal components (PC) explained 99.31 per cent of the total variation for number of seeds per pod. Genotypes L_5 and C_1 had higher projection from AEC abscissa whereas it was low for the genotype L_3 (Figure 1d). On ranking of genotypes L_1, L_2, L_3 and L_4 were found close to ideal genotype with L_3 being the closest (Figure 2d)

4.5.1.5 Grain yield per plant

The first two principal components (PC) explained 98.95 per cent of the total variation. Genotype L_4 had the highest projection while L_1 had the lowest from AEC abscissa for grain yield per plant (Figure 1e). Genotypes were ranked in terms of ideal genotype and genotypes L_1 and L_2 were located very close to the ideal genotype with L_1 being the closest (Figure 2e).

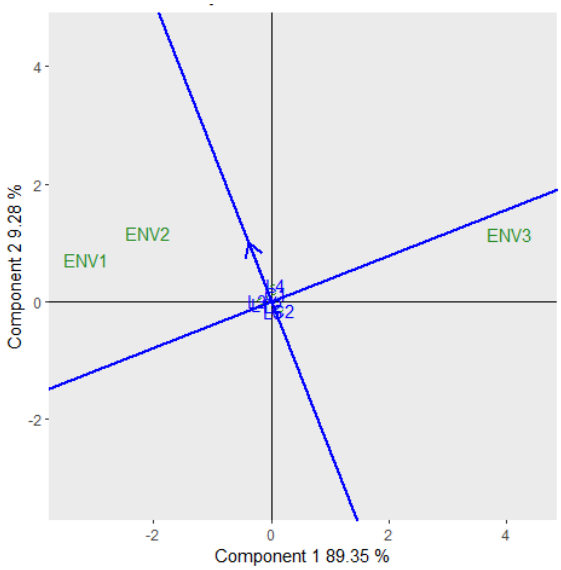


Figure 1a. Days to first flowering

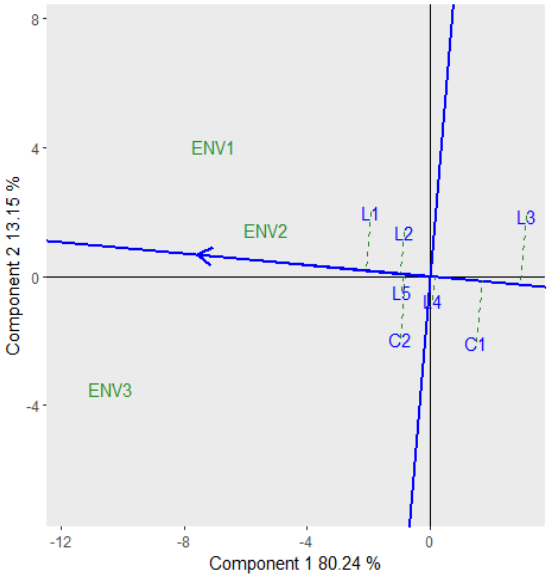


Figure 1b. Days to last harvest

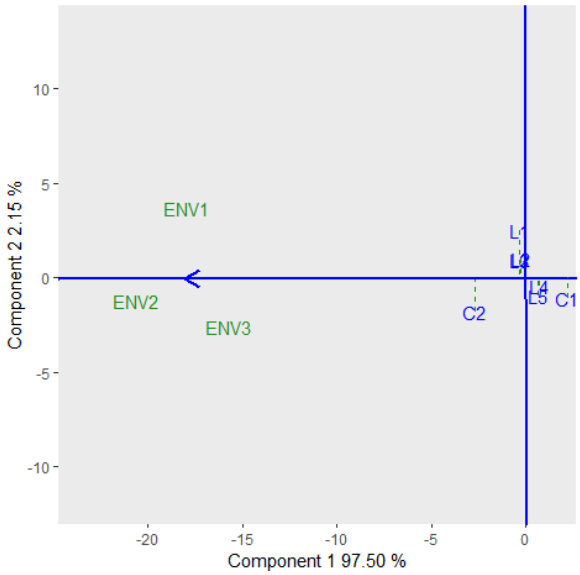


Figure 1c. Number of pods per plant

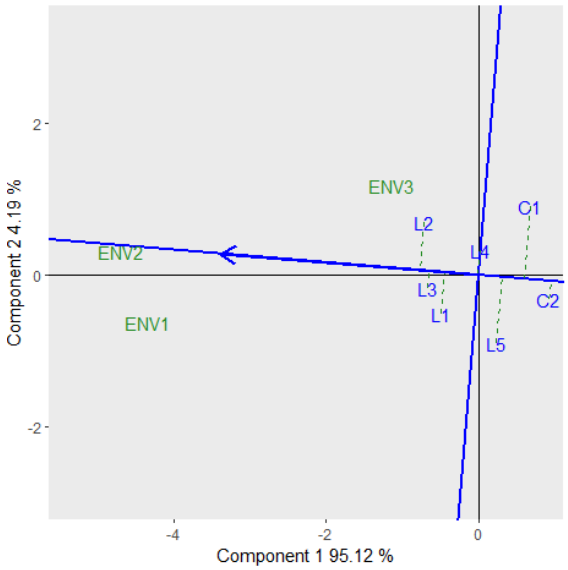


Figure 1d. Number of seeds per pod

Figure 1 (a to d). Mean versus stability graph of the genotypes

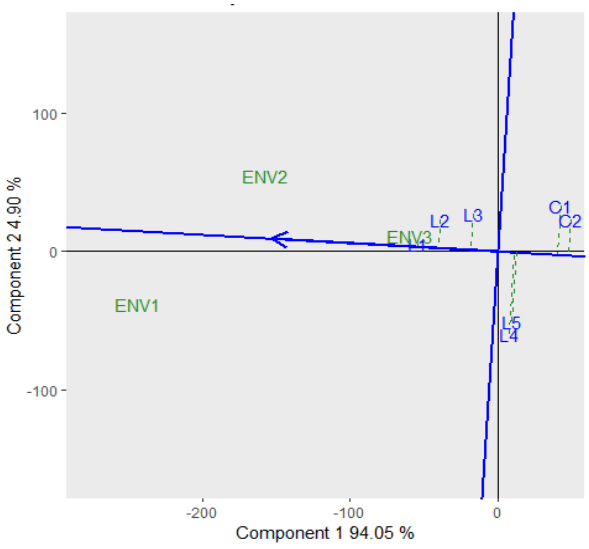


Figure 1e. Grain yield per plant

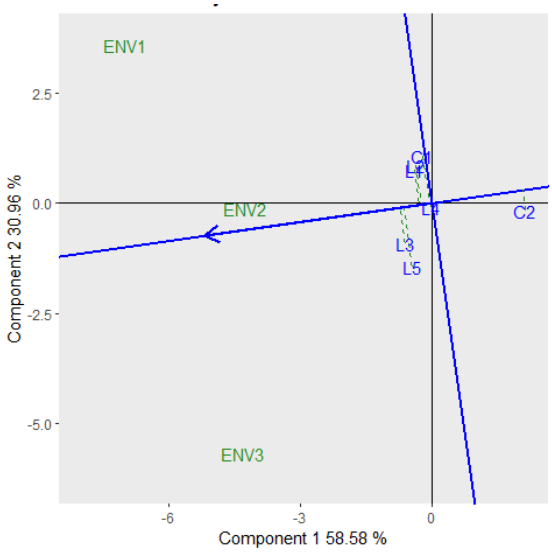


Figure 1f. Protein content

Figure 1 (e & f). Mean versus stability of the genotypes

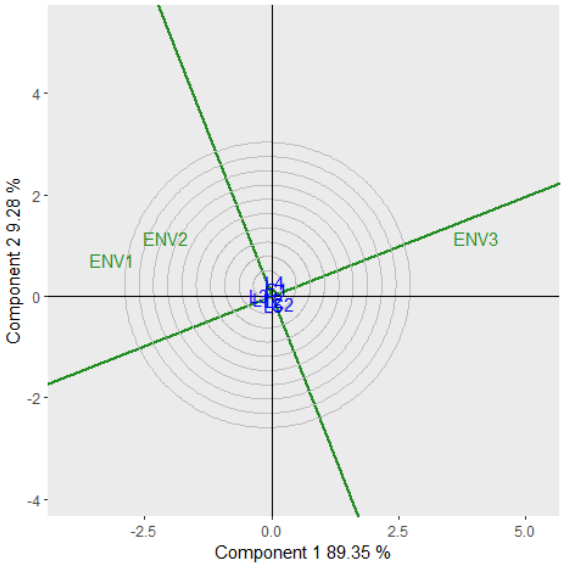


Figure 2a. Days to first flowering

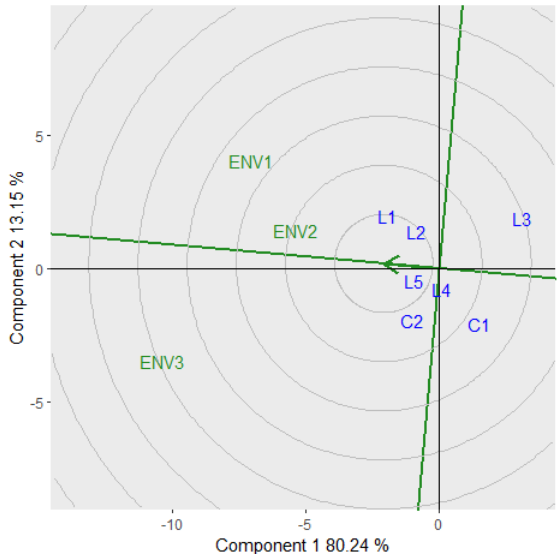


Figure 2b. Days to last harvest

Figure 2 (a & b). Ranking of genotypes relative to an ideal genotype

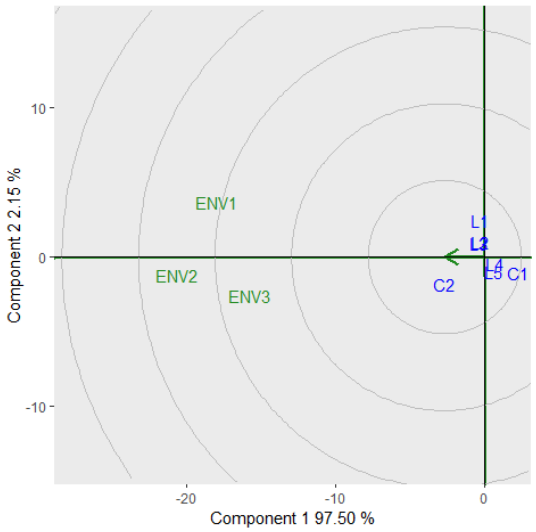


Figure 2c. Number of pods per plant

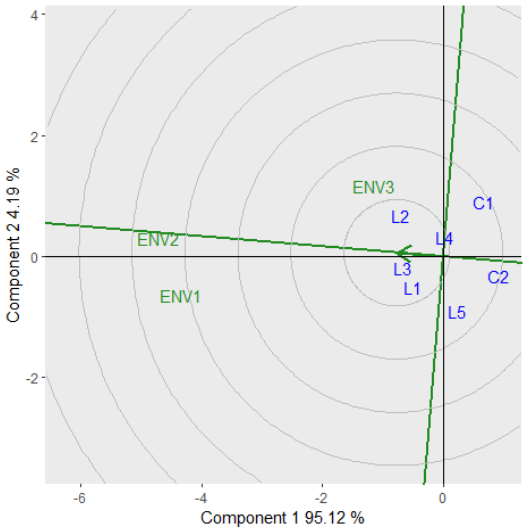


Figure 2d. Number of seeds per pod

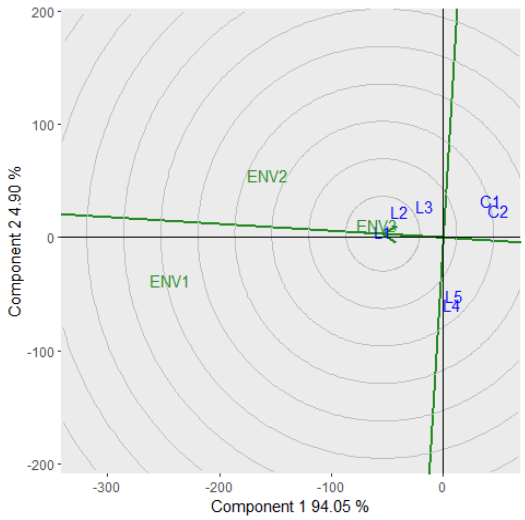


Figure 2e. Grain yield per plant

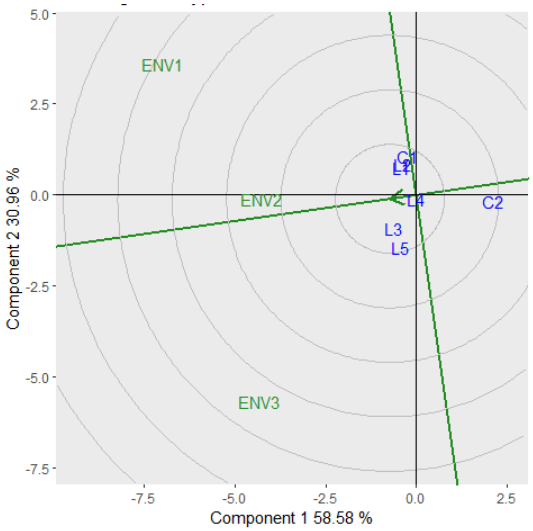


Figure 2f. Protein content

Figure 2 (c to f). Ranking of genotypes relative to an ideal genotype

4.5.1.6 Protein content

The first two principal components (PC) explained 89.54 per cent of the total variation. Genotype L_5 had the highest projection from AEC abscissa and the projection was lowest in L_4 for protein content (Figure 1f). While ranking of genotypes, L_4 was located closer to the ideal genotype (Figure 2f).

4.5.2. Evaluation of environment

The relationship among the environments were studied using Column Metric Preserving SVP and Tester-Centered G+GE with no scaling for each character and the results obtained are as follows.

4.5.2.1 Days to first flowering

The angle between environment vectors of environment 1 and environment 2 was acute for days to first flowering but it was obtuse between environment 1 and environment 3 as well as between environment 2 and environment 3 (Figure 3a).

4.5.2.2 Days to last harvest

The angle between environment vectors for days to last harvest was acute for all the environments (Figure 3b).

4.5.2.3 Number of pods per plant

The angle between environment vectors for number of pods per plant was acute for all the environments (Figure 3c).

4.5.2.4 Number of seeds per pod

The angle between environment vectors for number of seeds per pod was acute for all the environments (Figure 3d).

4.5.2.5 Grain yield per plant

The angle between environment vectors for grain yield per plant was acute for all the environments (Figure 3e).

4.5.2.6 Protein content

The angle between environment vectors for grain yield per plant was acute for all the environments (Figure 3f).

4.5.3 Which-won-where analysis

Which-won-where graphs were constructed by joining the farthest genotypes forming a polygon. Perpendicular lines (equality lines) from the origin of the biplot to each side of the polygon were drawn, thereby separating the polygon into different sectors with one genotype at the vertex of the polygon. Genotypes at the vertices of the polygon performs best or poorest in one or more environments. The genotype at the vertex of the polygon performs best in the environment falling within the sectors (Yan and Tinker 2006). Which-won-where biplots for days to first flowering, days to last harvest, number of pods per plant, number of seeds per pod, grain yield per plant and protein content were constructed.

4.5.3.1 Days to first flowering

Polygon for the days to first flowering was not well distributed and had fewer vertices (Figure 4a). The equality line divided the biplot into five sectors of which two retained all the three locations.

4.5.3.2 Days to last harvest

Polygon for the days to last harvest with four vertices was well distributed with genotypes L_1, L_3, C_1 and C_2 at the vertices for days to last harvest (Figure 4b). The equality line divided the biplot into four sectors of which two retained all the three locations.

4.5.3.3 Number of pods per plant

Polygon for the number of pods per plant had fewer vertices and the locations were not well separated (Figure 4c). The equality line divided the biplot into six sectors of which one retained all the three locations.

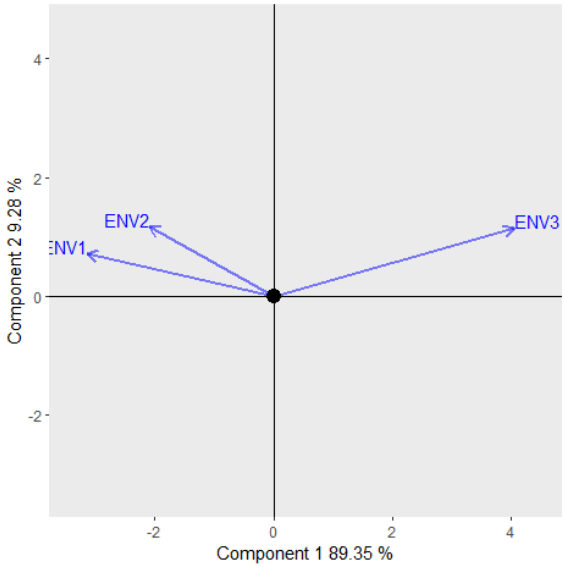


Figure 3a. Days to first flowering

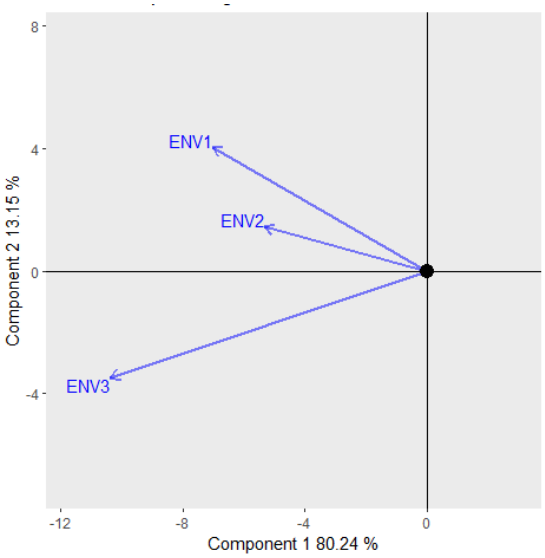


Figure 3b. Days to last harvest

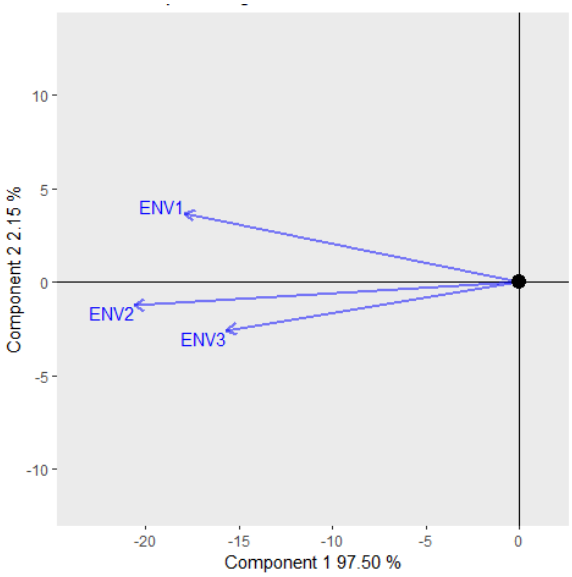


Figure 3c. Number of pods per

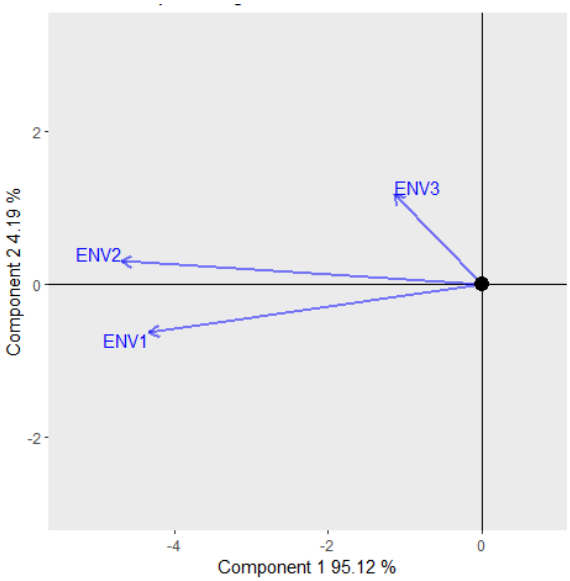


Figure 3d. Number of seeds per pod

Figure 3 (a to d). Environment evaluation for genotypes

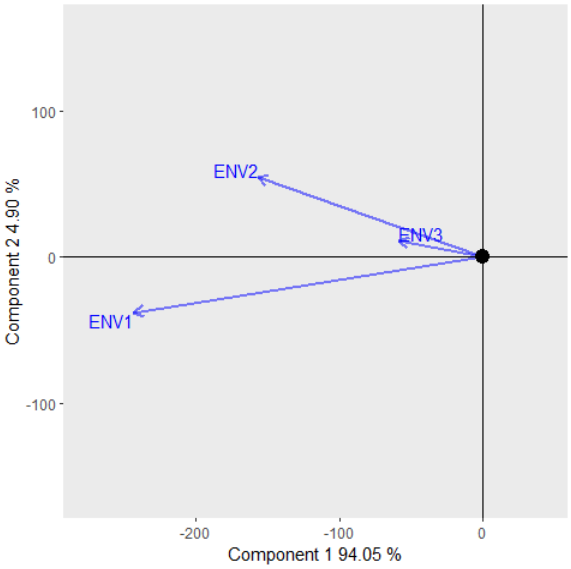


Figure 3e. Grain yield per plant

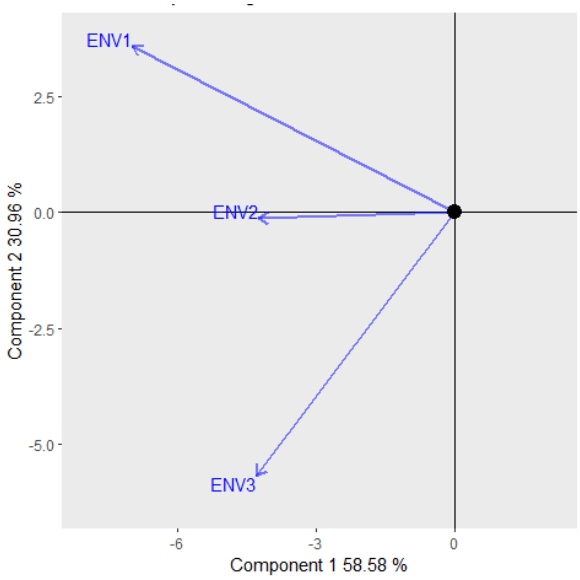


Figure 3f. Protein content

Figure 3 (e & f). Environment evaluation for genotypes

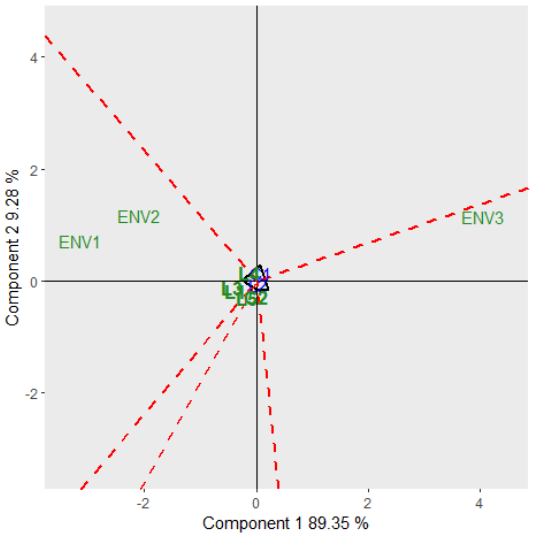


Figure 4a. Days to first flowering

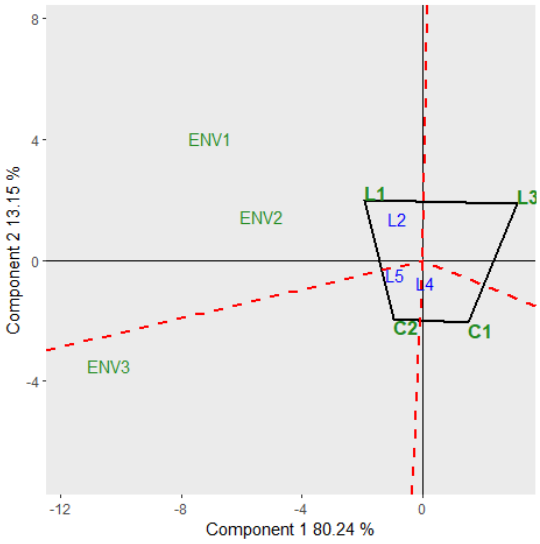


Figure 4b. Days to last harvest

Figure 4 (a & b) .Which-won-where analysis of the genotypes

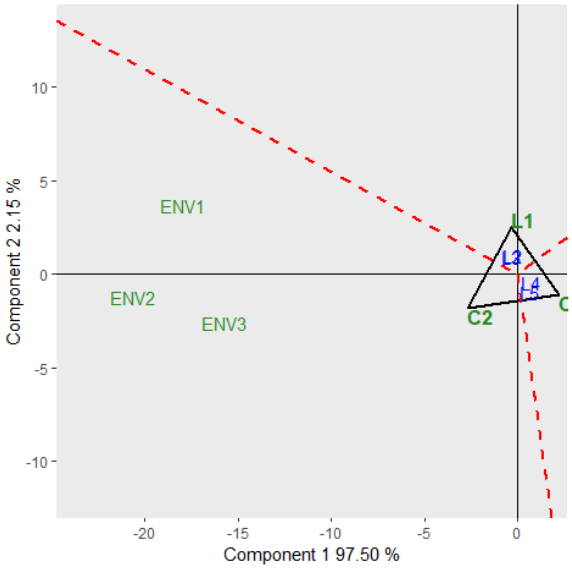


Figure 4c. Number of pods per plant

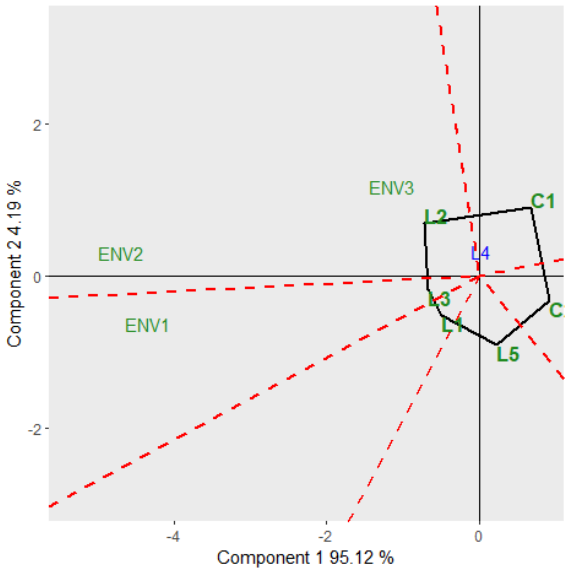


Figure 4d. Number of seeds per pod

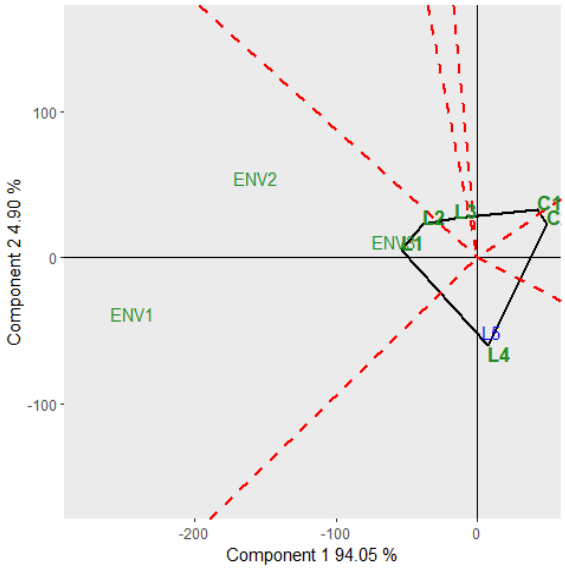


Figure 4e. Grain yield per plant

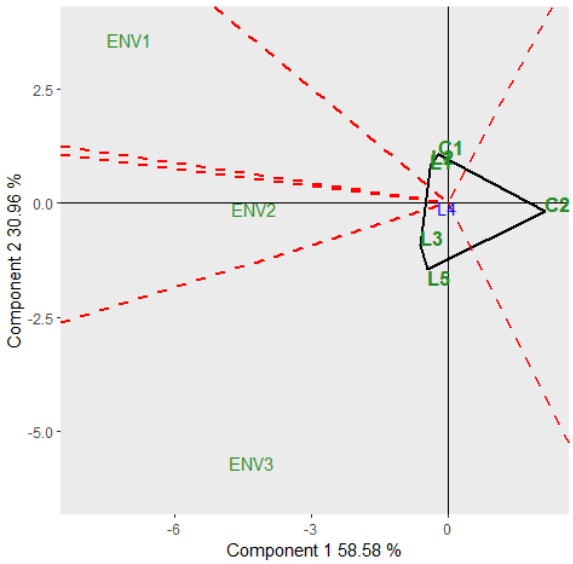


Figure 4f. Protein content

Figure 4c to figure 4f. Which-won-where analysis of the genotypes

4.5.3.4 Number of seeds per pod

Polygon for the number of seeds per pod with six vertices was well distributed with genotypes L_1, L_2, L_3, L_5, C_1 and C_2 at the vertices (Figure 4d). The equality line divided the biplot into six sectors of which two retained all the three locations.

4.5.3.5 Grain yield per plant

Polygon for the grain yield per plant with five vertices was well distributed with genotypes L_1, L_2, L_3, L_4, C_1 and C_2 at the vertices (Figure 4e). The equality line divided the biplot into six sectors of which only one retained all the three locations.

4.5.3.6 Protein content

Polygon for the protein content with five vertices was well distributed with genotypes L_1, L_2, L_3, L_5, C_1 and C_2 at the vertices of the polygon (Figure 4f). The equality line divided the biplot into six sectors with three sectors, each one accommodating one of the environment.

Discussion

5. DISCUSSION

Cowpea (*Vigna unguiculata* (L.) Walp.) is a versatile warm season pulse crop grown in tropical as well as subtropical zones of Asia, Africa and USA. India and Ethiopia are regarded as the primary centre of origin for cowpea and China as a secondary centre (Vavilov, 1951). Cowpea serves as a very good source of proteins, carbohydrates with low amounts of fat, fiber, amino acids and minerals (Kabas *et al*., 2007).

In India, pulses play an important role in healthy diets, sustainable food production and in a larger context it contributes towards food security. India produced 23.03 million tonnes of pulses during the 2019-2020 crop year but had to import 26-28 million tonnes so as to meet the national requirements (Anonymous, 2020).

Besides providing proteins and carbohydrates, tender leaves of cowpea are also edible and are highly recognised for its capability in providing nutritious fodder for the livestock. Being a resourceful crop, cowpea restores soil nitrogen content, leading to enhancement of soil fertility to grow cereal as an alternate crop (Singh, 2005). Cowpea can be grown under diverse climatic and soil conditions because of its phenotypic plasticity. Its canopy suppresses weed growth thereby maintaining soil moisture and at the same time retains soil health and microbial diversity.

Cowpea is one of the most important legume crops cultivated in Kerala because of its use, both as a vegetable as well as grain purpose. Under Kerala conditions, cowpea can be grown throughout the year as a floor crop in coconut gardens and as an intercrop in Tapioca during May to September. It can also be grown as a pure crop in rice fallows during rabi and summer seasons. One of the major constraints in cowpea production is the lack of high yielding varieties stable over diverse environments. The present work has been conceived with an objective of assessing the genotype x environment interaction in advanced breeding lines of cowpea. The identified lines possessing higher yield were developed at the Department of Plant Breeding and Genetics, CoA Vellanikkara, through hybridization followed by pureline selection.

The experiment was conducted with five cowpea cultures in stabilized F_7 generation and two check varieties over three locations. Two varieties released by KAU, Anaswara and Kanakamony both having wider acceptability because of its dual purpose nature and high yield were the check varieties used. Field trials were conducted at RARS Pattambi, CoA Vellanikkara and RRS Vyttila so as to find out the cultures that are better performing and stable over three locations and the results of the study are presented in this chapter.

5.1 Performance of cowpea genotypes under each environment

Cowpea an important legume crop of India, can tolerate summer drought as well as water stagnant conditions of the rainy season (Panchta *et al*., 2021). Among the Kharif season legumes, cowpea is considered to have the highest productivity potential (Singh and Sharma, 1996). The present study was undertaken over three locations (RARS Pattambi, CoA Vellanikkara and RRS Vyttila) during the month of Feb 2021-May 2021.

5.1.1 Performance of cowpea genotypes under environment 1

Variability available within the tested genotypes were significant for all the characters under study in the first environment. Kharde *et al*. (2014) reported significant differences among 20 genotypes of cowpea for all the characters evaluated. In an experiment conducted in 30 genotypes of cowpea, all the 14 characters exhibited significant variations (Thorat and Gadewar. 2013). Significant differences among all the thirty one genotypes for all the twelve characters studied was observed by Ugale *et al*. (2020). One hundred and eighty genotypes of cowpea were evaluated and analysis of variance revealed significant differences among the genotypes for all the 13 characters recorded (Devi and Jayamani, 2018).

Phenotypic Coefficient of variation (PCV) and genotypic coefficient of variation (GCV) values were classified as low (<10%), moderate (10% - 20%) and high (>20%) by Sivasubramanian and Madhavamenon (1973). Johnson et al. (1955) classified genetic advance as per cent of mean as low (<10%), moderate (10% - 20%) and high (>20%).

The traits, days to first flowering, days to first harvest, days to last harvest and protein content recorded low phenotypic (PCV) and genotypic (GCV) coefficients of variation. Moderate PCV was observed in plant height, number of branches, number of pods per plant, length of pod, pod weight, number of seeds per pod and test weight. The characters plant height, number of branches and pod weight had low GCV. Moderate GCV was found for characters number of pods per plant, length of pods, number of seeds per pod and test weight. High GCV and PCV was obtained for grain yield per plant. The magnitude of difference between phenotypic and genotypic coefficients of variation were high for the characters plant height and number of branches suggesting that these characters were under the control of environment with little role of genetic constitution on the phenotypic expression of these characters. When low influence of environment is observed compared to genetic factors it suggests that the traits are under the genetic control rather than the environment and further improvement can be achieved through selection (Vange and Egbe, 2009).

Low genetic advance as percentage of mean was observed for plant height, days to first flowering and days to last harvest. Genetic advance was moderate for number of branches, days to first harvest and protein content. It was high for number of pods per plant, length of pod, pod weight, number of seeds per pod, test weight and grain yield per plant.

Manggoel *et al*. (2012) observed high PCV and GCV for all the characters studied except for pod length and seeds per pod. Moderate PCV and GCV were recorded for plant height and number of pods per plant and moderate PCV coupled with low GCV was recorded for number of branches, number seeds per pod and seed yield per plant (Dinesh *et al*., 2017). Palve *et al*. (2018) obtained high GCV and PCV values for pod yield per plot, pod length, number of seeds per pod, number of pods per plant, average pod weight, and number of clusters per plant. In a study conducted by Borah and Khan (2000), low genetic advance as percent of mean was exhibited by crude protein content, days to 50 per cent flowering, stem thickness, and leaf length and width.

Heritability was classified as low (< 30%), medium (30% - 60%) and high (> 60%) by Johnson *et al*. (1955). It was observed that the character plant height exhibited low heritability while number of branches had moderate heritability. All other

characters: days to first flowering, days to first harvest, days to last harvest, number of pods per plant, length of pod, pod weight, number of seeds per pod, test weight, grain yield per plant and protein content exhibited high heritability.

High heritability with high genetic advance (GA) indicates that the heritability is due to additive gene action so that selection for such traits can be effective (Nadarajan and Gunasekharan, 2008). According to this criteria, number of pods per plant, length of pod, pod weight, number of seeds per pod, test weight and grain yield per plant were detected to be under the influence of additive gene action so that further selection can improve these traits.

High heritability with high genetic advance were observed for green pod yield per plant, plant height, pod length, pod width, number of seeds per pod, number of pods per plant, pod weight, number of pods per cluster and hundred fresh seed weight (Khanpara *et al*., 2016). High heritability along with moderate genetic advance as per cent of mean was recorded for pod wall proportion, seed yield per plant and pod length (Meena *et al*., 2015).

In the present study high heritability with moderate or low GA was observed for days to first flowering, days to first harvest, days to last harvest and protein content. This refers to the presence of non- additive gene action and selection for such characters can turn ineffective. Low heritability coupled with low genetic advance observed in plant height indicates the dominance of environmental effects over the trait.

5.1.2 Performance of cowpea genotypes under environment 2

The cowpea genotypes in the second environment exhibited significant variation for all the characters studied with an exception for plant height. Magashi *et al*. (2017) observed significant variation for plant height, number of days to fifty per cent flowering, number of days to maturity, number of pods per plant, pod length, number of seeds per pod, test weight and protein content. High and significant variation was observed for all the characters excluding pod width by Chandrakar *et al*. (2016).

The magnitude of difference between PCV and GCV was high for plant height and number of branches per plant indicating that these characters are governed by environment than the genotype. The magnitude of difference was low for the traits

length of pod, pod weight, number of seeds per pod, test weight and protein content. Since the expression of these traits are largely controlled by the genetic constitution with little or no effects from the environment, further improvement through selection is possible.

Grain yield per plant exhibited high PCV and GCV. High PCV was observed for number of pods per plant. Moderate PCV was observed for plant height and number of branches. Moderate PCV and GCV were recorded for length of pod, pod weight, number of seeds per pod and test weight. Moderate GCV was observed for number of pods per plant. Low PCV and GCV were observed for days to first flowering, days to first harvest, days to last harvest and protein content. Characters plant height and number of branches exhibited low GCV. High values of GCV and PCV was observed for pod yield per plot, pod length, number of seeds per pod, number of pods per plant, average pod weight, and number of clusters per plant (Palve *et al*., 2018). Sabale *et al.* (2018) reported low GCV and PCV for days to flowering and days to maturity.

High heritability coupled with high genetic advance as per cent of mean was observed for number of pods per plant, length of pod, pod weight, number of seeds per pod, test weight and grain yield per plant. Selection for such characters are effective since they are controlled by additive gene action. High broad-sense heritability was recorded for grain yield per plant whereas lowest heritability was observed for the character number of seeds per pod (Nkoana *et al*., 2019). High heritability with moderate and low genetic advance was observed in days to first flowering, days to first harvest and protein content and these traits were under the control of non- additive genes for which selection will not be effective. Low heritability along with low genetic advance was observed for plant height and number of branches which shows the predominant effect of environment over these traits. Ajayi *et al*. (2014) observed high broad sense heritability values for all the traits studied except for plant height.

5.1.3 Performance of cowpea genotypes under environment 3

The characters plant height and number of branches showed no variability in the third environment. This was in contradiction to Kharde *et al*. (2014) wherein significant variations were observed among genotypes for all the characters evaluated. High PCV

was observed for plant height. Moderate PCV and GCV were observed for number of pods per plant, length of pod, pod weight, test weight and protein content. Plant height showed moderate GCV while days to first flowering, days to first harvest, days to last harvest and number of seeds per pod exhibited low PCV and GCV. Moderate PCV was observed for number of branches and grain yield per plant and low GCV was observed for number of branches.

Large difference was observed between the magnitude of PCV and GCV for the characters plant height and number of branches. This explained the predominance of environmental effects in the expression of these characters. The difference in magnitude was considerably less for length of pod, pod weight, number of seeds per pod and protein content. Since these characters are little manipulated by environmental effects further improvement in these characters can be achieved through selection. Moderate PCV and GCV were recorded for plant height and number of pods per plant (Dinesh *et al*., 2017). Lowest GCV and PCV was observed for days to first flowering and days to maturity (Sabale *et al*., 2018).

Heritability and genetic advance was high for number of pods per plant, length of pod, pod weight, test weight and protein content indicating the predominance of additive gene action so that selection for such characters can be effective. High heritability along with high genetic advance expressed as percentage of mean was observed for number of pods per plant, 100 fresh seeds weight, 10 pods weight, green pod yield per plant and plant height (Sapara *et al*., 2014). Chattopadhyay *et al*. (2014) have observed high broad sense heritability coupled with higher genetic advance for number of pods per plant, pod yield per plant, pod weight, number of seeds per pod and pod length. High heritability accompanied with moderate and low genetic advance was observed in days to first flowering, days to last harvest, number of seeds per pod and grain yield per plant. Selection for such traits can be misleading since they are under the control of non- additive gene action. Low heritability with low genetic advance was observed in plant height and number of branches indicated the prominent effects of environment on these traits.

5.1.4 Comparison of genetic components over locations

The present study conducted at three locations revealed significant differences between genotypes with respect to most of the characters and the magnitude of variability differed according to locations. Phenotypic and genotypic variation observed in cowpea cultures at three locations showed that the characters were showing low, medium as well as high PCV and GCV. Previous studies regarding the heritability indicated that the magnitude of heritability and other genetic parameters for a character in cowpea differed from location to location (Omoigui *et al*., 2006).

Additive gene action reflected through high heritability and high genetic advance was observed for number of pods per plant, length of pod, pod weight, number of seeds per pod, test weight and grain yield per plant in environment 1 whereas number of pods per plant, length of pod, pod weight, number of seeds per pod, test weight and grain yield per plant recorded high heritability coupled with high genetic advance in the second environment. In the third environment, number of pods per plant, length of pod, pod weight, test weight and protein content had high heritability and genetic advance. Based on the observation from all the three environments, it can be inferred that number of pods per plant, length of pod, pod weight and test weight were found to be controlled by additive gene action suggesting further possible improvement of these traits through selection.

Non additive gene action was found to be influencing the traits days to first flowering, days to first harvest, days to last harvest and protein content in environment 1 since they had high heritability with moderate or low genetic advance. Similarly in environment 2, days to first flowering, days to first harvest and protein content had high heritability with moderate or low genetic advance. It was found that days to last harvest and grain yield per plant were controlled by non additive gene action in the third environment. The character days to first flowering, days to first harvest, days to last harvest and protein content were under the influence of non additive gene action under two environments indicating the inefficiency of these traits towards selection.

The traits, plant height and number of branches were greatly under the influence of environment in two and three locations.

5.2 Stability parameters

One among the major challenges faced by every crop improvement programme is in assuring stable performance of selected genotypes across contrasting environments. It is important for a breeder to ensure the perfect combination of genotypic stability and high yield while selecting a genotype. It should be a goal of plant breeding to develop varieties that are adaptable towards unpredictable and temporary environmental variations (Allard and Bradshaw, 1964).

The relative magnitude of genotypic effect, environment and their interactions are major constraints in cowpea cultivation and production (Hall, 2003). Hence while developing a variety, interaction between genotypes and environment has also to be considered. Many a times, low levels of interactions are preferred for some characters so as to maximize the stable performance across a number of environments and under particular situations high beneficial interactions are also being explored (Nath and Dasgupta, 2013).

5.3 Stability parameters (Eberhart and Russell model)

Genotype x environment interactions are of major consideration for a plant breeder while developing improved varieties. Relative ranking of genotypes varies when performance of varieties are compared across different environments. This in turn reflects in the difficulty of explaining the significant superiority of any variety. It has been proven statistically that large genotype x environment interactions of a genotype can reduce its progress from selection (Comstock and Moll, 1963).

Various statistical attempts have been devised to explain the behaviour of genotypes in response to varying environments. Among those attempts, statistical approach of regression by Finlay and Wilkinson (1963) has proven to be useful in measuring the phenotypic stability of a genotype. This approach was further improved by Eberhart and Russell (1966), by introducing the component deviation from regression (S^2di), enabling consideration for unpredictable irregularities in the response of genotype to different environments.

Eberhart and Russell (1966) defined a stable variety as the one having high mean yield, regression coefficient (bi) near unity and deviation from regression (S^2di) around

zero. Regression indicates the measure of response of a genotype and the deviation from regression, the measure of its stability (Samuel *et al*., 1970).

5.3.1 Stability parameters (Eberhart and Russell) under three environments

The data collected for cowpea genotypes across three environments were subjected to pooled ANOVA and it was observed that the Genotype- environment interaction was found to be significant for the characters days to first flowering, days to last harvest, number of pods per plant, number of seeds per pod, grain yield per plant (g) and protein content (%). This indicated the combined effect of genotype and environment in determining the phenotype for the specified characters. The stability analysis of cowpea genotypes were performed for each character and discussed character wise.

5.3.1.1 Days to first flowering

For days to first flowering, even though the mean values ranged between 38.66 of C_2 and 39.91 of L_4, none of the genotypes had significant bi and S^2di value. This indicated that all the genotypes were stable across three environments for the character days to first flowering. Similar results were obtained by Patel and Jain (2012) in eleven genotypes of cowpea where pooled analysis of variance revealed significant differences for all the characters except for days to fifty per cent flowering. However, studies by Adewale *et al*. (2010) in eleven genotypes of Cowpea observed that out of the total characters studied days to fifty per cent flowering was significantly influenced by the effect of genotype, year and their interactions.

5.3.1.2 Days to last harvest

Significant bi value was shown by genotypes L_3 and C_2 and S^2di values were observed significant for the genotypes L_3, C_1 and C_2 for days to last harvest. All other genotypes L_1, L_2, L_4 and L_5 were showing stability for the character under consideration. Among these stable genotypes, the one having extended period for days to harvest (L_1 and L_2) can be considered superior. The results were in contradiction to Sabale *et al*. (2018), where lesser variations were observed for the character days to maturity.

5.3.1.3 Number of pods per plant

For number of pods per plant significant values for bi were observed for the genotypes L_1 and C_2 and significant S^2di values for L_1 and C_1. All other genotypes L_2, L_3, L_4 and L_5 without significant bi and S^2di values were considered stable for the character. Among these, the genotypes possessing potential for producing more than 40 pods per plant (L_2 and L_3) can be considered as superior. According to Cholin *et al*. (2010), Variances due to genotype, environment, genotype x environment, environment + (genotype x environment), environment (linear) were found significant for pods per plant. Similar results of significant difference among genotypes, environment and genotype x environment was reported for all the evaluated genotypes of cowpea by Teixiera *et al*. (2007). They could also observe differential response of cowpea genotypes to the environment as indicated by significant E (linear) and G x E (linear).

5.3.1.4 Number of seeds per pod

Significant bi values were shown by L_5 and C_2 and S^2di values were found significant for C_1 and C_2 for the character number of seeds per pod. All other genotypes L_1, L_2, L_3 and L_4 can be considered stable for the character. Among these genotypes, the ones having seventeen and more number of seeds per pod (L_1, L_2 and L_3) can be considered as superior. These results were in harmony with the results obtained by Torres *et al*. (2008), wherein significant differences among the tested genotypes, environmental effects and interaction between genotype and environment were observed between the evaluated genotypes of cowpea. Most of these interactions were in linear function with the environmental values and the estimated value for E + (G x E) were also found significant. Ten cowpea genotypes were evaluated for grain yield and other reproductive characters at three locations and significant effects for year, location, variety and year × location interactions were observed for most of the parameters evaluated including number of seeds per pod (Akande and Balogun, 2009).

5.3.1.5 Grain yield per plant (g)

Genotypes L_4, L_5, C_1 and C_2 had significant bi values and L_4, L_5 and C_1 had significant S^2di value for the character grain yield per plant. Genotypes L_1, L_2 and L_3 were considered as stable varieties. Among the stable genotypes, the ones with higher

yield L_1 and L_2 can be considered as superior. In a study conducted by Singh *et al*. (2020) in thirty eight accessions of cowpea including three checks, the genotype C-863 with higher mean performance as compared to check with non-significant deviation from regression line and regression coefficient less than unity was regarded as most suitable for favourable environments for the characters seed yield per plant. In another study by Manivannan *et al*. (2019) among fourteen genotypes of cowpea, the genotypes VCP 12006, VCP 13001 and VCP 15006 with a unity regression coefficient and deviation from regression equal to zero were found to be stable across the environments for seed yield.

5.3.1.6 Protein content (%)

For protein content, bi values were found significant for L_5, C_1 and C_2 while C_1 and C_2 had significant S^2di value. Genotypes L_1, L_2, L_3 and L_4 were recognized as stable varieties for protein content. 36 genotypes of cowpea were evaluated over four seasons and the magnitude of genotype x environment linear and pooled deviation from linearity was observed high for protein content (Chaudhari *et al*., 2013).

5.3.2 Overall stability

The present study identified L_2 as a stable genotype for all the characters under consideration. In a study conducted by Cholin *et al*. (2010) among twenty genotypes of cowpea for stability analysis of five yield related traits, only eight genotypes were found to be stable. According to the Eberhart and Russell model, superior and stable genotypes are the ones with high mean value and non significant bi and S^2di values. On the basis of yield and yield contributing traits, the genotypes were ranked according to the criteria suggested by Arunachalam and Bandyopadhyay (1983). For stable genotypes, rank 1 was given and rank 2 for unstable genotypes. The genotypes were ranked from 1 to 7 for the traits considered: days to first flowering, days to last harvest, number of pods per plant, number of seeds per pod, grain yield per plant and protein content. Based on the ranks, each genotype was given a specific total score as presented in Table 19a and Table 19b. The genotype with lowest score was given rank one followed by subsequent ranks according to the increasing order of their total scores.

Genotype L_2 had the lowest score followed by L_1 and L_3. This indicates the suitability of the above mentioned genotypes for general cultivation over three locations.

5.4 Stability analysis (AMMI model)

Superiority in yield and other agronomic traits for a new variety should be reliable over a wide range of environmental conditions. In reality, the relative performance of genotypes vary according to different environmental conditions. This variation in performance of the genotypes across different environments cannot be explained using variance component models. The major constraint faced in the regression model is its adequacy in describing these variations only when the genotypic response is linear. Further, when the deviation component from the linear regression is significant, joint regression fails in recognizing dominant interactive effects. This in turn affects the accuracy in determining the performance of a variety over range of environments (Raju, 2002). Non-linear genotype and environmental interaction is a complex phenomenon resulting from various characteristics of different genotypes in relation to different environments (Varghese *et al*., 2006). Stability analysis from the Eberhart and Russell model could reveal that for certain traits, the G x E linear were not significant as observed in the ANOVA and insignificant G x E linear can hinder the interpretation of stability parameters. This is because ANOVA identifies G x E interaction as a source of variation but does not analyse its multiplicative effect. These multiplicative formulations allows in interpreting the interaction as a differential genotypic sensitivity to environmental variables (Varghese *et al*., 2006).

The Additive Main effects and Multiplicative Interaction effect (AMMI) model is a hybrid model that encompasses both the additive as well as the multiplicative components of the two way data structure. G x E interaction patterns can be interpreted in an effective way through AMMI biplot analysis. The principal component analysis (PCA) provides a multiplicative model and can be applied to analyse the interaction effect from the additive ANOVA model. The PCA scores when plotted against each other in a biplot enables visual interpretation of G x E interactions. Integration of the

Table 19a. Total scores and ranking of genotypes

Genotypes	Days to first flowering			Days to last harvest			Number of pods per plant			Number of seeds per pod		
	Mean	Score	Stability	Mean	Score	Stability	Mean	Score	Stability	Mean	Score	Stability
L_1	39.35	4	1	88.37	1	1	43.41	3	2	17.68	3	1
L_2	39.08	3	1	86.04	2	1	43.07	4	1	18.33	1	1
L_3	39.53	5	1	79.05	7	2	43.59	2	1	18.01	2	1
L_4	39.91	7	1	84.35	5	1	38.3	6	1	16.66	4	1
L_5	38.83	2	1	85.67	4	1	38.75	5	1	16.02	5	2
C_1	39.57	6	1	81.23	6	2	30.69	7	2	15.39	6	2
C_2	38.66	1	1	85.73	3	2	55.02	1	2	14.68	7	2

Table 19b. Total scores and ranking of genotypes

Genotypes	Grain yield per plant (g)			Protein content (%)			Total score	Rank
	Mean	Score	Stability	Mean	Score	Stability		
L_1	140.49	1	1	24.34	2	1	21	2
L_2	133.21	2	1	24.77	1	1	19	1
L_3	121.49	3	1	20.66	5	1	31	3
L_4	105.44	5	2	23.14	3	1	37	6
L_5	105.53	4	2	19.59	7	2	36	5
C_1	91.31	6	2	19.99	6	2	48	7
C_2	84.51	7	2	21.01	4	2	34	4

visual observations from biplot display and genotypic stability statistics enables the classification of genotypes according to their similarities in performance across diverse environments (Mukherjee *et al*., 2013). In order to obtain accurate interpretations regarding the stability of seven genotypes tested under three environments, the data was analysed using AMMI model and the results are discussed here.

5.4.1.1 Days to first flowering

Mean values of days to first flowering for the genotypes ranged between 38.66 of C_2 and 39.91 of L_4 (Table 18a). Positive values for IPCA 1 were observed for genotypes L_1 and L_3 and environments E_1 and E_2. IPCA 2 values were positive in genotypes L_3, L_4 and C_2 and environment E_2. Based on the biplot 1 (Fig.5) L_1 and L_3 had similar main effects while L_5 and L_2 had similar interaction effects. The L_5 and L_2 placed near to the origin of biplot 1 were stable for the trait days to first flowering. Based on biplot 2 (Fig.6), the environment 3 (RRS Vyttila) having a long spoke exerted strong interactive forces on the genotypes. The environment E_2 (CoA, Vellanikkara), exerted lesser interaction on the genotype. Genotypes L_5 and L_2 that are present near to the origin were non sensitive to interactive patterns. Comparatively, these genotypes had early flowering also. Hence, these genotypes can be selected for days to first flowering.

5.4.1.2 Days to last harvest

Mean values for days to last harvest for the genotypes ranged from 79.05 of L_3 and 88.37 of L_1. Positive values for IPCA 1 were observed for the genotypes L_1, L_2, L_3 and L_4 and environment E_1 and E_2. IPCA 2 values were observed positive for the genotypes L_1, L_2, L_3 and L_5 and environment E_1 and E_3. Based on the biplot 1 (Fig.7), L_2, L_5 and C_2 had similar main effects while L_1 and L_4 had similar interaction effects. Genotypes L_1 and L_4 present near to the origin of biplot 1was found stable for days to last harvest. Based on biplot 2 (Fig. 8), the environment 3 (RRS, Vyttila) having a long spoke exerted strong interactive forces on the genotypes when compared with environments 1 (RARS, Pattambi) and 2 (CoA, Vellanikkara). Genotype L_1, L_2 and C_1 present near to the origin was found to be non sensitive towards interactive patterns.

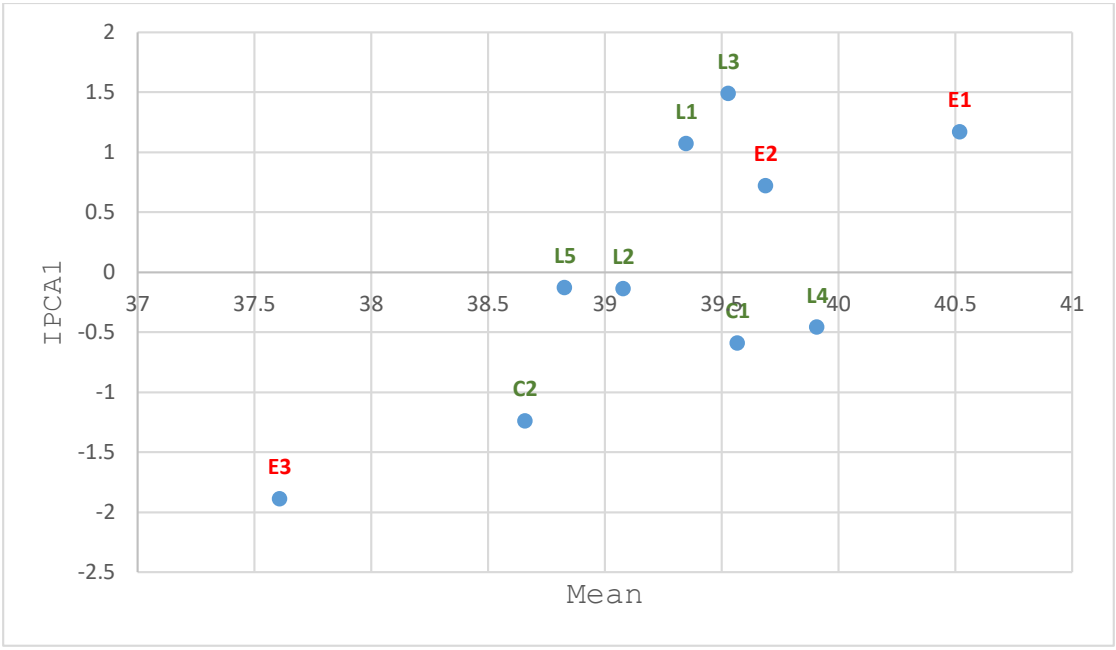


Fig. 5. Biplot (AMMI 1) for days to first flowering

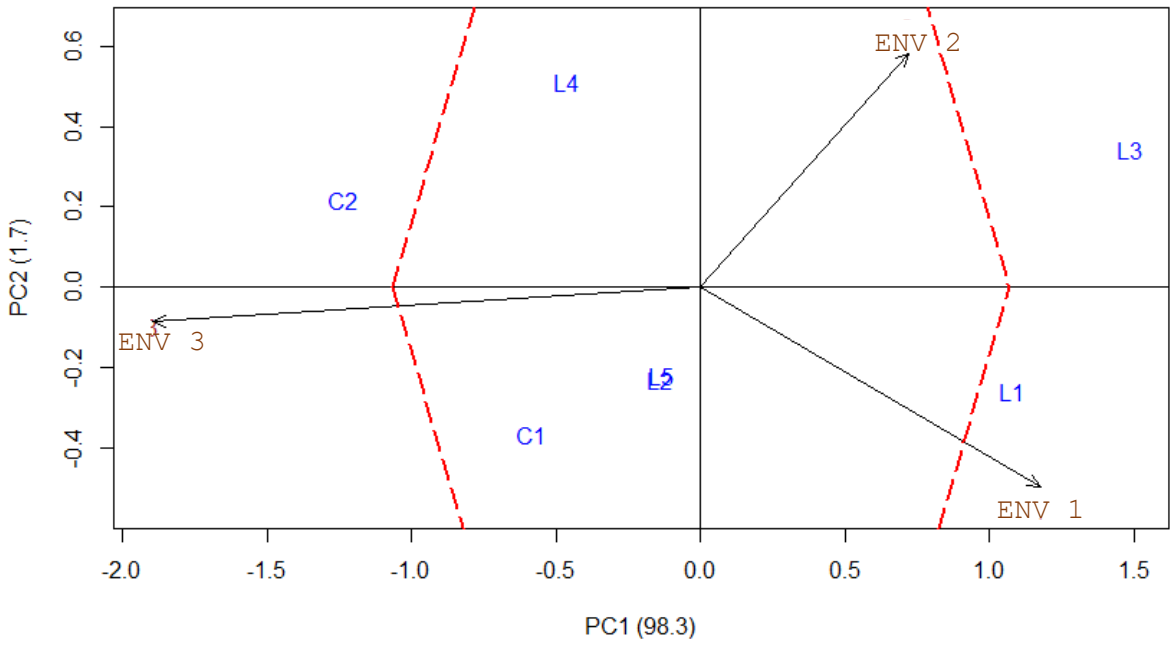


Fig. 6. Interaction biplot (AMMI 2) for days to first flowering

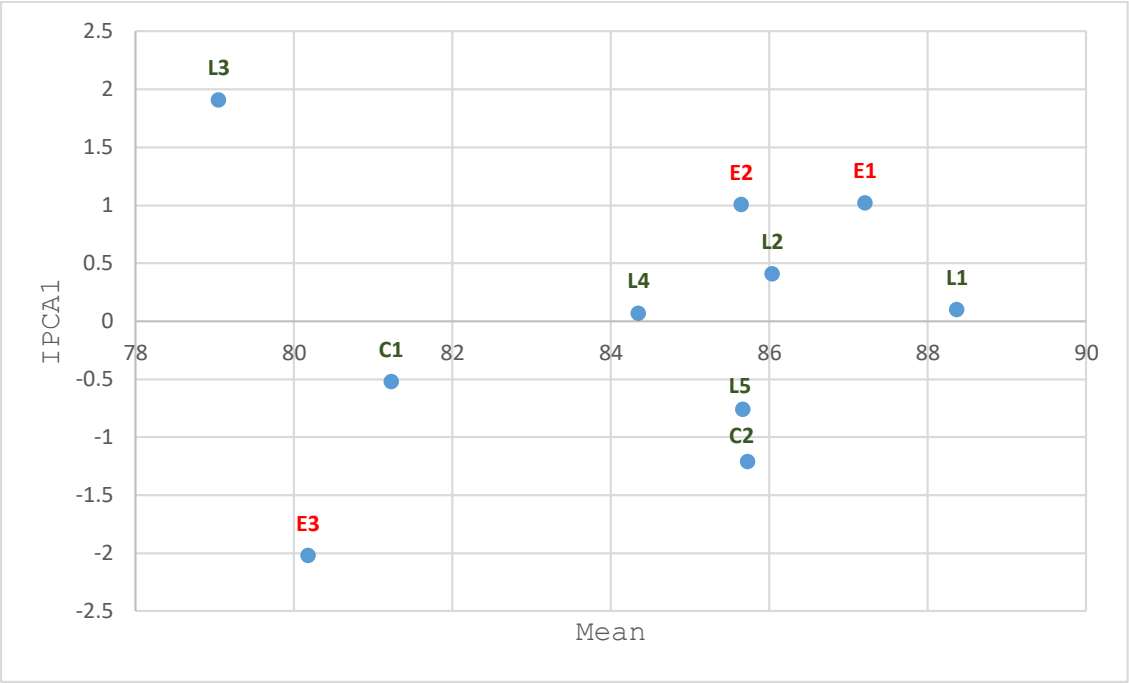


Fig. 7. Biplot (AMMI 1) for days to last harvest

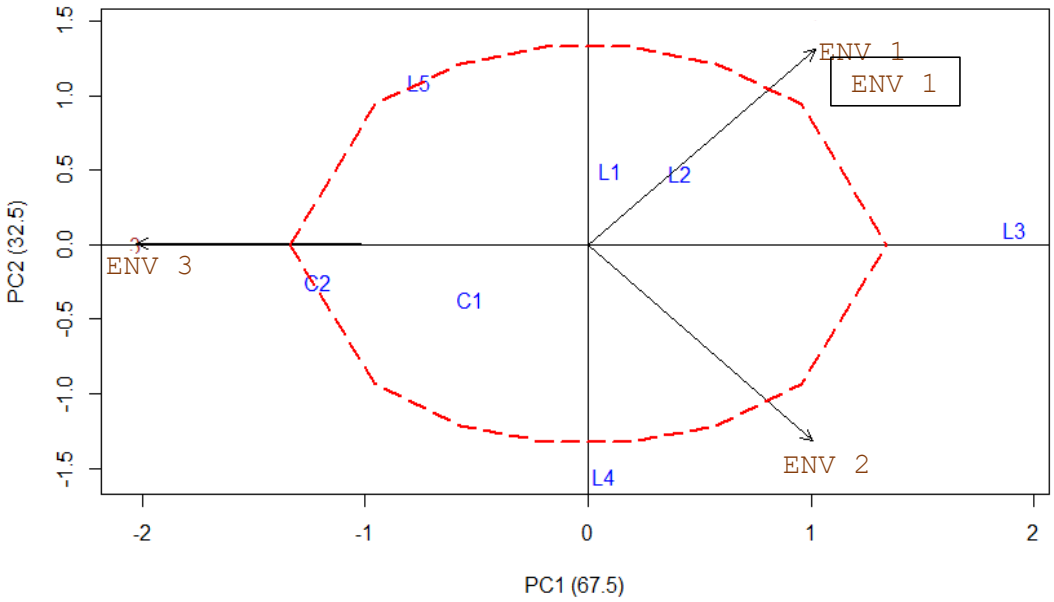


Fig. 8. Interaction biplot (AMMI 2) for days to last harvest

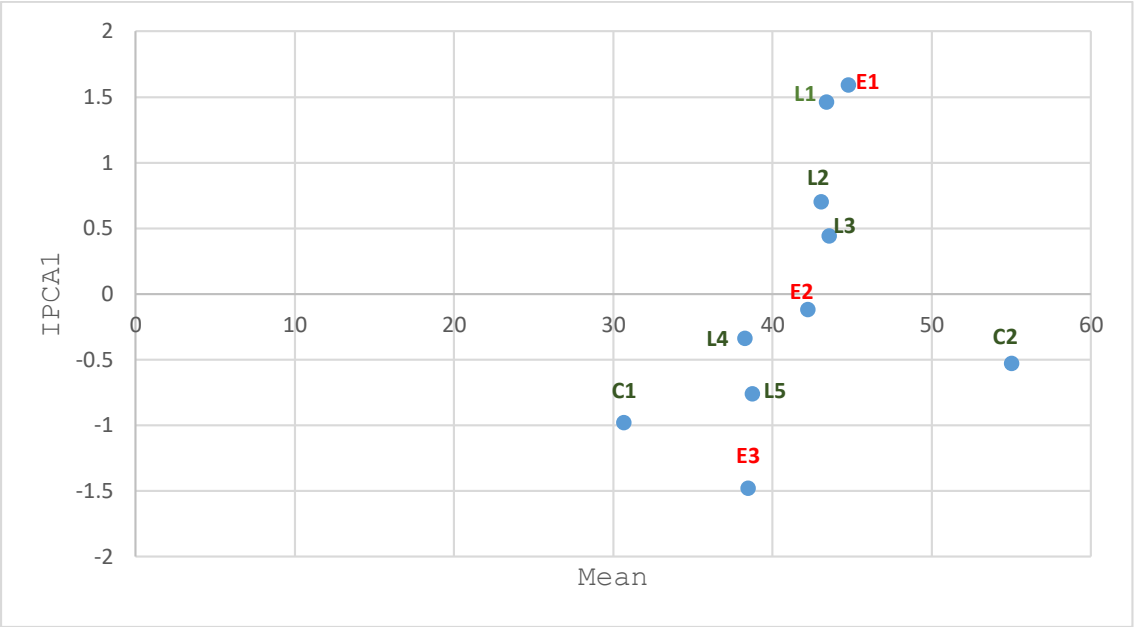


Fig. 9. Biplot (AMMI 1) for number of pods per plant

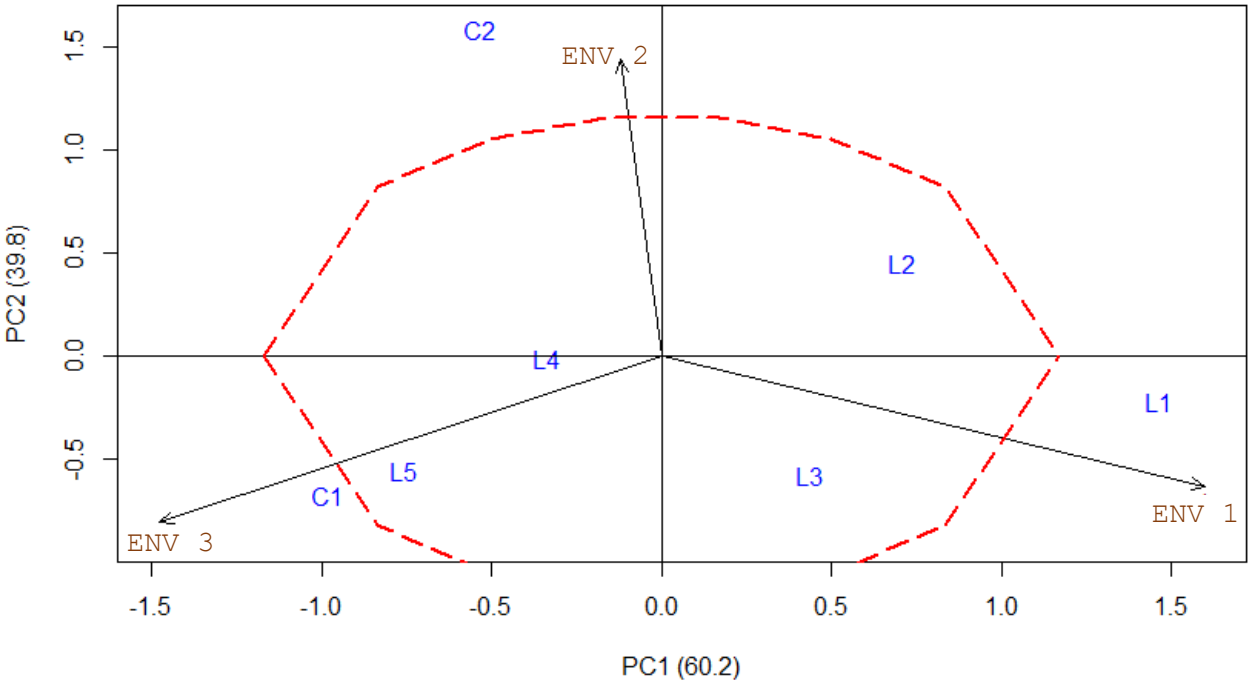


Fig. 10. Biplot (AMMI 2) for number of pods per plant

Among these, genotypes L_1 and L_2 had extended days for last harvest. Hence genotypes L_1 and L_2 can be selected for days to last harvest.

5.4.1.3 Number of pods per plant

Mean values for number of pods per plant varied from 30.69 of C_1 to 43.59 of L_3. Positive values for IPCA 1 were observed for the genotypes L_1, L_2 and L_3 and for the environment E_1. IPCA 2 values were observed positive for the genotypes L_2 and C_2 and for the environment E_2. From biplot 1 (Fig. 9), L_1, L_2 and L_3 and L_4 and L_5 had similar main effects. Genotypes C_1 and L_5 had similar interaction effects. Genotype L_4 present near to the origin of biplot 1 was determined as the stable genotype for number of pods per plant. Considering biplot 2 (Fig. 10), environment 1 (RARS, Pattambi) and environment 3 (RRS Vyttila) with long spoke exerted strong interactive forces on the genotype. Genotypes L_2, L_3, L_4 and L_5 present near to the origin were found non sensitive to interactive patterns. Among these, genotypes L_2, L_3 and L_4 with more number of pods can be selected. Considering the analysis of AMMI, the genotypes P290, P-508 showed high yield and good stability for the character yield of immature pods (Aquino *et al*., 2016).

5.4.1.4 Number of seeds per pod

Mean values for number of seeds per pod for the genotypes ranged between 14.68 of C_2 and 18.33 of L_2. Positive values of IPCA 1 were obtained for L_1, L_2, L_3 and L_5 and for the environment E_1 and E_2. Positive values of IPCA 2 were obtained for the genotypes L_1, L_5 and C_2 and for the environment E_1. On the basis of biplot 1 (Fig. 11), it was observed that L_1, L_2 and C_2 had similar main effects. Genotypes L_4 and L_5 located closer to the origin of biplot 1 were accepted as stable for the trait number of seeds per pod. From biplot 2 (Fig. 12), environment 3 (RRS Vyttila) with longer spoke exerted stronger interactive force on the genotypes compared to environment 1 (RARS Pattambi) and 2 (CoA Vellanikkara). Genotype L_2, L_4 and L_5 were present near to the origin and hence concluded to be non sensitive to interactive patterns. Among these L_2 and L_4 with more number of seeds can be selected. In a study conducted by Dhanasekar *et al*. (2010), with an aim to identify grain cowpea possessing low pod wall proportion and high pod filling index with least environment interaction, the AMMI model

identified C 440 as the most stable genotype with least number of unfilled locules. For yield of immature seeds per pod and good stability, the genotypes CPCR3F6L15, PC951015D01E and PC950409D02E expressed better yield and stability when determined through AMMI model (Aquino *et al*., 2016).

5.4.1.5 Grain yield per plant (g)

Mean values for grain yield per plant for the genotypes ranged between 84.51 of C_2 and 140.50 of L_1. Positive values for IPCA 1 were observed for the genotypes L_1, L_2, L_3, L_4 and L_5 and environment E_1. Positive values for IPCA 2 were observed for L_1, L_2, L_3, C_1 and C_2 and environments E_2. From biplot 1 (Fig. 13), it can be inferred that L_4 and L_5 had similar main effects. Genotypes L_3 and L_5 located close to the origin of biplot can be considered as stable for the character grain yield per plant. From biplot 2 (Fig. 14), environment 1 (RARS Pattambi) and environment 3 (RRS Vyttila) exerted strong interactive forces on the genotype as indicated by their longer spokes. Genotypes L_2, L_3, L_4 and L_5 were located near to the origin of biplot 2 hence, was found non sensitive to interactive patterns. Among these genotypes L_3 had higher grain yield among the stable genotypes. Hence genotype L_3 can be selected for the trait grain yield per plant. Singh *et al*. (2019) through biplot-AMMI analysis and yield stability index, incorporating the AMMI stability value and yield in a single non-parametric index identified G135, G125, G104, G112 and G144 as promising genotypes for grain yield. Simion *et al*. (2018), determined TVU as the most stable genotype with mean yield above the mean grain yield of considered genotypes.

5.4.1.6 Protein content (%)

Mean values of protein content for the genotypes ranged between 19.59 of L_5 and 24.77 of L_2. Positive values for IPCA 1 were observed for the genotypes L_1, L_2 and L_3 and genotype E_3. Positive values for IPCA 2 were observed for genotypes L_1, L_5 and C_2 and environment E_1 and E_3. From biplot 1 (Fig. 15), it was observed that L_1 and L_2, L_3 and C_2 and L_5 and C_1 had similar main effects while L_2 and L_3 had similar interactive effects. C_1 placed near to origin was found stable for protein content. From biplot 2 (Fig. 16) environment 3 (RRS, Vyttila) exerted strong interactive forces on the genotypes compared to environment 1 (RARS, Pattambi) and environment 2 (CoA, Vellanikkara).

Genotypes L_2, L_3, L_4, C_1 and C_2 placed near to the origin of biplot 2 seem to be insensitive to interactive patterns. Among these L_2 and L_4 had comparatively higher protein content associated with stability and hence, can be selected. In a study conducted on twenty nine genotypes of cowpea for protein stability and adaptability under diverse environments, genotypes BRS Pujante, C1J, C2Q and CIT expressed high protein levels with high stability and wide adaptability (Ddamulira *et al*., 2015).

5.4.2 Overall stability

To select genotypes with higher yield stability over the environments, the AMMI stability value (ASV) and yield stability index (YSI) were calculated according to Oliveira *et al*. (2014). The rank of ASV (rASV) and the rank of performance for each character (rY) followed by stability index (SI) was calculated for each genotype and presented in Table 20a and Table 20b. The lower the SI value, higher is its mean performance and stability (Iseki *et al*., 2021). Scoring was done accordingly for yield and yield contributing traits by AMMI model. The total score of the genotype is given in Table 21. It was observed that genotype L_2 ranked the best genotype with lowest total score followed by L_1 and L_5.

Comparison of results from stability analysis by AMMI with Eberhart and Russell model showed that the most stable and promising genotypes were the same, L_1 and L_2 by both the models.

5.5 GGE Biplot (Genotype main effect plus Genotype-by-Environment Biplot) analysis

Very less importance is being given on the genotype x environment interaction during the process of release of new cultivars using multi locational data while major emphasis is on its agronomic superiority over the ruling cultivar. While analysing the data from multi-locational trials, genotypic evaluations are often limited on genotype main effects, that genotype x environment interactions (GEI) are ignored as noise or confounding factors (Yan and Tinker, 2006). Various statistical models have been employed so as to understand this complex interaction between genotype and environment. When the traditional methods of ANOVA, PCA and linear regression failed in many aspects while describing its complexity, the AMMI model that integrated

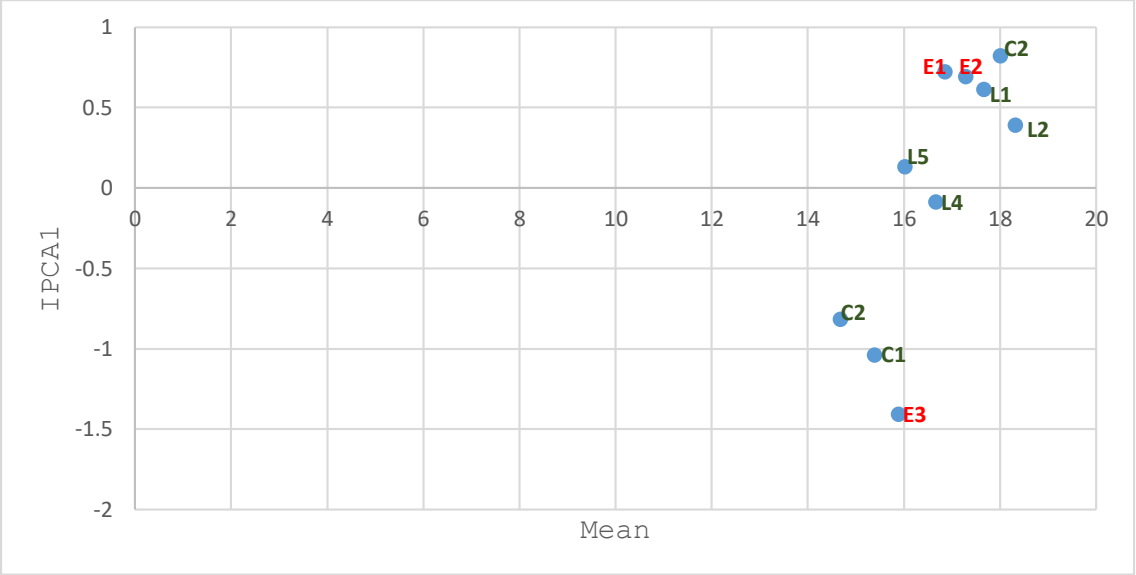


Fig. 11. Biplot (AMMI 1) for number of seeds per pod

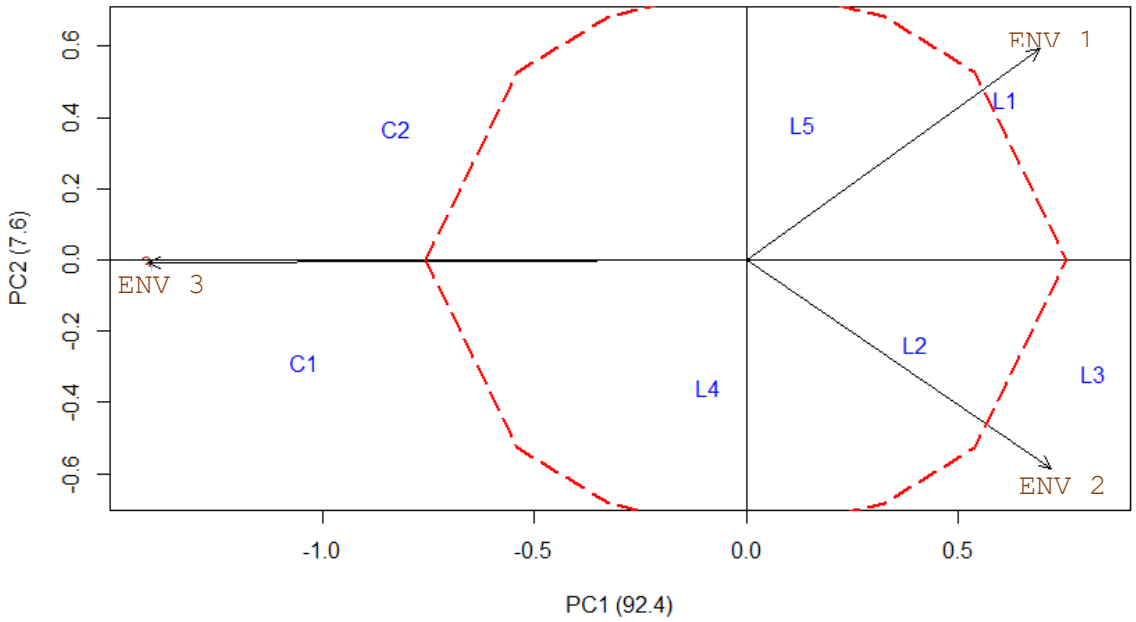


Fig. 12. Biplot (AMMI 2) for number of seeds per pod

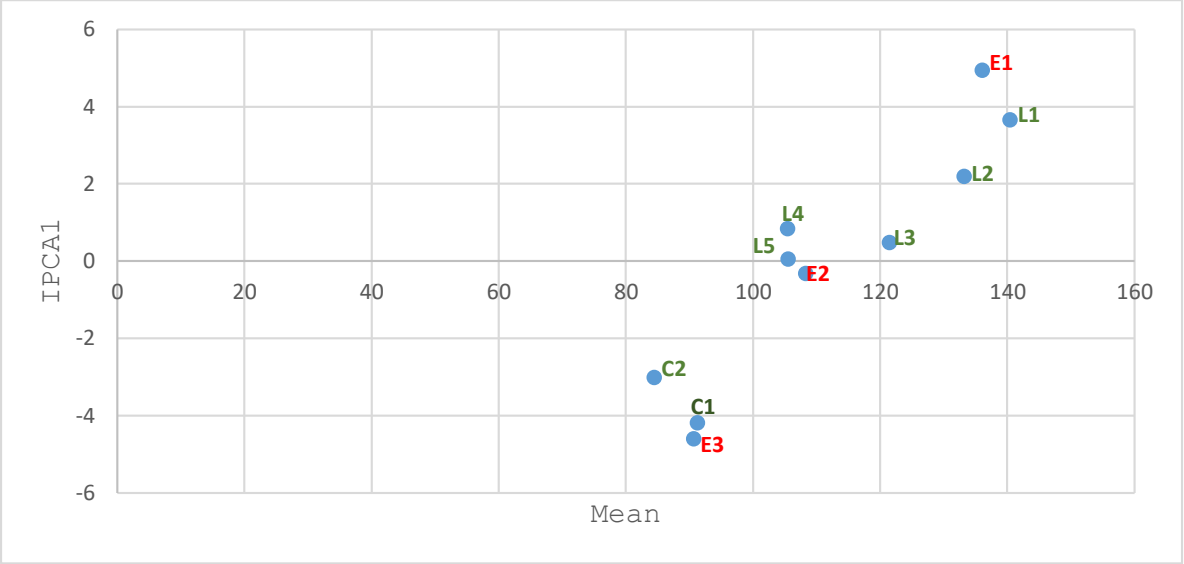


Fig. 13. Biplot (AMMI 1) for grain yield per plant

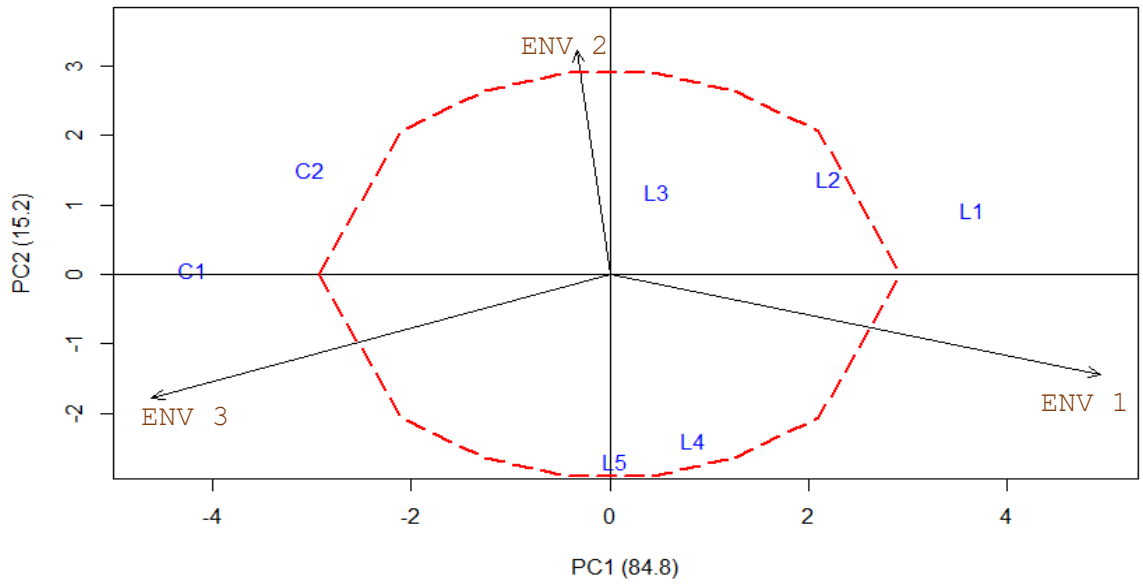


Fig. 14. Biplot (AMMI 2) for grain yield per plant

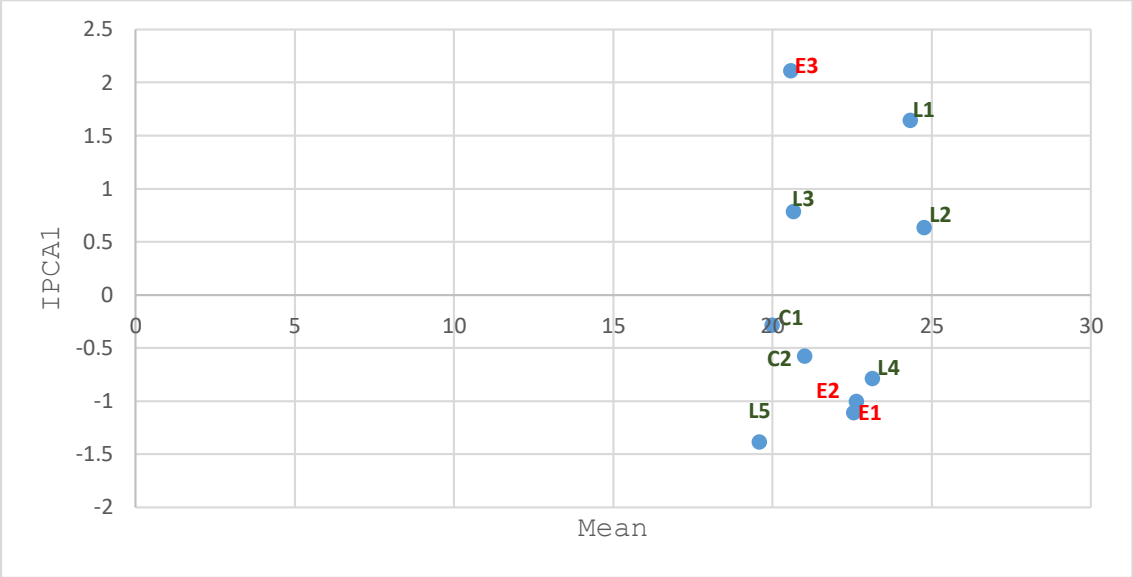


Fig. 15. Biplot (AMMI 1) for protein content

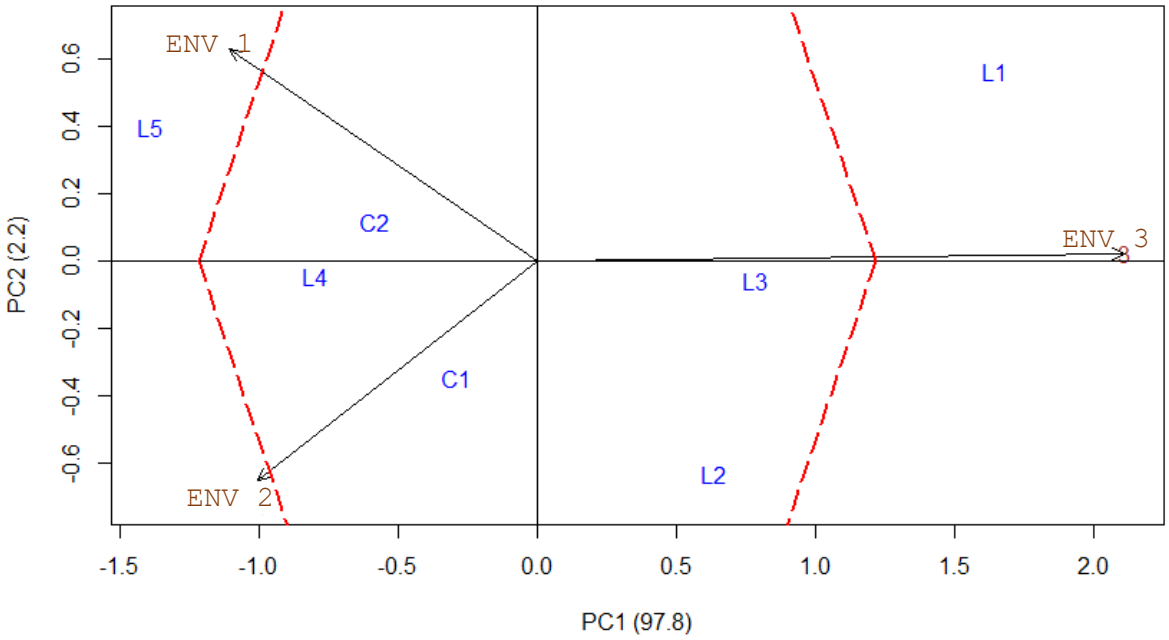


Fig. 16. Biplot (AMMI 2) for protein content

additive and multiplicative components into a combined and powerful least square analysis could explain the GEI much more accurately. Emergence and propagation of biplot enabled easier understanding of GEI complexity through graphical manner. The AMMI biplot and the GGE biplot are the most commonly used biplots. The G + GE biplot in GGE removes the E and integrates the G with the GE interaction effect of a G x E data (Yan *et al*., 2000). GGE biplot is comparable with the best AMMI models when different AMMI family models were considered (Ma *et al*., 2004) and is more logical and biological in explaining PC1 score that represents genotypic effect than additive main effect (Yan, 2002).

5.5.1 Mean performance and stability of the genotypes across environments

Mean performance and stability of genotypes across locations were visualized graphically through 'mean versus stability' graph. An ideal genotype is the one with high performance and high stability across environments (Yan and Tinker, 2006) and ranking of genotypes in terms of ideal genotype was performed graphically. Interpretations of these graphs are discussed here.

5.5.1.1 Days to first flowering

When the absolute length of its projection onto the AEC abscissa is larger, genotypes are less stable. The average yield of a genotype in producing the specified character can be approximated by the projections of their marker to the AEC abscissa (Kaya *et al*., 2006). Accordingly it was observed that all the genotypes were equally stable with regard to days to first flowering as they produced relatively similar length of projection on to the AEC abscissa (Figure. 1a). So was the result obtained while ranking of genotype (Figure. 2a) where all the genotypes performed similar with equal stability on comparison with ideal genotype.

5.5.1.2 Days to last harvest

Based on the 'mean versus stability' graph obtained, it can be inferred that genotype L_1 was the best performing genotype and L_3 appeared to be the poor performer with regard to days to last harvest (Figure. 1b). With higher projection from AEC abscissa, genotypes L_3 and C_2 were least stable for days to last harvest and the genotype L_5 with the lowest projection as the highly stable. L_1 even though, being a best performer

was found not to be stable. L_4 despite being stable, was not a good performer as compared to L_5. On ranking of genotypes (Figure. 2b), L_5 and L_2 was determined to be the genotype with superior performance and high stability across test environments.

5.5.1.3 Number of pods per plant

Based on the 'mean versus stability' graph, it was observed that C_2 was the best performer and C_1 the least performer when considering the number of pods per plant. Genotypes L_1 and C_2 with higher projection from AEC abscissa were found to be the least stable and genotypes L_2 and L_4 with low projection to be stable. C_2 the better performer was least stable. L_1, L_2 and L_3 had similar performance for number of pods per plant, but L_1 was less stable compared to the other two (Figure. 1c). This was in accordance with the results obtained from ranking of genotypes (Figure. 2c) where, L_2 and L_3 were found located very close towards the ideal genotype.

5.5.1.4 Number of seeds per pod

For number of seeds per pod L_2 was the better performer and C_2 was the least performer. Genotypes L_5 and C_1 with higher projection from the abscissa were considered to be the least stable while L_3, L_4 and C_2 with low projection were considered as the most stable for number of seeds per pod. C_2 was stable but poor in performance while L_1 was a better performer but not stable. It can be observed that the genotype L_3 was a better performer for number of seeds per pod with relatively high stability (Figure. 1d). Similar were the results obtained on ranking genotypes in terms of ideal genotype where L_3 was determined as a high performing and stable variety across test environments (Figure. 2d).

5.5.1.5 Grain yield per plant

On considering grain yield per plant, genotype L_1 was the good yielder and C_2 poor in yield. L_4 with highest projection was observed to be the least stable while L_1 with its lowest projection to be the most stable genotype for grain yield per plant. On a combined basis it can be interpreted that L_1 was the most stable and better yielder over three environments (Figure. 1e). The results were in accordance with the ones obtained

Table 20a. AMMI Stability Values (ASV) and Stability Index (SI) of the genotypes

Genotypes	Days to first flowering					Days to last harvest					Number of pods per plant				
	Mean	rY	ASV	rASV	SI= rASV + rY	Mean	rY	ASV	rASV	SI= rASV + rY	Mean	rY	ASV	rASV	SI= rASV + rY
L_1	39.35	4	1.06	5	9	88.37	1	0.18	1	2	43.41	3	0.88	7	10
L_2	39.08	3	0.14	2	5	86.04	2	0.32	2	4	43.07	4	0.46	3	7
L_3	39.53	5	1.46	7	12	79.05	7	1.29	7	14	43.59	2	0.35	2	4
L_4	39.91	7	0.46	3	10	84.35	5	0.50	4	9	38.30	6	0.20	1	7
L_5	38.83	2	0.13	1	3	85.67	4	0.62	5	9	38.75	5	0.51	4	9
C_1	39.57	6	0.58	4	10	81.23	6	0.37	3	9	30.69	7	0.65	5	12
C_2	38.66	1	1.22	6	7	85.73	3	0.82	6	9	55.02	1	0.71	6	7

Table 20b. AMMI Stability Values (ASV) and Stability Index (SI) of the genotypes

Genotypes	Number of seeds per pod					Grain yield per plant (g)					Protein content (%)				
	Mean	rY	ASV	rASV	SI= rASV + rY	Mean	rY	ASV	rASV	SI= rASV + rY	Mean	rY	ASV	rASV	SI= rASV + rY
L_1	17.67	3	0.56	4	7	140.50	1	3.09	6	7	24.33	2	1.60	7	9
L_2	18.33	1	0.37	3	4	133.21	2	1.87	4	6	24.77	1	0.62	3	4
L_3	18.01	2	0.75	5	7	121.49	3	0.44	2	5	20.66	5	0.77	4	9
L_4	16.67	4	0.09	1	5	105.44	5	0.79	3	8	23.14	3	0.78	5	8
L_5	16.03	5	0.12	2	7	105.53	4	0.41	1	5	19.55	7	1.36	6	13
C_1	15.39	6	0.96	7	13	91.31	6	3.55	7	13	19.99	6	0.28	1	7
C_2	14.68	7	0.76	6	13	84.51	7	2.57	5	12	21.01	4	0.57	2	6

Table 21. Total scores and ranking of genotypes (AMMI model)

Genotypes	Total score	Rank
L_1	44	2
L_2	30	1
L_3	51	5
L_4	47	4
L_5	46	3
C_1	64	7
C_2	54	6

from ranking of genotypes where the genotype L_1 was determined as the stable best performer (Figure. 2e).

5.5.1.6 Protein content

For protein content, genotype L_3 was the better performer and C_2 was the poor performer. Genotype L_4 was found to be the most stable with lowest projection. On the contrary, L_5 with the highest projection was regarded as the least stable. L_5 being a better performer was the least stable and L_4 was the most stable but an average performer for protein content (Figure. 1f). The result was in slight disagreement with the ones obtained while ranking of genotypes (Figure. 2f) where L_4 was observed to be the stable and superior performing genotype across test environments.

In the present study, the first two principal components (PC) explained more than 80% of the total variation. When the first two PCs explain more than 60% of the variability in the data, then it can be inferred that the biplot sufficiently approximates the variability in G x E data (Yang *et al*., 2009). Hence the biplots were effective in representing the variability present in data collected over three locations. The highest performing genotype may not always be the stable one. This was evident from the observations of L_1 for days to last harvest, C_2 for number of pods per plant, L_1 for number of seeds per pod and L_5 for protein content. It was also observed that genotypes showing stability for one trait failed while considering other traits. This can be explained by the fact that each trait is controlled by a different set of genes which when under the influence of environment, the cumulative effect of each set will vary accordingly (Dehghani *et al*., 2006).

Genotypes located closer to the ideal genotype are considered as the most desirable one. Based on this criteria, all the genotypes were found desirable for days to first flowering with its best performance at environment 3 and near average performance at environment 1 and environment 2 (Figure. 17a). L_5 was the most desirable genotype for days to last harvest with its best performance at environment 3 and above average stability at environment 1 and environment 2 (Figure. 17b). For number of pods per plant, L_2 and L_3 were the desirable genotypes with the best performance at environment 1 and above average performance at environment 2 and

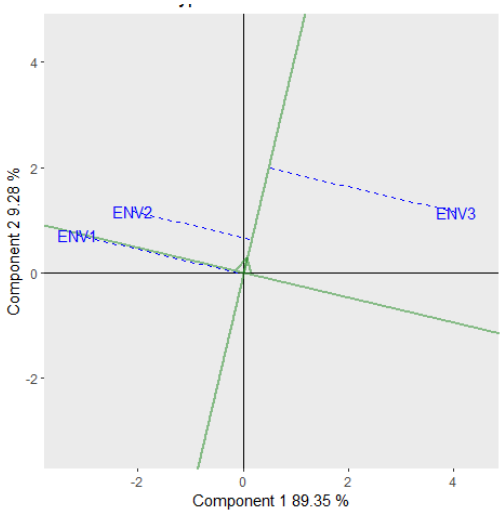


Fig. 17a. Days to first flowering, selected genotype: L_4

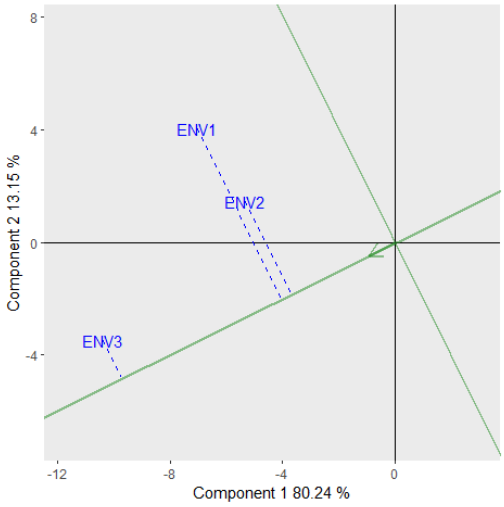


Fig. 17b. Days to last harvest, selected genotype: L_5

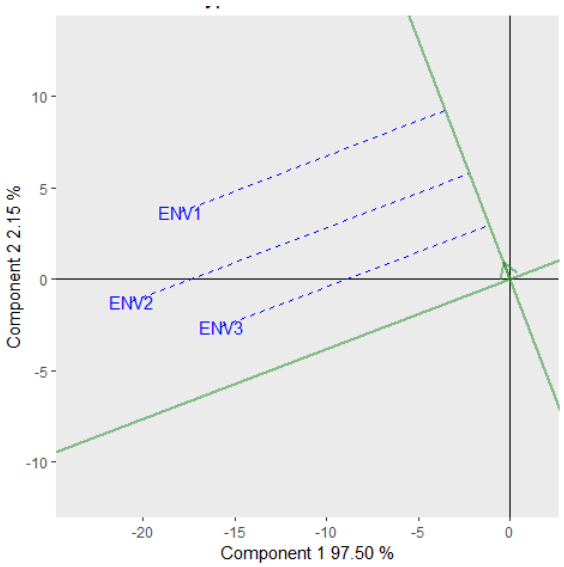


Fig. 17c. Number of pods per plant, selected genotype: L_2 and L_3

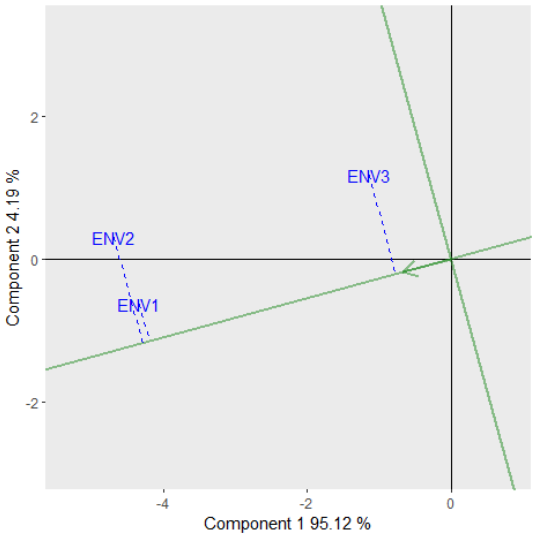


Fig. 17d. Number of seeds per pod, selected genotype: L_3

Fig. 17a to Fig. 17d. Ranking of environments based on the best performing genotype

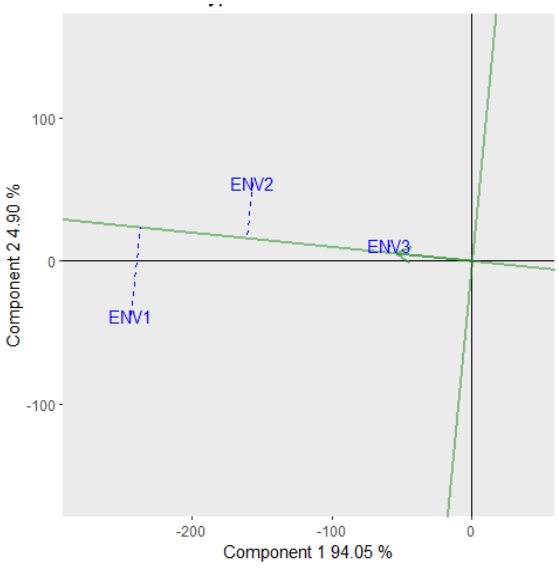


Fig. 17e. Grain yield per plant, selected genotype: L_1

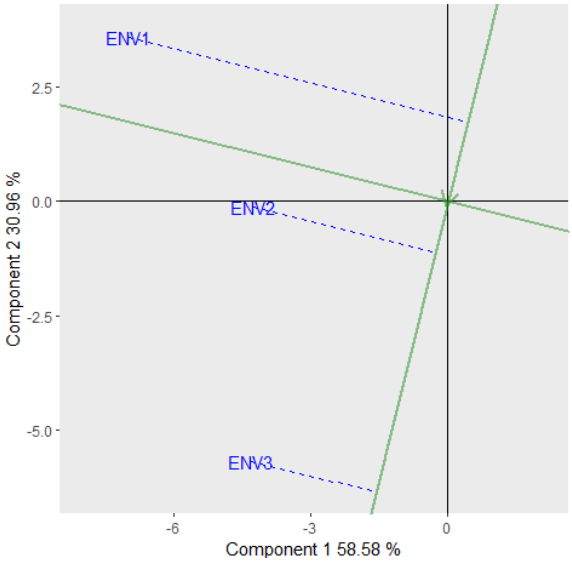


Fig. 17f. Protein content, selected genotype: L_4

Fig. 17e and Fig. 17f. Ranking of environments based on the best performing genotype

environment 3 (Figure. 17c). L_3 was observed as the most desirable genotype for number of seeds per pod with its better performance at environment 1 and environment 2 and near average stability at environment 3 (Figure. 17d). L_1 the most desirable genotype for grain yield per plant performed better in environment 1 followed by above average performance in environment 2 and near average performance at environment 3 (Figure. 17e). L_4 was observed to be the most desirable genotype for protein content performed best in environment 3, near average at environment 2 and below average at environment 1 (Figure. 17f). The above observations suggested that the order of genotypes on the basis of their performance varied according to the environment or there exist crossover GE interaction.

High crossover GE interaction was observed wherein the most ideal genotype for grain yield SPH 1606, performed best at Buldana, while near average yielded at Mauranipur and Bhavanisagar, and lower than average yield at Deesa (Rakshit *et al*., 2014).In a study conducted by Kaya *et al*. (2006), different genotypes produced highest grain yield in different environments. They observed that genotypes G7, G17 and G20 (Gerek-79) possessed the highest yield in environments E4 (Eregli), E8 (Uflak) and E3 (Obruk), respectively. In a study conducted on lentil (*Lens culinaris* Medik) it was observed that the best genotype in one location was not always so in other test locations (Sabaghnia *et al*., 2008).

In a study conducted on sixteen genotypes of cowpea at seven environment so as to evaluate the genotype x environment interactions through GGE biplot it was identified that variety TVU was the most stable with mean yield above mean grain yield of the genotypes (Simion *et al*., 2018).

A study was conducted to evaluate genotype by environment interactive effects and yield stability among elite cowpea selections derived by gamma irradiation and the biplot explained 75.57 per cent of the total variation observed of which 63.57 per cent was explained by the first principal component (PC1) while the second principal component (PC2) explained 12 per cent (Horn *et al*., 2018).

5.5.2 Evaluation of environment

Relationship among the environments were studied and combined analysis over three locations for days to first flowering, days to last harvest, number of pods per plant, number of seeds per pod, grain yield per plant and protein content showed that majority of the angles between their vectors are acute. Acute vector angles suggest closer relationship among the environments and non existence of crossover GE (Yan and Tinker, 2006). Therefore it can be inferred that majority of the environments are highly correlated with an exception between environment 1 and environment 3 as well as between environment 2 and environment 3 for days to first flowering which was obtuse (Figure. 3a). This indicated strong negative correlation between the environments and existence of crossover GE. In a study conducted by Rakshit *et al.* (2012), majority of the locations were found to be highly correlated with an exception between Udaipur and Deesa for grain yield and between Buldhana and Deesa for harvest index. In a study conducted by Fan *et al.* (2007) for evaluating the yield stability of maize in multi environment trial, mixture of crossover as well as non-crossover types of G x E interaction was obtained.

5.5.3 Which-won-where analysis

Which-won-where analysis is one among the exclusive features of GGE biplot that enables to study the G x E interactions, the mega environment differentiation and the specific genotype adaptation through graphical representation (Oral *et al*., 2018). A polygon is formed by joining the farthest genotypes. Genotypes at the vertices of the polygon performs best or poorest in one or more environments. The genotype at the vertex of the polygon performs best in the environment falling within the sectors (Yan and Tinker, 2006). Out of the six which-won-where biplots constructed, it can be observed that the biplots for days to first flowering and number of pods per plant produced polygons with few vertices and were not well distributed. Hence being less informative they were not considered further.

5.5.3.1 Days to last harvest

For the days to last harvest it was observed that genotypes L_4, L_5 and C_2 performed best in environment 3 while genotype L_1 and L_2 performed best in

environment 1 and environment 2 (Figure. 4b). The equality line dividing the biplot partitioned the test environments into two mega-environments: one with environment 1 and environment 2 consisting of genotypes L_1 and L_2 as the winning genotypes and the other with environment 3 with L_4, L_5 and C_2 as the winning genotype.

5.5.3.2 Number of seeds per pod

For the number of seeds per pod it was observed that genotypes L_2 and L_4 performed best in environments 2 and 3. The equality line dividing the biplot partitioned the test environments into two mega-environments: one with environment 2 and environment 3 comprising of genotypes L_2 and L_4 as the winning genotypes for number of pods per plant and the other with environment 1 with no winning genotypes (Figure. 4d).

5.5.3.3 Grain yield per plant

For grain yield per plant, the environments were not separated and belonged to one sector of biplot with genotype L_1 performing best in all the three environments (Figure. 4e).

5.5.3.4 Protein content

For protein content, the equality line accommodated each one of the environments to three different sectors with L_3, L_4 and L_5 as the winning genotype in environment 3 for protein content (Figure. 4f).

In which-won-where analysis, for each character the environments were partitioned into mega-environments and winning genotypes for each mega-environment were determined.

In a study conducted by Dehghani *et al*. (2006), three mega-environments for Barley were identified through biplot analysis. The first mega-environment contained locations Khoy, Mashhad, Miandoab, Karaj and Nyshabour, where genotype Bahtim7-D1/79-w40762 was the winner. The second mega-environment contained locations Tabriz, Hamedan, Ardabil, and Arak, where genotype Walfajre/W1-2291 was the winner. The third mega-environment containing the location of Zanjan had 73-M4-30 as the winner.

In an experiment conducted by Owusu *et al*. (2020) to assess the yield stability of eight advanced breeding lines of cowpea and to identify mega-environments for cowpea production in Ghana, the genotypes were evaluated across five environments and the genotypes SARI-6-2-6 and IT07K-303-1 were adapted to Damongo, Nyankpala, and Tumu, whereas the genotype SARI-2-50-80 was adapted to Yendi and Manga.

In a study conducted to evaluate genotype by environment interactive effects and yield stability among elite cowpea selections derived by gamma irradiation, genotypes G3, G6, G9, G24, and G29 were situated at the corners of the "which won where" polygon and indicated that they were outstanding genotypes in particular environments. Among these genotypes, G9 was the highest yielding genotype in all the test environments (Horn *et al*., 2018).

5.5.4 Overall stability

On ranking of genotypes it was observed that all the genotypes were equally stable for days to first flowering over three environments. Genotypes L_2 and L_5 were the stable and superior performing ones for days to last harvest while it was L_1, L_2 and L_3 for number of pods per plant. L_3 was determined as the best and stable performing genotype for number of seeds per pod and L_1 as the best and stable performing genotype for grain yield per plant. For protein content, the most stable genotype with better performance was genotype L_4. On an overall basis it can be concluded that L_1, L_2 and L_3 as the most stable and promising genotypes.

Comparison of results from stability analysis by GGE with Eberhart and Russell and AMMI model showed that the most stable and promising genotypes were the same L_1 and L_2 by all the three model

Summary

6. SUMMARY

An experiment entitled "Genotype x environment interaction in advanced breeding lines of cowpea (*Vigna unguiculata* (L.) Walp.)" was carried out at the Department of Plant Breeding and Genetics, College Of Agriculture, Vellanikkara during February 2021- May 2021. The study was undertaken with an objective of assessing the genotype x environment interaction in advanced breeding lines of cowpea. The study was conducted at three different locations namely RARS Pattambi, CoA Vellanikkara and RRS Vyttila. The study emphasised on the development of high yielding and stable genotypes of cowpea to be used as a dual purpose type (both as grain purpose type and as vegetable purpose type). Important findings from the study are summarised below.

Performance of cowpea genotypes under environment 1

- Cowpea cultures exhibited wide variability in yield and other traits at environment 1 (RARS, Pattambi)
- Low phenotypic (PCV) and genotypic (GCV) coefficient of variation was observed for the traits of days to first flowering, days to first harvest, days to last harvest and protein content (%)
- High GCV and PCV was observed for grain yield per plant (g)
- The magnitude of difference between PCV and GCV was high for the character plant height (cm) and number of branches suggesting that these traits are largely influenced by environment with little role of their genetic constitution on the expression of these characters
- Additive gene action was observed for number of pods per plant, length of pod, pod weight, number of seeds per pod, test weight and grain yield per plant since the characters had high heritability and high genetic advance
- Non additive gene action was prominent in days to first flowering, days to first harvest, days to last harvest and protein content (%)
- Dominance of environmental effect as indicated by low heritability coupled with low genetic advance was observed for plant height (cm)

Performance of cowpea genotypes under environment 2

- Cowpea genotypes exhibited significant variation for all the characters studied except for plant height in the second environment (CoA, Vellanikkara)
- High PCV and GCV was observed for grain yield per plant (g) and high PCV was observed for number of pods per plant
- Low PCV and GCV were observed for days to first flowering, days to first harvest, days to last harvest and protein content (%)
- The magnitude of difference between PCV and GCV was high for plant height (cm) and number of branches per plant indicating that these characters are governed by environment than by their genotype
- The magnitude of difference between PCV and GCV was low for the traits pod length (cm), pod weight (g), number of seeds per pod, test weight (g) and protein content (%) indicating that the traits are controlled by genotype than the environment
- High heritability coupled with high genetic advance as per cent of mean was observed for number of pods per plant, length of pod (cm), pod weight (g), number of seeds per pod, test weight (g) and grain yield per plant (g) and hence can be concluded that these traits are controlled by additive gene action
- Non additive gene action was found in the characters days to first flowering, days to first harvest and protein content (%)
- Low heritability along with low genetic advance was observed for plant height (cm) and number of branches which shows the predominant effect of environment over these traits

Performance of cowpea genotypes under environment 3

- Cowpea genotypes exhibited significant variation for all the characters studied except for plant height and number of branches in the third environment (RRS, Vyttila)
- High PCV was observed for plant height (cm) while moderate PCV and GCV were observed for number of pods per plant, length of pod (cm), pod weight (g), test weight (g) and protein content (%)

- Predominance of environmental effects in the expression of characters, plant height (cm) and number of branches as indicated by the large difference between PCV and GCV was observed
- Additive gene action was observed for number of pods per plant, length of pod (cm), pod weight (g), test weight (g) and protein content (%)
- Non additive gene action was observed in days to first flowering, days to last harvest, number of seeds per pod and grain yield per plant (g)
- Low heritability with low genetic advance was observed in plant height (cm) and number of branches indicated the prominent effects of environment on these traits

Comparison of genetic components over three environments

- Based on the observation from all the three environments, it can be inferred that number of pods per plant, length of pod (cm), pod weight (g) and test weight (g) were found to be controlled by additive gene action suggesting further possible improvement of these traits through selection
- The character days to first flowering, days to first harvest, days to last harvest and protein content (%) were under the influence of non additive gene action under two environments indicating the inefficiency of these traits towards selection
- The traits, plant height (cm) and number of branches were greatly under the influence of environment in two and three locations

Bartlett's test for homogeneity of error variance

- Error variance was found to be homogenous for only six characters among the twelve characters considered
- The six characters namely days to first flowering, days to last harvest, number of pods per plant, number of seeds per pod, grain yield per plant (g) and protein content (%) were proceeded further with pooled analysis of variance

Pooled analysis of variance

- Pooled analysis of variance revealed significant difference between genotypes for the six characters pooled except for days to first flowering

- Environment was found to be significant for the six characters from pooled analysis of variance
- Genotype x Environment (G x E) interaction was found to be significant for the six characters considered

Stability analysis: Eberhart and Russell model

- Analysis of variance for Eberhart and Russell model revealed significant difference between genotypes for all the characters except for days to first flowering
- All the genotypes exhibited non significant bi as well as S^2di values for the character days to first flowering and hence all the genotypes were considered as stable for the character days to first flowering
- Genotypes L_1 and L_2 with non significant bi and S^2di values and extended days to last harvest can be selected as stable and better performing for the character days to last harvest
- Genotypes L_2 and L_3 with non significant bi and S^2di values with more than forty number of pods per plant can be selected as stable for the character number of pods per plant
- Genotypes L_1, L_2 and L_3 with non significant bi and S^2di values with more than seventeen seeds per pod can be selected as stable and better performing genotypes for the character number of seeds per pod
- Genotypes L_1 and L_2 with non significant bi and S^2di values can be selected as stable and better performing for the character number of seeds per pod
- Genotypes L_1, L_2, L_3 and L_4 with non significant bi and S^2di values were determined as stable for the character protein content (%)
- Genotypes were ranked according to the criteria suggested by Arunachalam and Bandyopadhyay in 1983 and on an overall basis genotypes L_2, L_1 and L_3 were determined as the stable and better performing genotypes from Eberhart and Russell model

Stability analysis by Additive Main effects and Multiplicative Interactive effects (AMMI) model

- Analysis of variance for AMMI model revealed significant difference between genotypes for the six characters except for days to first flowering
- G x E interactions partitioned into IPCA 1 and IPCA 2 was found to be significant for the six characters
- Stability parameters of AMMI namely, mean and IPCA 1 were plotted against each other to construct AMMI biplot 1
- Stability parameters of AMMI namely, IPCA 1 and IPCA 2 were plotted against each other to construct AMMI biplot 2
- Biplot analysis for days to first flowering identified L_2 and L_5 as the stable and better performing genotypes
- Biplot analysis for days to last harvest identified L_1 and L_2 as the superior and stable performing genotype
- Genotype L_4 was determined as the stable and better performing genotype for the character number of pods per plant from biplot analysis
- Biplot analysis for number of seeds per pod identified L_2 as the stable and better performing genotype
- Genotype L_3 was identified as the superior and stable performing genotype for the character grain yield per plant (g)
- Biplot analysis identified L_4 as the stable and superior genotype for the character protein content (%)
- Overall stability so as to identify the most stable and better performing genotype from AMMI model was performed on the basis of stability index (SI) value and L_2, L_1 and L_5 were determined as the superior and stable genotypes

Stability analysis by Genotype main effects plus Genotype-by-Environment (GGE) model

- Mean performance and stability of the genotypes as well as ranking of genotypes on the basis of ideal genotype was performed

- All the seven genotypes were found to be stable as well as better performing for the character days to first flowering with their better performance at environment 3 (RRS, Vyttila)
- Genotypes L_2 and L_5 were determined as the stable and better performing genotypes for the character days to last harvest with their best performance at environment 3 (RRS, Vyttila)
- Genotypes L_2 and L_3 were identified as the stable and better performing genotype for the character number of pods per plant with its best performance at environment 1 (RARS, Pattambi)
- Genotype L_3 was determined as the stable and superior performing genotype for the character number of seeds per pod with its better and stable performance at environment 1 (RARS, Pattambi)
- L_1 was determined as the stable genotype for the character grain yield per plant (g) with its better performance at environment 1 (RARS, Pattambi)
- Genotype L_4 was determined as the stable and better performing genotype for the character protein content (%) with its better performance at environment 3 (RRS, Vyttila)
- Obtuse angle was observed between environment vector 1 (RARS, Pattambi) and environment vector 3 (RRS, Vyttila) as well as between environment vector 2 (CoA, Vellanikkara) and environment vector 3 (RRS, Vyttila) indicating strong negative correlation between the environments
- Which-won- where analysis was performed so as to interpret G x E interactions, for delineating mega environments and to assess specific adaptation of genotype towards a particular environment
- Which- won- where graphs were less informative for the characters of days to first flowering and number of pods per plant and hence was not considered further for analysis
- L_1 was determined as the winning genotype for the mega environment comprising environment 1 (RARS, Pattambi) and environment 2 (CoA, Vellanikkara) whereas genotype C_2 was determined as the winning genotype at environment 3 (RRS, Vyttila) for the character days to last harvest

- Genotype L_2 was determined as the winning genotype for the environment 2 (CoA, Vellanikkara) and environment 3 (RRS, Vyttila) for the character number of seeds per pod
- Genotype L_1 and L_2 were observed as the winning genotypes at all the three environments for the character grain yield per plant (g)
- For the character of protein content, genotypes L_3 and L_5 were identified as the winning genotypes at environment 3 (RRS, Vyttila)
- On an overall basis genotypes L_1, L_2 and L_3 were determined as the stable and better performing genotypes through GGE biplot model
- Comparison from all the three models (Eberhart and Russell model, AMMI model and GGE biplot model) revealed L_1 and L_2 as the most stable and better performing genotypes

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GENOTYPE x ENVIRONMENT INTERACTION IN ADVANCED BREEDING LINES OF COWPEA (*Vigna unguiculata* (L.) Walp)

By

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ABSTRACT OF THE THESIS

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ABSTRACT

Cowpea (*Vigna unguiculata* (L.) Walp) is an important tropical and subtropical annual legume crop grown for its green pods, grains and is also being used as a forage crop. It is one among the widely cultivated and consumed grain legumes, globally. As the grains contain high amount of protein (23.4 %) possessing better biological value on dry weight basis, cowpea is often considered as "vegetable meat". Its ability to fix atmospheric nitrogen and drought tolerance makes it a suitable component in all major cropping systems.

The present study entitled 'Genotype x environment interaction in advanced breeding lines of Cowpea (*Vigna unguiculata* (L.) Walp)' was an attempt to identify suitable and stable lines for general cultivation as a dual purpose type (both as grain purpose and vegetable purpose). Materials used for the study comprised of five cowpea cultures in stabilized F_7 generation developed as a result of pedigree selection from two crosses at the Department of Plant Breeding and Genetics, College of Agriculture, Vellanikkara, along with two check varieties, Anaswara and Kanakamony. The crop was raised during February 2021 to May 2021 over three environments *viz*., RARS Pattambi, CoA Vellanikkara and RRS Vyttila. Field experiments were laid out in plots of size 65 m^2 adopting randomized block design (RBD) with three replications. Observations were recorded on twelve characters: plant height (cm), number of branches, days to first flowering, days to first harvest, days to last harvest, number of pods per plant, pod length (cm), pod weight (g), number of seeds per pod, test weight (g), grain yield per plant (g) and protein content (%). All the observations were recorded at the time of harvest except for days to first flowering.

The recorded observations were subjected to individual, location wise analysis of variance (ANOVA) followed by pooled analysis of variance (pooled ANOVA) over three locations. From the pooled ANOVA, the characters that exhibited significant genotype x environment (G x E) interaction were further assessed for stability using three models of stability. The Eberhart and Russell model, the Additive Main effects and Multiplicative Interaction effects (AMMI) model and the Genotype main effects plus Genotype-by-Environment interaction effect (GGE) biplot were the three models of stability used for the study.

ANOVA revealed significant difference between lines for all the twelve characters considered. However, the Bartlett's test for examining the homogeneity of error variance was found to be significant only for six characters. These six characters *viz.*, days to first flowering, days to last harvest, number of pods per plant, number of seeds per pod, grain yield per plant and protein content were subjected to pooled ANOVA across three environments. Significant G x E interaction was observed in the six characters considered and were hence forwarded for analysing the stability.

The Eberhart and Russell model recognizes a stable genotype as the one with high mean performance, non-significant regression (bi) as well as deviation from regression (S^2di) values. The genotypes were ranked according to their mean values and stability parameters and it was observed that genotype L_2 with the lowest score was the most stable one followed by L_1 and L_3 respectively.

The AMMI model with its additive as well as multiplicative formulations could interpret the complex G x E patterns effectively through the AMMI biplots. Genotypes were scored and then ranked, according to their stability index (SI) value computed on the basis of rank of AMMI stability value (rASV) and the rank of performance for each character (rY). It was observed that L_2 with its lowest score ranked as the best and stable genotype followed by L_1 and L_5.

The GGE biplot model enabled effective interpretation of genotype x environment interaction by providing visual understanding of genotype and test-environment evaluation through mean versus stability graph, ranking of genotypes, ranking of environments and which won where analysis. On an overall basis it was identified from GGE biplot method that L_1, L_2 and L_3 were the most stable and superior performing genotypes.

Comparison of results from the three models of stability confirmed L_1 and L_2 as the most stable and promising genotypes. Hence these genotypes can be evaluated in large fields so as to confirm with the results and for checking the suitability of these genotypes to be released as a variety.

സംഗ്രഹം

പച്ച കായ്കൾക്കും ധാന്യങ്ങൾക്കും വേണ്ടി വളർത്തുന്ന ഒരു പ്രധാന വാർഷിക ഉഷ്ണമേഖലാ, ഉപ ഉഷ്ണമേഖലാ പയർവർഗ്ഗ വിളയാണ് വൻപയർ. ആഗോളതലത്തിൽ വ്യാപകമായി കൃഷി ചെയ്യുന്നതും ഉപഭോഗം ചെയ്യുന്നതുമായ ധാന്യ പയർവർഗ്ഗങ്ങളിൽ ഒന്നാണിത്. ധാന്യങ്ങളിൽ ഉയർന്ന അളവിലുള്ള പ്രോട്ടീൻ (23.4%) അടങ്ങിയിരിക്കുന്നതിനാലും, ഉണങ്ങിയ ഭാരത്തിന്റെ അടിസ്ഥാനത്തിൽ മെച്ചപ്പെട്ട ജൈവ മൂല്യമുള്ളതിനാലും വൻപയർ പച്ചക്കറികളിൽ വൻ പ്രാധാന്യം അർഹിക്കുന്നു. അന്തരീക്ഷ നൈട്രജൻ മണ്ണിൽ ഉറപ്പിക്കുവാനുള്ള കഴിവും, വരൾച്ച സഹിഷ്ണുതയും വൻപയറിനെ എല്ലാ പ്രധാന വിള സമ്പ്രദായങ്ങളിലും അനുയോജ്യമായ ഒരു ഘടകമാക്കുന്നു.

'വൻപയറിലെ (വിഗ്ന അങ്കിക്കുലേറ്റ (എൽ.) വാൽപ്പ്) നൂതനമായ ബ്രീഡിംഗ് ലൈനുകളുടെ വിവിധ പരിസ്ഥിതികൾക്ക് അനുയോജ്യമായ ഇനങ്ങളുടെ തിരഞ്ഞെടുക്കൽ' എന്ന തലക്കെട്ടിലുള്ള ഇപ്പോഴത്തെ പഠനം, പൊതുകൃഷിക്ക് അനുയോജ്യവും സുസ്ഥിരവുമായ ധാന്യ ആവശ്യത്തിനും പച്ചക്കറി ആവശ്യത്തിനും ഉപയോഗിക്കാവുന്ന ലൈനുകൾ തിരിച്ചറിയാനുള്ള ശ്രമമായിരുന്നു. വെള്ളാനിക്കരയിലെ കാർഷിക കോളേജിലെ പ്ലാൻഡ് ബ്രീഡിംഗ് ആൻഡ് ജനറ്റിക്സ് വിഭാഗത്തിലെ രണ്ട് സങ്കരങ്ങളിൽനിന്നുള്ള നിർദ്ധാരണത്തിലൂടെ വികസിപ്പിച്ചെടുത്ത എഫ് 7 തലമുറയിലെ അഞ്ച് പയർ ലൈനുകളും, രണ്ട് ചെക്ക് ഇനങ്ങളായ അനശ്വര കനകമണി എന്നിവയുമാണ് പഠനത്തിന് ഉപയോഗിച്ച വസ്തുക്കൾ. 2021 ഫെബ്രുവരി മുതൽ 2021 മെയ് വരെയുള്ള കാലയളവിൽ ആർ. എ. ആർ. എസ് പട്ടാമ്പി, സി. ഒ. എ വെള്ളാനിക്കര, ആർ. ആർ. എസ് വൈറ്റില എന്നിങ്ങനെ മൂന്ന് പരിതസ്ഥിതികളിലായാണ് വിള വളർത്തിയത്. 65 ചതുരശ്ര മീറ്റർ വലിപ്പമുള്ള പ്ലോട്ടുകളിൽ മൂന്ന് പകർപ്പുകളുള്ള റാൻഡമൈസ്ഡ് ബ്ലോക്ക് ഡിസൈൻ (ആർ ബി ഡി) സ്വീകരിച്ചുകൊണ്ട് ഫീൽഡ് പരീക്ഷണങ്ങൾ നടത്തി. ചെടിയുടെ ഉയരം (സെ.മീ.), ശാഖകളുടെ എണ്ണം, ആദ്യത്തെ പൂവിടുന്ന ദിവസം, ആദ്യത്തെ വിളവെടുപ്പ് ദിനം, അവസാനത്തെ വിളവെടുപ്പ് ദിനം, ഓരോ ചെടിയുടെയും കായ്കളുടെ എണ്ണം, കായ്കളുടെ നീളം (സെ.മീ), കായ് ഭാരം (ഗ്രാം), ഓരോ കായിലുമുള്ള വിത്തുകളുടെ

എണ്ണം, ടെസ്റ്റ് ഭാരം (ഗ്രാം), ഒരു ചെടിയിൽ നിന്നുള്ള ധാന്യ വിളവ് (ഗ്രാം), പ്രോട്ടീന്റെ അളവ് (%) എന്നീ പന്ത്രണ്ട് സ്വഭാവങ്ങളുടെ നിരീക്ഷണങ്ങൾ രേഖപ്പെടുത്തി.

രേഖപ്പെടുത്തിയ സ്വഭാവങ്ങൾ വ്യക്തിഗത, ലൊക്കേഷൻ തിരിച്ചുള്ള വേരിയൻസ് വിശകലനത്തിന് (അനോവ) വിധേയമാക്കി, തുടർന്ന് മൂന്ന് സ്ഥലങ്ങളിലുമായ സംയോജിത വേരിയൻസിന്റെ പ്രൂൾഡ് അനോവ) വിശകലനം നടത്തി. സംയോജിത വിശകലനത്തിൽ നിന്ന് സുപ്രധാന ജനിതകമാതൃക x പരിസ്ഥിതി (ജി x ഇ) ഇടപെടൽ പ്രദർശിപ്പിച്ച സ്വഭാവങ്ങൾ സ്ഥിരതയുടെ മൂന്ന് മോഡലുകൾ ഉപയോഗിച്ച് സ്ഥിരതയ്ക്കായി കൂടുതൽ വിലയിരുത്തി. എബർഹാർട്ട്, റസ്സൽ മോഡൽ, അഡിറ്റീവ് മെയിൻ ഇഫക്റ്റുകളും മൾട്ടിപ്ലിക്കേറ്റീവ് ഇന്ററാക്ഷൻ ഇഫക്റ്റുകളും (എഎംഎംഐ മോഡൽ), ജീനോടൈപ് മെയിൻ ഇഫക്റ്റുകൾ ജീനോടൈപ് x എൻവയോൺമെന്റ് ഇന്ററാക്ഷൻ ഇഫക്റ്റ് (ജിജിഇ) ബൈപ്ലോട്ട് എന്നിവയാണ് പഠനത്തിനായി ഉപയോഗിച്ച സ്ഥിരതയുടെ മൂന്ന് മോഡലുകൾ.

പരിഗണിച്ച പന്ത്രണ്ട് സ്വഭാവങ്ങൾക്കും ലൈനുകൾ തമ്മിലുള്ള കാര്യമായ വ്യത്യാസം അനോവ വെളിപ്പെടുത്തി. എന്നിരുന്നാലും, സ്വഭാവങ്ങളുടെ ഏകതാനത പരിശോധിക്കുന്നതിനുള്ള ബാർട്ട്ലെറ്റിന്റെ പരിശോധന ആറ് സ്വഭാവങ്ങൾക്ക് മാത്രമാണ് പ്രാധാന്യമുള്ളതായി കണ്ടെത്തിയത്. ആദ്യത്തെ പൂവിടുന്ന ദിവസം, അവസാനത്തെ വിളവെടുപ്പ് വരെയുള്ള ദിനം, ഒരു ചെടിയിലെ കായ്കളുടെ എണ്ണം, ഒരു കായ്യിലെ വിത്തുകളുടെ എണ്ണം, ഒരു ചെടിയിൽ നിന്നുള്ള ധാന്യ വിളവ്, പ്രോട്ടീന്റെ അളവ് എന്നിങ്ങനെ ഈ ആറ് സ്വഭാവങ്ങൾ മൂന്ന് പരിതസ്ഥിതികളിൽ സംയോജിത അനോവയ്ക്ക് വിധേയമാക്കി. പരിഗണിച്ച ആറ് സ്വഭാവങ്ങളിൽ കാര്യമായ ജി x ഇ ഇടപെടൽ നിരീക്ഷിക്കപ്പെട്ടു, അതിനാൽ സ്ഥിരത വിശകലനം ചെയ്യുന്നതിനായി മുന്നോട്ട് കൊണ്ടുപോയി.

എബർഹാർട്ട് റസ്സൽ മോഡൽ സ്ഥിരതയാർന്ന ജനിതകരൂപത്തെ ഉയർന്ന ശരാശരി പ്രകടനം, പ്രാധാന്യമില്ലാത്ത റിഗ്രഷൻ അതുപോലെ റിഗ്രഷൻ മൂല്യങ്ങളിൽ നിന്നുള്ള വ്യതിയാനം എന്നിവയായി അംഗീകരിക്കുന്നു. ജനിതകരൂപങ്ങളെ അവയുടെ ശരാശരി

മൂല്യങ്ങളുടേയും, സ്ഥിരത പരാമീറ്ററുകളും അനുസരിച്ച് റാങ്ക് ചെയ്തു. ഏറ്റവും കുറഞ്ഞ സ്കോർ ഉള്ള ജനിതക തരം എൽ 2, തുടർന്ന് എൽ 1, എൽ 3 ആയും നിരീക്ഷിക്കപ്പെട്ടു.

എഎംഎംഐ മോഡലിന് അതിന്റെ സങ്കലനവും ഗുണിത ഘടകങ്ങളിലൂടെയും, ബൈപ്ലോട്ടുകളിലൂടെയും സങ്കീർണ്ണമായ ജി x ഇ ഇടപെടലുകളെ ഫലപ്രദമായി വ്യാഖ്യാനിക്കാൻ കഴിയും. എഎംഎംഐ സ്ഥിരത മൂല്യത്തിന്റെ റാങ്കിന്റെയും, ഓരോ പ്രതീകത്തിന്റെയും പ്രകടനത്തിന്റെ റാങ്കിന്റെയും അടിസ്ഥാനത്തിൽ അവയുടെ സ്ഥിരത സൂചിക മൂല്യം അനുസരിച്ച് ജനിതകരൂപങ്ങൾ സ്കോർ ചെയ്യുകയും റാങ്ക് ചെയ്യുകയും ചെയ്തു. ഏറ്റവും കുറഞ്ഞ സ്കോറുള്ള എൽ 2 മികച്ചതും സ്ഥിരതയുള്ളതുമായ ജനിതകരൂപമായി റാങ്ക് ചെയ്യപ്പെട്ടതായി നിരീക്ഷിച്ചു, തുടർന്ന് എൽ 1 ഉം എൽ 5 ഉം.

ജിജിഇ ബിപ്ലോട്ട് മോഡൽ ജി x ഇ സംവേദനത്തിന്റെ ഫലപ്രദമായ വ്യാഖ്യാനം പ്രാപ്തമാക്കി. ജനിതകമാതൃകയും പരീക്ഷണ-പരിസ്ഥിതി വിലയിരുത്തലും, ശരാശരിക്ക് എതിരായി സ്ഥിരതയുടെ ഗ്രാഫ്, ജനിതകമാതൃകകളുടെ റാങ്കിംഗ്, പരിതസ്ഥിതികളുടെ റാങ്കിംഗ്, ഏതാണ് വിജയിച്ചത്-എവിടെ വിശകലനം എന്നിവയിലൂടെ. മൊത്തത്തിലുള്ള അടിസ്ഥാനത്തിൽ, ജിജിഇ ബൈപ്ലോട്ട് രീതിയിൽ നിന്ന് എൽ 1, എൽ 2, എൽ 3 എന്നിവ ഏറ്റവും സ്ഥിരതയുള്ളതും മികച്ചതുമായ ജനിതകരൂപങ്ങളാണെന്ന് തിരിച്ചറിഞ്ഞു.