

ASSESSMENT OF GENETIC DIVERSITY AND VARIABILITY
FOR PRODUCTIVITY AND QUALITY TRAITS IN HORSE GRAM
[*Macrotyloma uniflorum* (Lam.) Verdc]

POORNIMA B. S.

DEPARTMENT OF GENETICS AND PLANT BREEDING
COLLEGE OF AGRICULTURE, VIJAYAPUR
UNIVERSITY OF AGRICULTURAL SCIENCES
DHARWAD – 580 005

JUNE, 2015

ASSESSMENT OF GENETIC DIVERSITY AND VARIABILITY
FOR PRODUCTIVITY AND QUALITY TRAITS IN HORSE GRAM
[*Macrotyloma uniflorum* (Lam.) Verdc]

*Thesis submitted to the
University of Agricultural Sciences, Dharwad
in partial fulfilment of the requirement for the*

Degree of

Master of Science (Agriculture)

in

GENETICS AND PLANT BREEDING

By

POORNIMA B. S.

DEPARTMENT OF GENETICS AND PLANT BREEDING
COLLEGE OF AGRICULTURE, VIJAYPUR
UNIVERSITY OF AGRICULTURAL SCIENCES
DHARWAD – 580 005

JUNE, 2015

DEPARTMENT OF GENETICS AND PLANT BREEDING
COLLEGE OF AGRICULTURE, VIJAYPUR – 586 101
UNIVERSITY OF AGRICULTURAL SCIENCES,
DHARWAD – 580 005

CERTIFICATE

This is to certify that the thesis entitled “ASSESSMENT OF GENETIC DIVERSITY AND VARIABILITY FOR PRODUCTIVITY AND QUALITY TRAITS IN HORSE GRAM [*Macrotyloma uniflorum* (Lam.) Verdc]” submitted by Ms. POORNIMA B. S., for the award of Degree of MASTER OF SCIENCE (AGRICULTURE) in GENETICS AND PLANT BREEDING to the University of Agricultural Sciences, Dharwad, is a record of research work carried out by her during the period of her study in this university under my guidance and supervision, and the thesis has not previously formed the basis of the award of any degree, diploma, associateship, fellowship or other similar titles.

DHARWAD
JUNE, 2015

(G. M. SAJJANAR)
CHAIRMAN

Approved by:

Chairman: _____
(G. M. SAJJANAR)

Members: 1. _____
(B. D. BIRADAR)

2. _____
(V. S. SURAKOD)

3. _____
(KASHIBAI KHYADAGI)

ACKNOWLEDGEMENT

With regards to sweet memories.....

Any tedious task is made light and smooth by God's grace. At this moment, I would remember 'the almighty god', who has made each impossible work a reality in my life. The fruit of which, I am expressing here.

I would consider myself lucky to have worked under the excellent guidance of Dr.G.M. SAJJANAR Principal Scientist and head, AICSIP on Sorghum, Regional Agricultural Research Station, Vijayapur, University of Agricultural Sciences, Dharwad and the esteemed chairman of my advisory committee without whose appreciation, constant encouragement, critical suggestion, valuable advice, keen interest, constructive criticism and everlasting patience throughout the endeavor and devoting her time amidst her busy schedule. This task would not have been accomplished. I would never forget her constant support throughout my career in moulding my personality by acting as teacher, counsellor and philosopher through her elderly advice. It is proud and privilege for me to be one of her student.

I avail this opportunity to express sincere thanks to my advisory committee consisting Prof. like Dr. B. D. BIRADAR Professor, Department of Genetics and Plant breeding, Agriculture college, Vijayapur. University of Agricultural sciences, Dharwad. Prof .V. S. SURAKOD Agronomist, AICRP on Dryland Agriculture, Regional Agricultural Research Station, Vijayapur, University of Agricultural Sciences, Dharwad and Dr. KASHIBAI KHYADAGI, Associate Professor, Department of Food Science and Nutrition, College of Agriculture, Vijayapur for their constant help, valuable suggestions during the investigation, sensible criticism in animating and ameliorating its manuscript and valuable counsel during the period of study and I owe them a lot for this small venture of mine.

I avail myself of this opportunity to express my sincere thanks to My seniors Mr. Deepak G. C., Siddarth Garla and Ishwar Boodi for the valuable suggestions and encouragement in pursuit of the study. I also express my sincere and heartfelt gratitude at all the staff members of Department of Genetics and Plant Breeding, UAS, Dharwad for their help and cooperation throughout the M. Sc. Programme. I never forget the enormous and timely help by Mahadev Nucchi Field Assistant, Sharu, Shabbu,

Thayamma, Shaila, Ramakka, Shilpa and other field workers, during the course of my research work

Very importantly, I would like to thank Dr. O. Sridevi Professor and Head Department of Genetics and Plant Breeding, Dr. Hunshal Dean (PGS), Technical Officer Dean (PGS) office, and all the staff of Dean (PGS) office for timely completing the office correspondence.

This thesis would be incomplete if do not reckon the love, affection and support of my beloved parents, Suresh B. and Shobha B. S., my brother Adarsh B. S., and other relatives without whose affection, care and blessings this task would not have been possible.

I have been highly fortunate in having many friends in whose company; I never felt the burden of studies. Their helping hand was evident at every stage of tension, anxiety and achievement. To mention the names of only a few petals this together as a flower scented my life with an elegant fragrance. I must begin with, Radha, Appaji, Bhagi, Bassu, Chandru, Mallu, Om, Sumith, Chummy, Shashi, Harsha, Gulzar, Tippeswamy and Bharath, and for their everlasting source of inspiration and love. Finally I am thankful to my batch mates, junior friends and senior friends of UG, Diploma and PG degree programme for their kind support.

I cannot express the role that whole lot of my friends played during those difficult steps I had gone through, cheer to friendship of Lacchi, Vijju, Shashi, Kavi, Vinu, Nethra, Sruthi, Sushmitha, Vidya, Preethi, Manasa, Roselin, and Manisha which has made my stay in college a memorable one in my life.

One last word; since it is practically impossible to list all the names who contributed contributions to my work, it seems proper to issue a blanket of thanks for those who helped me directly or indirectly during the course of study.

.....Omission of any names in this brief acknowledgement does not mean lack of gratitude.

VIJAYAPUR

JUNE, 2015

(POORNIMA B. S.)

CONTENTS

Sl. No.	Particulars
	CERTIFICATE
	ACKNOWLEDGEMENT
	LIST ABBREVIATIONS
	LIST OF TABLES
	LIST OF FIGURES
	LIST OF PLATES
	LIST OF APPENDICES
I.	INTRODUCTION
II.	REVIEW OF LITERATURE
	2.1 Genetic diversity analysis
	2.2 Variability parameters
	2.3 Correlation
	2.4 Path Coefficient
	2.5 Varietal evaluation for nutritional quality
	2.6 Qualitative characters studies
III.	MATERIAL AND METHODS
	3.1 Experimental location
	3.2 Experimental material
	3.3 Methodology
	3.5 Statistical analysis
IV.	EXPERIMENTAL RESULTS
	4.1 Analysis of variance
	4.2 Genetic diversity
	4.3 Genetic variability parameters

Sl. No.	Particulars
	4.4 Correlation studies
	4.5 Path coefficient analysis
	4.6 Evaluation of genotypes for quality traits
V	DISCUSSION
	5.1 Analysis of variance
	5.2 Genetic diversity analysis
	5.3 Genetic variability parameter
	5.4 Correlation coefficients
	5.5 Path coefficient analysis
	5.6 Screening genotypes for quality traits
	5.7 Performance of genotypes over check
VI	SUMMARY
VII	REFERENCES
	APPENDICES

LIST OF ABBREVIATIONS

%	:	Per cent
/	:	Per
° C	:	Degree Celsius
Anon,	:	Anonymous
ANOVA	:	Analysis of Variance
CV (P=0.05%)	:	Coefficient of variation at 5 per cent level
cm	:	Centimetre
<i>et al.</i>	:	And others
Fig.	:	Figure
g	:	Grams
GA	:	Genetic Advance
GAM	:	Genetic Advance as per cent of Mean
h^2b	:	Broad sense heritability
ha	:	Hectare
<i>i.e.</i> ,	:	That is
kg/ha	:	Kilogram per hectare
mha	:	Million hectares
mt	:	Million tonnes
N	:	North
No.	:	Number of
<i>Per se</i>	:	As such mean
S	:	South
<i>viz.</i> ,	:	Namely

LIST OF TABLES

Table No.	TITLE
1a	List of Horse gram germplasm lines used in the present study
1b	Details regarding local collections of horse gram used in the present study
2	Analysis of variance for yield and yield attributing characters in horse gram germplasm lines
3	Clustering pattern of germplasm lines of horse gram based on D ² analysis
4	Average intra and inter cluster distance among germplasm lines of horse gram for yield and yield related traits
5	Percent contribution of character towards total divergence in horse gram germplasm lines
6	Cluster means of germplasm lines of Horse gram for yield and yield related traits
7	Estimates of range, mean, variability, heritability and genetic advance for different characters of horse gram germplasm lines
8	Phenotypic correlation co-efficient between different traits in germplasm lines of horse gram
9	Direct and indirect effects on seed yield at phenotypic level in germplasm lines of horse gram
10	Evaluation horse gram genotypes for grain protein, micronutrients contents, plant nitrogen and plant protein content
11	Grouping of genotypes under different category for seed quality traits among horse gram germplasm lines
12a	Top ten genotypes identified for different traits among 111 germplasm lines of horse gram
12b	List of genotypes showing significantly better performance over check GPM-6 for various traits

LIST OF FIGURES

Figure No.	Title
1	Clustering pattern of 111 horse gram germplasm lines into different cluster
2	Graphical representation of estimates of percent contribution of different traits
3	Graphical representation of Estimates of GCV and PCV for productive traits
4	Graphical representation of Estimates Heritability and Genetic advance as per cent means for different characters
5	Phenotypic path diagram for yield and its related traits in horse gram germplasm lines

LIST OF PLATES

Plate No.	Title
1	General view of experimental plot of germplasm lines of horse gram
2	General view and varietal differences for maturity early v/s late among germplasm lines of horse gram
3	Difference in seed colour and seed size of germplasm lines of horse gram
4	Difference in stem colour of germplasm lines of horse gram

LIST OF APPENDICES

Sl. No.	Title
1	Meteorological data for the year 2014-15 and average data of 32 years (1981-2013) at RARS, Vijayapur
2	Mean values of the 13 characters for the 111 entries of horse gram germplasm lines
3	Qualitative characters observed in horse gram germplasm lines

I INTRODUCTION

Arid legumes form very important source of food and nutrients, rich in protein for human beings especially in the dryland regions. Horse gram (*Macrotyloma uniflorum* (Lam.) Verdc) is one among them which is an important component in the dryland crop production system, due to its ability to withstand drought with minimum management. Although it grows under a wide range of soil and climatic conditions but it is well known for its hardiness, adaptability to poor soil and adverse climatic conditions. Like other pulses it plays role as food & fodder (dual purpose), as green manure crop, as good cover crop in controlling soil erosion, enhancing soil fertility and having ability of fixing atmospheric nitrogen into the soil. It is usually grown as catch crop for late *kharif* or with the rains after a prolonged drought conditions and aberrant weather conditions.

India is the major country in the world growing horse gram crop. It is cultivated most extensively in southern India (Smartt, 1990) and the crop is indigenous to the southeastern regions of India. Globally horse gram is distributed in tropical Africa encompassing countries in East and North East Africa such as Sudan, Ethiopia, Zaire, Kenya, Tanzania, Zimbabwe, South Africa, Mozambique and Angola. In Asia, India is a major producer of horsegram. China, Philippines, Bhutan, Pakistan, Sri Lanka and few other countries in Asia also produce large amounts of horse gram. It is cultivated in small areas within Queensland in Australia.

It is considered that horse gram originated in South-East Asia and most probably in Peninsular India, where it is still an important cultivated crop. The region of maximum genetic diversity is considered to be in the Old World Tropics, especially in India and Himalayas (Zeven and de Wet 1982). This crop is native to different parts of India and is spread all over the country from Uttarakhand in North to Southern tip in Tamil Nadu and Gujarat in West to Bengal in East. It is extensively grown in Karnataka, Andhra Pradesh, Tamil Nadu, Madhya Pradesh and parts of Maharashtra, Bihar, Orissa and, to some extent, in hilly slopes of Himachal Pradesh and Uttar Pradesh. Horse gram is cultivated over an area of 2.1 million hectares with production of 1.07 million tonnes of grain and average productivity of 507 kg/ha (Anon., 2007-2012). The yield per hectare is highest in Kerala (829 kg/ha). The largest area is found in Karnataka (1.22 million hectares), and the state is the major producer of horse gram (0.62 million tonnes). The crop is raised both during *kharif* and *rabi* seasons with 58.7 area in *kharif* and 41.3% in *rabi* seasons in 2005-06.

Grains serve as excellent source of protein, minerals (iron, calcium, molybdenum), and polyphenols which have high antioxidant capacity (Ramesh *et al.*, 2011), and hemagglutinin which is a substance found in antibodies and autoimmune functions. Horse gram is having highest calcium content among all the established pulses and arid legumes. Recent studies have confirmed that horse gram is having anti-hyperglycemic and plays role in life style diseases like diabetics. Apart from its good nutritional composition, it has many therapeutic uses (to treat renal stones, piles, edema etc.), which makes it as potential food source for future. It is consumed as a whole seed, as sprouts, or as whole meal by a large population in rural areas of Southern India.

The horse gram grain can also be used as a concentrated feed for cattle, and fodder being rich in protein, is widely used as a feed to milch animals and horses. The protein content of 18-29 per cent puts the crop in equivalence to the other pulse crop that are commonly grown in tropics. Horse gram fodder contain around 12 % protein and considerable amount of fiber with good digestibility. The palatability of the fodder is very much liked by the milch animals. Lightly boiled or parched grain and boosa are used as concentrate for milch animals. It also makes excellent hay and green manure (Nagaraja, 1997).

When monsoon is delayed too much, the only crop that can be thought of is horse gram. It can produce a normal crop by utilizing rainfall of the tail end part of the south west monsoon and the early morning fog that falls during November-December. Consequently it has become popular as a crop for August–September sowing. It is also grown as a relay crop with maize, jowar and ragi. The average yield of the crop is low because it is usually grown on poor soils where no other pulse crops can be grown (Nagaraja, 1997).

In spite of greater adoptability and its multiplicity of uses, work on genetic improvement is meager. Considering its inherent abilities, high yielding varieties certainly play major role in enhancing the productivity under dryland conditions. All the varieties developed/recommended to date are mainly by single plant selection from locals. There is greater need to increase the yield and quality of this crop by breeding while understanding the genetic makeup of this crop. Hence, it is essential to generate new variability through hybridization and mutation to strengthen the breeding programs in horse gram which otherwise has been neglected.

Assessment of genetic diversity and variability existing in the germplasm collection for yield and its attributes is prerequisite for any successful breeding programme. This could be known through the precise estimation of genotypic and phenotypic co-efficient of variances for various traits. Diversity analysis helps in the cluster formation of similar and diverse genotypes. Partitioning of the observed phenotypic variability into its heritability and non-heritable components will help the breeder in selection programme.

In addition, information on the degree and direction of correlation of yield with other characters would help in selecting desirable genotypes. Correlation co-efficient merely describe the existence of association between pairs of variable characters. It is rather difficult to explain a system of correlation, as the indirect association of character increases. As correlation is the sum of direct and indirect effects of an independent character on dependent character, path co-efficient analysis which provides this information become necessary. So that the relative influence of each component character on the yield could be assessed. Selection indices which indicate the weightage to be given to different characters in selecting for a dependent character like yield would be further helpful.

The knowledge of degree of variability and diversity and association existing between yield and its attributes and further among the yield components is very important for selection. Considering the importance of the crop and the above indicated facts, present study was planned to assess the genetic variability, genetic diversity and associations among horse gram germplasm lines maintained at U.A.S Dharwad involving released varieties, single plant selection derivatives & local collections for various qualitative and quantitative traits. As horse gram is an important source as grain and plant protein, it is essential to study varietal differences for identification of genotypes with high protein content.

Objectives

1. To assess the genetic variability and diversity for yield and yield components among horse gram germplasm lines.
2. To study the association between yield and yield components among the genotypes.
3. To assess the selected genotypes of horse gram for grain nutrients and plant nitrogen content

II REVIEW OF LITERATURE

Horse gram [*Macrotyloma uniflorum* (Lam.) Verdc formerly *Dolichos biflorus* L.] is an excellent source of proteins & other nutrients, thus supplementing the staple cereal based diet, a good source of energy, minerals, antioxidants and vitamins. It is also used in Ayurvedic medicine for treating several ailments. In spite of all these, the cultivation of this pulse crop has not received due attention. It needs to be explored for many advantageous traits by development and cultivation of high yielding varieties. At present the productivity is low, which could be due to cultivation of local genotypes, their cultivation on poor or marginal soils etc. Breeding for high yielding varieties is hindered by narrow genetic variability within germplasm collection. Proper identification of diverse genotypes for hybridization offers the scope for generating potential genotypes that provide higher variability. Therefore, several investigators have studied horse gram for assessing genetic variability and diversity for choosing distinct parents for further breeding programme, grain nutrient for diet, plant nitrogen content estimation for green manure purpose and livestock feed as fodder, and also character association study.

A summary of literature related to the present study is given below under the following headings.

- 1 Diversity (D^2) analysis
- 2 Genetic variability, heritability and genetic advance
- 3 Correlation coefficients
- 4 Path analysis
- 5 Varietal evaluation for quality traits

2.1 Studies on diversity (D^2) analysis

One of the reasons for very low productivity in horse gram is limited variability (Maloo, 1999). The selection of genetically diverse parents for hybridization programmes is most crucial for generating genetic variability in the crop. Hence, it needs to be assessed the nature and magnitude of variability in the horse gram genotypes available. The present horse gram germplasm includes released varieties from different states, locally cultivated varieties and a germplasm collection, representing the diverse nature of the existing horse gram cultivars. Proper identification of diverse genotypes for hybridization offers the scope for generating

potential genotypes that provide higher variability. It is reported from genetic diversity analysis that selection of genotypes from the most divergent clusters may exhibit a high heterosis. Therefore, hybridization between the genetically diverse parents in breeding programmes may produce large variability and better recombinants in the segregating generation. Hence, several workers studied genetic diversity within available germplasm.

Ramkrishnan *et al.* (1978) reported that hundred seed weight and dry weight of nodular tissue are chief components to total divergence in horse gram. Ganeshaiah (1979) reported that days taken for flowering, days to maturity, number of pods per plant and hundred seed weight were the contributions towards the discrimination of the entries to total divergence. Ghorpade (1985) analyzed data on morphological and maturity variation. It revealed that 216 varieties of horse gram studied could be classified into 3 groups on the basis of days to 50 per cent flowering.

Sunil *et al.* (2009) reported that nine characters contributing to seed yield were observed on 20 accessions of horse gram, and subjected to genetic divergence analysis. Genotypes were grouped into five clusters. Genetic diversity was not related to eco-geographical distribution. The greatest inter-cluster distance separated clusters II and V, followed by clusters IV, and V, III and IV. Entries in clusters V and II appear suitable as parents for horse gram improvement. The Rayalaseema region is the source of useful variation for days to flowering, maturity and yield.

Genetic divergence among 50 accessions was estimated by Dasgupta *et al.* (2005). The genotypes formed 10 different clusters. No relationship was found between genetic divergence and geographic origin in the formation of clusters. Wide variability among the germplasm was noticed. Flowering duration, seed yield per plant, 100-seed weight, soluble protein percentage and days to flowering were the major contributors to divergence.

Cluster analysis among 35 genotypes of horse gram grouped the genotypes into 9 clusters (Kalia and Dogra, 2006). At the inter cluster level, crop growth rate contributed maximum towards genetic divergence followed by seed yield and harvest index, whereas at genotypic level, seed yield per plant contributed maximum towards genetic divergence followed by harvest index and pods per plant. Cluster analysis in another study revealed that plant height, number of days to 50% flowering, number of days to maturity, number of primary

branches per plant, number of pods per plant, seed yield per plant, biological yield per plant, and harvest index were important characters contributing to maximum genetic divergence.

Singhal *et al.* (2010) worked on genetic divergence and revealed the existence of wide diversity among the genotypes. On the basis of the results obtained, these 88 genotypes were grouped into ten clusters. The varieties belong to clusters VIII and IX having great statistical distance may be selected for hybridization programme as they are expected to produce good segregants.

Prakash *et al.* (2010) studied on 100 germplasm lines that were grouped into eighteen different clusters based on D² analysis revealed that Cluster I was the largest with 19 genotypes followed by cluster III (14) and cluster V (13). Cluster XII showed the maximum mean value for seed yield. The intra and inter cluster divergence among the genotypes was varying in magnitude. Further it was implied that intra-cluster distance was maximum in cluster III followed by clusters XI and XIII. The widest inter cluster distance was noted between cluster XII and XV giving scope for hybridization programme with improvement of genotypes. The distance between clusters X and V was minimum indicating close relationship between those clusters. They also reported that character contribution in cluster divergence revealed that the maximum contribution in cluster formation was attributed by seed yield (94.93) followed by number of pods per plant (3.17), plant height (1.21) and number of seeds per pod (0.65), whereas, remaining traits played minor role in cluster divergence.

Arun *et al.* (2010) studied on a total of 54 horse gram landraces collected from three altitudinal zones (lower hills, mid hills and higher hills) of Himalayan region, and these genotypes were characterized and evaluated for nine quantitative characters. Accessions collected from lower and higher hills were more diverse and differed significantly from mid hills accessions for characters viz., days to flowering, days to physiological maturity, plant height and grain yield per plant. It reveals a less variability among the landraces collected from same altitudinal group but high variability among the landraces collected from different altitudes.

Geetha *et al.* (2011) studied on genetic divergence among 100 germplasm accessions and these were grouped into sixteen different clusters. The cluster VI was the largest with 43 genotypes followed by cluster I (14) and cluster XV (11). The cluster XIV showed the maximum mean value for seed yield followed by cluster VII. The intra and inter cluster

divergence among the genotypes was varying in magnitude. Further it implies that the intra-cluster distance was maximum in cluster I followed by clusters II and XV. The widest inter cluster distance was noted between cluster I and XIII. The distance between clusters X and XII was minimum.

Kanaka *et al.* (2014) reported using Mahalanobis D² statistics. Grouped all the 23 cultivars of horse gram into six clusters. The cluster's strength varied from single/solitary genotypes to fourteen genotypes. Cluster I had fourteen cultivars, cluster II had five cultivars and the other four clusters (III, IV, V and VI) had a single genotype each. The inter cluster distance between cluster IV and cluster V was the maximum. The characteristic of cluster V was that it showed a considerably higher mean value for leaf width, the numbers of primary branches per plant and secondary branches per plant, seed yield per plant, test weight and seedling length. The intra cluster distance ranged from 0 (clusters III, IV, V and VI) to 15.17 (cluster I). The maximum intra cluster distance in cluster I indicated that genotypes in this cluster were relatively more diverse than the genotypes within other clusters. The other high inter cluster distances were noticed between clusters IV and VI (61.20), clusters III and VI (59.95), and clusters III and V (57.72).

Thirty eight horse gram accessions were characterized and evaluated during *post rainy* 2005-06 and 2006-07 for six qualitative and nine quantitative traits by Sunil *et al.* (2014). All the accessions had trailing growth habit and determinate growth but showed variation in vigour, stem colour, flower colour and seed colour. Plant height, number of primary branches, number of clusters per plant and seeds per pod were found to be significant traits. The multivariate cluster analysis grouped the accessions into two clusters. Promising lines for number of clusters per plant and seeds per pod were identified based on analysis.

2.2 Genetic variability, heritability and genetic advance

All the self-pollinated crops are characterized by two important virtues a) extreme homozygosity found within populations and b) variability found between the populations. Homozygosity assures the fixed nature of the character selected whereas variability between populations helps in selection for superior population. The plant breeder has to progress in improving a plant type by initial step the variability existing between the populations. Later, the

success of the selected population depends on upon the stability of the characters under selection. Thus, understanding of the genetic makeup of the crop is basic for a plant breeder.

The apparent variability in a crop can be divided into i) variability due to genotypes, ii) variability due to environment and iii) variability due to interaction between genotypes and environment. The genotypic heritability is the actual heritable component of the apparent variability and is expressed as the heritability. So heritability is defined as the proportion of the phenotypic (apparent) variability that is due to genotype. The genotypic variability is the result of additive and non additive effects. So heritability is defined in the two ways by Fisher *et al.*, 1932. Pense, 1940. Lush, 1949 and Mather, 1949. Lush (1949) has proposed heritability as the ratio of additive variance to total variance in narrow sense. The heritability in broader sense was proposed by Hanson *et al.* (1956) as the ratio of genetic variance to the total variance.

However, the gain from selection for a particular character is the function of its heritability, selection pressure and the variance existing in the basal population and thus the genetic gain was expressed by Burton and Devan (1953) as the product of heritability, phenotypic standard deviation and selection differential. Though, the heritability indicates the relative value of the selection based on phenotypic expression of a character, the genetic advance is more useful in judging the actual value of selection as shown by Johnson *et al.* (1955).

Johannsen (1909) studied the contribution of genetic and environmental components to the total variance, and showed that genetic components are the relatively constant in every generation, in the self-pollinated crops. Nilson Ehle (1909) and East (1916) confirmed the results obtained by the Johannsen (1909). Powers (1942) separated genotypic variance from the total variance since the studies on the heritability, genetic advance (GA) and their variance components are estimated for most of the yield contributing characters.

Sreekantaradya *et al.* (1975) studied 48 varieties of horse gram for variability and observed highest phenotypic and genotypic variance for plant height, pods per plant and seeds per pods. The estimates of phenotypic co-efficient of variation and genotypic co-efficient of variation were also high for these characters. Seed yield exhibited moderate variance. High heritability was observed for seeds per pod and pods per plant. Moderate

heritability and genetic advance was observed for seed yield. Genetic advance (GA) was highest for seeds per pod followed by pods per plant.

Aggarwal and Kang (1976) reported low values of PCV, GCV and low values of heritability associated with low genetic advance for plant height and high heritability and high genetic advance for number of branches per plant, pods per plant and seed yield and moderate heritability for hundred seed weight. For days to maturity, low values of PCV, GCV and high heritability with moderate genetic advance were reported.

Shivashankar *et al.* (1977) reported low values of PCV, GCV and heritability associated with low genetic advance for plant height, days to maturity, pods per plant, seeds per pod and seed yield. While hundred seed weight exhibited moderate heritability, high heritability and genetic advances were observed for number of branches per plant. Ganeshiah (1979) reported moderate GCV and PCV values with high heritability and genetic advance for plant height, number of branches per plant, and high GCV, PCV, heritability and genetic advance for number of fruiting nodes per plant, pods per plant and seeds per pod. Pods per node showed the lower estimates of PCV, GCV, heritability and genetic advances. And the lowest values for GCV (genotypic co-efficient of variations) and PCV (phenotypic co-efficient of variations) obtained for seeds per pod, days to maturity, threshing percentage, hundred seed weight, days to flower and number of pods per plant in genetic advance for horse gram.

Suraiya (1980) obtained the highest genotypic and phenotypic variance for plant height and days to 50 per cent flowering in a study conducted with 15 genotypes of horse gram. Days to 50 percent flowering showed the highest and hundred seed weight showed the lowest genotypic and phenotypic co-efficient of variation estimates.

Kallesh (1981) reported moderate values of heritability and genetic advances for pod bearing nodes. High genetic and phenotypic variances, high heritability and genetic advance were noticed for pods per plant and seed yield, while high heritability with moderate genetic advance was observed for days to maturity.

Ramkrishnan *et al.* (1978) reported high estimates of heritability and genetic advance for seed yield per plant, plant height, and number of branches per plant. Kanaka (2014) reported that highest GCV was observed for pod hulm per plant, followed by pods per plant and seed yield per plant. Senapati *et al.* (1998) reported the highest PCV and GCV values for

seed yield per plant in horse gram, and low GCV estimates were noticed for the germination rate, seedling length and seedling vigour index I. Seed yield per plant exhibited the highest heritability, followed by the pod hulk per plant, leaf width, leaf length, test weight, number of seeds per pod and the number of pods per plant. They also observed high heritability estimates for the number of pods per plant, seeds per pod and seed yield per plant. On the other hand, the number of primary branches per plant, plant height and seedling length exhibited the lowest heritability; selection for such traits will be ineffective.

Ganeshaiah *et al.* (1982) revealed the high heritability estimate (94.23 per cent) for days taken to 50 per cent flowering. Patil and Deshmukh (1982) observed high heritability and genetic advance for number of branches per plant, pods per plant and seed yield per plant.

Birari *et al.* (1987) studied 21 varieties of horse gram and observed that higher heritability values were recorded for yield per hectare, number of days to first flowering, pod maturity and number of seed weight and relatively low heritability value for number of pods per plant and number of seeds per pod. Highest genetic advance was expected for yield per hectare followed by number of seeds per pod.

Yarguntappa (1987) reported comparatively high GCV and PCV, heritability and genetic advance for seed yield per plant, number of pods per plant, number of nodes per plant and dry weight per plant. Moderate values of PCV, GCV, and genetic advance were observed for hundred seed weight and plant height with high heritability values noticed for all these estimates and number of seeds per pod while days to 50 per cent flowering and days to maturity showed the lower values of PCV and GCV coupled with high heritability.

Suraiya *et al.* (1988) reported that 13 diverse horse gram genotypes showed considerable variation for all the characters studied. Pods per plant, plant height, days to 50 per cent flowering and days to maturity showed the highest, and hundred seed weight the lowest genotypic variances. Their study also revealed high genotypic co-efficient of variation for plant height and branches per plant. Further, they reported high heritability and genetic advance for days to 50 per cent flowering, days to maturity, plant height and branches per plant, but low heritability and genetic advance for seed yield per plant and number of pods per plant.

Kabir and Sen (1990) revealed that the additive genetic variance was important for days to flower, pod length, pod width and hundred seed weight. Whereas non additive genetic variance was important for pod number and pod yield per plant. Both broad and narrow sense heritability values were high for days to flowering, pod length, pod width and hundred seed weight. These results indicated the prospect of improving these characters through selection in horse gram.

Singh (1990) studied nine characters in 40 horse gram genotypes and reported high heritability estimates for days to 50 per cent flowering and hundred seed weight. His study indicated lower heritability values for plant height, number of branches per plant and number of pods per plant.

In studies by Balan *et al.* (1991) the phenotypic and genotypic variances were maximum for pod number followed by plant height and node number. High estimates of GCV were observed for pod number, seed yield and node number. High heritability coupled with high genetic advance were recorded for pod number, node number, pod weight, seed yield and plant height.

Savithramma (1994) studied 103 genotypes for 17 characters in which she obtained comparatively narrow differences between GCV and PCV for days to 50 per cent flowering, number of seeds per pod, hundred seed weight and pod yield in all the three seasons (*kharif*, *rabi* and *summer*) she studied. Moderate to high estimates of GCV and PCV were observed for days to maturity, plant height, number of primary branches per plant, biomass per plant, seed yield per plant, threshing percentage, number of secondary branches, number of pods per plant, pod length and harvest index. The broad sense heritability estimates were high with high genetic advance for days to 50 per cent flowering in *kharif*, but low in other environments. Medium heritability and GA were observed for primary branches per plant and number of seeds per pod. The secondary branches per plant, plant biomass, and pod yield per plant and harvest index exhibited low heritability coupled with medium to high genetic advance. Low to medium heritability, with low to high genetic advance was noticed for the traits number of pods per plant, seed yield per plant and per day productivity. Hundred seed weight showed medium to high heritability coupled with high genetic advance. But the trait threshing percentage exhibited low heritability with low genetic advance.

Rao and Chandrakar (1994) reported genetic parameters for 8 agro morphological characters in 9 horse gram genotypes. According to their results, the highest GCV and PCV were observed for plant height, pod bearing nodes per plant, number of seeds per plant and seed yield per plant. Heritability estimates were found to be medium to low for all the characters except days to maturity which showed high heritability estimates. The expected genetic advance exhibited range of 4.85 to 12.35 for these characters, and the highest GCV observed for pod bearing nodes and lowest for harvest index. Seed yield showed high GA with low heritability, high GCV and PCV.

A set of 23 genotypes in horse gram was analyzed for genetic variability by Dobhal and Rana (1994a) who reported that PCV, GCV, heritability and genetic advance were highest for number of internodes, clusters per plant and days to flowering.

Rao and Nanda (1994) studied 18 horse gram genotypes for seed yield and seven yield components during *rabi* 1991-92 and reported GCV values ranging from 1.37 to 16.29 and PCV values ranging from 5.79 to 32.81. Heritability estimates were low for all the characters studied by them. The genetic advance ranged from 0.56 to 16.66 and it was highest for seed yield followed by number of pods per plant.

Ten horse gram genotypes were evaluated by Sood *et al.* (1994) for seed yield and its components. They reported lower GCV and PCV for days to 75 % flowering, days to 75 % maturity and hundred seed weight, while seed yield showed higher co-efficient at both the levels. Heritability estimates were 73.60 % for seed yield, 73.80 % for 100 seed weight, and 76 % for days to 75 % flowering. They estimated very high genetic advance (233.67) for seed yield, moderate GA for days to 75 % flowering and days to 75 % maturity and very low GA for hundred seed weight (0.43).

Senapati *et al.* (1998) reported high heritability and moderate genetic advance (GA) for seeds/pod, moderate heritability and high GA for branches/plant, and moderate heritability and moderate GA for pods/plant which indicated additive gene effects.

Wide range of genetic variability was also noticed by Lad *et al.* (1998) for yield and yield components in horse gram. The phenotypic variance for all the characters studied was higher than the genotypic variance. The magnitude of genotypic variance was greater for almost all the characters except number of branches/plant, pod length, grains/pod and 100-

grain weight. Strong positive correlation with yield was noticed by Sharma (1995) in pods/plant, pod length, grains/pod and dry weight of pods/plant. Grain yield showed the highest coefficient of variation and had high heritability (43.9%).

Nehru *et al.* (2000) reported that high variability was observed for grain yield and biomass yield per plant, moderate variability for nodes on main stem, plant height, and nodes and pods on primary branches and low heritability for number of primary branches, pod length and number of seeds per pod. The highest genotypic coefficient of variation (GCV) was observed for nodes on primary branches, followed by pods on primary branches and biomass yield per plant, while the lowest GCV was observed for number of nodes on the main stem, pod length and number of primary branches. High genetic advance was observed for nodes on primary branches, pods on primary branches and biomass yield per plant, moderate genetic advance for grain yield per plant, and low genetic advance for pod length, number of primary branches, seeds per pod, nodes on main stem and pods on main stem.

Genotypic coefficient of variation (GCV), heritability and genetic advance were assessed by Venkateswarlu (2000) in 20 diverse genotypes of horse gram. Genotypes differed significantly for all the characters studied. Pods per plant and clusters per plant expressed high genetic advance coupled with high heritability and GCV, indicating thereby the preponderance of additive gene effects for these traits.

Joshi *et al.* (2000) studied genetic variability among 59 genotypes of horse gram (*Macrotyloma uniflorum*) during the *rabi* season. A wide range of genetic variability was observed for yield and yield contributing characters. All the characters evaluated, exhibited considerable magnitude of heritability in broad-sense and genetic advance. The magnitude of PCV was greater than that of GCV.

Eighteen genotypes of horse gram were studied by Ram *et al.* (2003) for grain yield and related characters during *kharif* season of 2000-01 in Rajasthan under 2 environments (E1 and E2; with 400 and 615 mm rainfall, respectively). Results showed that significant variations existed for days to flowering, days to maturity, plant height, branches per plant, pods per plant, seeds per pod, 100-seed weight, and stand at maturity and grain yield under both environments. High heritability with genetic advance, and high genetic coefficient of variation were observed for branches per plant, seeds per pod, 100-seed weight and grain

yield. High heritability and moderate genetic advance was observed for stand at maturity under E1 (adverse conditions), suggesting that indirect selection for these traits would be effective under E1 conditions.

Raina *et al.* (2007) evaluated 32 genotypes to assess variability in horse gram. Sufficient variability existed in the material under study. Leaf area, internode length, plant height, pods per plant and 100-seed weight were exhibited high heritability coupled with high genetic advance. However, economic traits *viz.* seed yield per plant and biological yield per plant exhibited moderate heritability and genetic advance.

Kalia and Dogra (2007) studied on 35 diverse genotypes of horse gram. Phenotypic and genotypic coefficients of variation were high for crop growth rate and seed yield per plant. The phenotypic coefficient of variation for pods per plant and harvest index was high, whereas the genotypic coefficient of variation for these traits was moderate. High heritability coupled with high genetic advance for leaf area index (70 days after sowing) and crop growth rate indicated the influence of additive gene action and consequently a likelihood of high genetic gain from phenotypic selection.

Singhal *et al.* (2010) studied 88 horse gram genotypes. The analysis of variance revealed highly significant differences among genotypes for all the traits. The phenotypic coefficient of variation (PCV) was higher than that of genotypic coefficient of variation (GCV) and found to be high to moderate for all traits except for days to 50% flowering. A set of 48 genotypes of horse gram was evaluated by Sahoo *et al.* (2010). High coefficient of variation both at phenotypic and genotypic levels were found for pods/cluster, number of clusters/plant, pod yield/plant, biological yield/plant, number of branches/plant, seed yield/day, biological yield/day, number of pods/plant and plant height. Also this study showed high heritability in broad sense except seeds/pod, 100 seed weight, harvest index, shelling per cent and pod length. But, high heritability with high genetic advance were observed for number of pods/cluster, clusters/plant, number of branches/plant, pods/plant, per plant, seed yield, pod yield and biological yield/plant and plant height indicating a positive response of selection expected for these characters.

Prabha *et al.* (2010) reported that among 11 genotypes, the highest mean value was recorded for plant height in genotype PRH 03 followed by PRH 06, highest number of

branches in PRH 01, pod length in PRH 6, number of seeds/pod in PRG 7 followed by PRH 10 and VL Gahat 1, pods/plant, seed yield/plant and seed yield/hectare in VL Gahat 1 followed by PRH 10. The mean performance for seed quality parameters was highest for seedling length, seedling fresh weight in genotype PRG 04 followed by PRH 03, PRH 01, and germination per cent recorded highest in PRH 01.

Kulkarni and Mogle (2011) carried out evaluation of twenty two horse gram [*Macrotyloma uniflorum* (Verdcourt)] genotypes for analysis of quantitative as well as qualitative characters. Among the different genotypes, IC-268213, IC-341283, IC-282590, IC-259326 and IC-341308 were the top ranking in terms of yields per plant. The early genotypes were IC-341294, IC-267282, IC-341307, IC-341308 and IC-341283 which had observed their average 50% flowering on 36.58, 36.78, 36.95, 37.14 and 38.13 days respectively, whereas the local selections C-I and C-II had shown very less yield per plant and also late in 50% flowering.

Khulbe *et al.* (2013) evaluated 26 horse gram accessions and observed the presence of moderate to high range of variation for all the characters. Coefficient of variation was high for pods/plant and yield/plant and low for days to maturity and seeds/pod. High broad sense heritability estimates were obtained for days to 50% flowering (73%), plant height (64%) and yield/plant (60%), and low for seeds/pod (14%). Genetic advance as per cent of mean was highest for pods/plant (19.32) and lowest for seeds/pod (0.14).

Latha *et al.* (2013) reported that except for hundred seed weight, PCV was marginally higher than their corresponding GCV, reflecting narrow influence of environment indicating that selection on a phenotypic basis will hold good for a genetic basis. High PCV and GCV (>20%) were recorded for plumule length, radicle length and vigour index. Both seed length and thickness recorded low estimate for both PCV and GCV indicating narrow range of variability. High heritability was recorded for hundred seed weight. High heritability coupled with high genetic gain for seed volume, hundred seed weight, germination percentage, plumule length, radicle length and vigour index indicated that these characters are controlled by additive gene action. It was reported that high heritability associated with high genetic advance for yield per plant, number of pods per plant and seeds per pod. Nevertheless, low PCV, GCV, genetic gain and moderate heritability were observed for seed length and thickness.

Thirty eight horse gram accessions were evaluated and characterized during two *post rainy* seasons by Sunil *et al.* (2014) from the Andhra Pradesh, and it was indicated that all the accessions had trailing growth habit and determinate growth but showed variation in vigor, at pod stem color, flower colour and seed colour. Plant height, number of primary branches, number of clusters per plant and seeds per pod were found to be significant traits.

2.3 Correlation co-efficients

Studies were made on association between yield and its components by several workers.

Aggarwal and Kang (1976) observed that the seed yield had positive and highly significant correlation, with pods per plant, plant height, seed size and number of branches. Shivashankar *et al.* (1977) noticed highly positive correlation of yield with plant height, pods per plant and seeds per pod. Ganeshaiah (1979) found that seed yield was highly and positively correlated with number of pods, days to maturity and branch number. He also reported that the number of pods was positively associated with seeds per pod but pods per plant was negatively associated with hundred seed weight.

Kallesh (1981) noticed highly positive correlation of yield with plant height, pods per plant and seeds per pod. He also reported the positive and significant correlation of number of fruiting nodes with pods per plant and seeds per plant. Patil and Deshmukh (1982b) reported that seed yield was positively correlated with number of pods per plant, number of secondary branches per plant and hundred seed weight. Patil *et al.* (1983) observed positive correlation of yield with pods per plant, number of secondary branches and hundred seed weight. Ghorpade (1985) reported that seed yield per plant was negatively correlated with pod number per plant and seed index was positively correlated with days to 50 per cent flowering.

Yarguntappa (1987) has reported that seed yield per plant possessed a strong and positive correlation with number of pods per plant, days to 50 per cent flowering, days to maturity, plant height, seeds per pod and hundred seed weight both at phenotypic and genotypic levels. Days 50% was positively correlated with seed yield, days to maturity, number of pods per plant and plant height at both the levels and with seeds per pod only at genotypic level. Days to maturity was correlated with days to 50 per cent flowering, pods per plant, seeds per pod and hundred seed weight. He also observed positive and significant

association of plant height with number of pods per plant, days to maturity, seeds per pod, days to 50 per cent flowering and seed yield at both levels. Seeds per pod was correlated with seed yield, pods per plant, plant height and days to maturity. Hundred seed weight was positively correlated with seed yield and days to maturity.

Kabir and sen (1989) reported that pod number, pod length and pod width as well as seeds per pod were strongly correlated positively with pod yield at genotypic and phenotypic level in horse gram. Days to flower and hundred seed weight showed significant positive correlation with pod yield at genotypic level only. Genotypic correlation co-efficient of pod width with pod yield was lower than the phenotypic correlation, the influence of environment in the association of the two characters at genetic level was observed. Positive correlation of yield with plant height, pods per plant and seeds per pod was observed. He also reported the positive and significant correlation of number of fruiting nodes with pods per plant and seeds per pod.

Dabhos *et al.* (1990) studied factor analysis on 61 diverse genotypes. Seed yield and pod yield were positively correlated with each other and also with cluster on the main stem, and branches per plant, pods on branches and per plant, and seeds per pod in horse gram. Singh (1990) gave information on genetic advance, variability and yield correlations derived from data on nine characters in 40 horse gram genotypes which revealed significant negative correlation between seed yield and days to flowering and maturity. He also reported positive and significant correlation between pod number per plant and seed yield per plant. Balan *et al.* (1991) reported that seed yield had significant, positive correlation with 10 characters in 55 horse gram genotypes.

Savithramma (1994) noticed positive and significant association of seed yield with biomass, pod yield and pods per plant at both genotypic and phenotypic levels. Harvest index was positively and significantly correlated with seed yield and pods per plant and per day productivity with seed yield and pod yield. Rao and Chandrakar (1994) reported highly significant, positive correlation of seed yield per plant with days to flower, days to maturity, plant height, number of primary branches per plant, number of pods per plant and number of seeds per pod. Days to maturity, plant height, number of primary branches and number of pods per plant were significantly and positively correlated with each other. Their study also

revealed significant, negative association of harvest index with days to maturity and plant height.

Rao and Nanda (1994) revealed positive and significant association of only harvest index with seed yield among 8 characters studied. Whereas days to maturity showed significant negative association with harvest index. The correlation co-efficient studied both at genotypic as well as phenotypic levels by Sood *et al.* (1994) revealed significantly negative correlation of seed yield with days to 75 per cent flowering and days to 75 per cent maturity. Seed yield showed significant positive correlation with number of inter nodes, branches per plant, clusters per plant and days to flowering (Dobhol and Rana, 1994b).

Total dry matter accumulation and daily rate of dry matter production were positively correlated with grain yield at different stages of growth (Sahane *et al.*, 1995). Sharma (1995) reported that character association revealed the importance of pod length, number of pods per plant, number of grains per pod and 100-grain weight in determining yield. Number of grains per pod affected grain yield through pod length. Lad *et al.* (1999) reported that strong positive correlation with yield was noticed by pods/plant, pod length, grains/pod and dry weight of pods/plant.

Savithramma (2002) reported that there were significant differences between genotypes for all characteristics in all seasons, except pod length. Eighteen genotypes through analysis of correlation in E-400 mm and E-615 mm environments (Pandya *et al.*, 2002). Grain yield was significantly correlated with components like 100 seed weight, seeds per pod, branches per plant and plant height under both the environments. Roopadevi *et al.* (2002) reported that Seed yield was positively and significantly correlated with growth parameters like plant height, number of leaves, number of branches and leaf area index. Positive significant correlation was also observed between seed yield and nodule number. The yield components number of pods per plant, number of seeds per pod, pod length and 1000-seed weight were positively and significantly correlated with seed yield. Correlation analysis by Paliwal *et al.* (2005) reported that seed yield had positive and significant correlation with branches per plant. Sarkar *et al.* (2005) reported that genotypic correlation coefficients were greater than the corresponding phenotypic correlation coefficients for the different characters. Seed yield per plant showed positive and significant association with days to 50% flowering and 100-seed weight.

Raina *et al.* (2007) reported that economic yield recorded strong positive association with biological yield per plant, fruiting nodes per plant, leaf area, 100 seed weight, plant height and internode length. Correlation was carried out by Rama *et al.* (2007) on 35 genotypes of horse gram showed that seed yield was positively and significantly correlated with leaf area index at 35 days after sowing (DAS), leaf area (at 70 DAS), leaf area index (at 70 DAS), pods per plant, seeds per pod and biological yield per plant at both genotypic and phenotypic levels.

Prabha *et al.* (2010) studied on seed yield was associated with pod length, plant height number of pods/plant and seed yield/plant. The pod length, plant height and number of seeds/pods were found to be most important characters for genetic improvement. It can be concluded that the genotypes PRH 01, PRH 10 along with VL Gahat 1 can be used in future crossing programme to develop superior high yielding genotypes.

Correlation studies were done by Latha *et al.* (2013) in order to analyze the relationship between the seed physical and physiological characters in horse gram accessions. positive significant correlation between length and breadth, length and volume, breadth and volume, thickness and volume, hundred seed weight and volume, hundred seed weight and germination percentage, germination percentage and seedling vigour (both plumule and radicle length), germination percentage and vigour index, plumule length with radicle length and vigour index, and between radicle length and vigour index (at 1 % level). Correlation was significant and positive at 5% level between thickness and breadth, hundred seed weight with length, breadth, and thickness and number of seed colours with length and breadth. Significant and positive correlation observed between number of pods per plant and yield per plant ($r = 0.73$) was recorded by Sunil *et al.* (2014).

Niveditha and Jagapathi (2014) reported out of 30 accessions, seven genotypes proved themselves to be most adoptive in bothe locations different agroclimatic condition. Correlation values between plant height vs pods/plant, plant height vs. leaf area, plant height vs. days to flowering, plant height vs. pod length, plant height vs. grains/pod and plant height vs. yield/plant were determined and exhibited.

Significant correlation between number of pods per plant and yield per plant was recorded among thirty eight horse gram accessions evaluated and characterized during two *post rainy* seasons by Sunil *et al.* (2014).

2.4 Path co-efficient analysis.

Path analysis in horse gram showed that pods per plant had high positive direct effect on yield (Aggarwal and kang, 1976). Ganeshiah (1979) reported that pod weight, pod number and hundred seed weight contributed more towards yield than seeds per pod. Plant height had low negative effect on yield.

Kallesh (1981) reported that pods per plant and number of fruiting nodes were the major yield contributing characters and the indirect effect of all the variables through fruiting nodes and pods per plant was high and positive. Yarguntappa (1987) reported that the number of pods per plant exerted the greatest direct and positive effect on seed yield and its indirect effect through pod bearing nodes per plant, days to 50 per cent flowering and pods per node are also moderate. Days to 50 per cent flowering had comparatively high direct effect on seed yield, but its indirect influence on yield through number of pods per plant was more than its direct effect. Its indirect influence through days to maturity and plant height was negative and very low through other characters. The direct effect of hundred seed weight on seed yield was closer to its phenotypic correlation co-efficient. The number of seeds per pod had low positive direct effect on yield. Its indirect contribution through pods per plant was more than its direct effect. At genotypic level he noticed that pod bearing nodes per plant to seed yield was positive and more followed by plant height, days to 50 per cent flowering and number of nodules per plant.

Kabir and Sen (1989) reported the highest positive direct effect of pod length on pod yield followed by pod number, pod width seeds per pod, while 100 seed weight and days to flowering exhibited negative direct effect. Singh (1990) observed in path analysis that pod number per plant was important yield component in horse gram. He also observed that pod yield was correlated with pod number, length and pod weight and pod length had the largest direct effect on pod yield followed by pod number and width and seeds per pod, while 100 seed weight and days to flowering exhibited negative direct effect in horse gram. Path analysis by Balan *et al.* (1991) revealed that pod weight per plant had the greatest direct positive effect on horse gram seed yield. Savithamma (1994) reported that the biomass and pod yield per plant showed high direct effect on seed yield. High indirect effect on seed yield *via* pod yield per plant was observed during *kharif*. During *rabi*, biomass per plant and harvest index exhibited high direct effects on seed yield. Much of the correlation observed between

pod yield and seed yield was due to high indirect effect *via* biomass per plant. During *summer*, much of the correlation of the pod yield and harvest index with seed yield was due to high direct effect of these traits on seed yield. Number of pods per plant exhibited high indirect effect *via* pod yield per plant on seed yield.

Balan and Das (1994) analyzed direct and indirect effects of several characters and reported that pod weight per plant had the greatest direct positive effect on seed yield. Sood *et al.* (1994) reported the direct and indirect effect of days to 75 per cent flowering and days to 75 per cent maturity on seed yield had negative direct effect. Hundred seed weight was masked by its indirect positive effects *via* days to 75 per cent flowering and days to 75 per cent maturity. Dobhal and Rana (1994a) noticed that clusters per plant exhibited maximum direct effect on grain yield followed by days to flowering and pods per plant in 21 horse gram genotypes

Nagaraja *et al.* (1999) studied on path co-efficient of twenty genotypes of horse gram, and reported that number of primary branches, pod bearing nodes per plant and pod yield showed direct effect on seed yield. Eighteen genotypes were evaluated in E-400 mm and E-615 mm environments (Pandya *et al.*, 2002). Path coefficient analysis revealed that branches per plant had highest direct effect on grain yield in the E1 environment, whereas seeds per pod in E2, 100-Seed weight, days to maturity and plant height have direct positive effects on grain yield under both the environments, which suggest that improvements in grain yield could be effective, if the selections are based on these characters.

In a study by Paliwal *et al.* (2005) path coefficients for seed yield and its components (days to flowering, days to maturity, plant height, branches per plant, pods per plant and 100-seed weight) were assessed in 10 horse gram genotypes grown. Path analysis indicated that branches per plant, pods per plant and 100-seed weight had positive direct effects on seed yield. It was concluded that selection for branches per plant, pods per plant and 100-seed weight would be effective in improving horse gram yield. In another study by Sarkar *et al.* (2005) days to 50% flowering showed the highest positive direct effect on seed yield, followed by 100-seed weight. Thus, days to 50% flowering appeared to be the most important character affecting yield in the present set of materials of horse gram.

Rama *et al.* (2007) reported that leaf area (at 70 DAS), biological yield per plant and harvest index exhibited high positive and direct influence on seed yield per plant, whereas leaf

area index (70 DAS) had a negative direct effect. Plant height, leaf area, leaf area index, pods per plant, seeds per pod and biological yield per plant had a high indirect effect via harvest index. In a study by Raina *et al.* (2007), path analysis revealed importance of biological yield per plant, pods per plant, fruiting nodes per plant and 100-seed weight for indirect selection for seed yield in this crop. Path analysis among fifty-nine genotypes of horse gram grown revealed that plant height exhibited the greatest direct effect at the genotypic level on seed yield per plant and number of primary branches per plant (Bhave *et al.*, 2007).

Khulbe *et al.* (2013) reported that Pods/plant and 100-seed weight had positive direct effect, while *plant* height exhibited negative direct effect on seed yield/plant. The study suggested that emphasis may be placed on pods/plant and 100-seed weight in selecting superior genotypes. Three accessions IC 355888, PGR G-8 and PGR G-18 exhibited significantly higher yield than the best check VLG-10, suggesting scope for genetic enhancement of the crop by exploiting natural variation among the local cultivars and land races.

2.5 Varietal evaluation for nutritional quality

Horse gram seeds contain good nutritional composition (protein, amino acids, fatty acids, flavonols and minerals), and hence will serve as nutritious and healthy food for use by malnourished and food deprived people worldwide. Therefore, studies were made by several workers to evaluate the varieties for grain nutritional quality.

Patil and Deshmukh (1985) were observed varietal differences for seed protein content among 50 genotypes in the range 17.9-28.8%, being the highest in White Shimoga and lowest in EC-7460. Estimates of heritability for protein content were high and for genetic advance low, indicating nonadditive gene action (Patil and Deshmukh, 1982a).

Sudha *et al.* (1995) reported nutrients and some anti-nutrients in horse gram (*Dolichos biflorus*). Proximate nutrients, calcium, and some anti-nutrients in 16 varieties of whole horse gram and their dehulled seeds were estimated. The protein, fat, and carbohydrate contents were higher in the dehulled samples than in the corresponding whole horse gram. However, the moisture, fibre, ash, and calcium contents of the dehulled samples were lower. A significant portion of the anti-nutrients studied were removed by dehulling.

Jayashri *et al.* (2001) evaluated ten horse gram genotypes to study their chemical composition and functional properties. Results revealed that genotype PHG-9 was found to contain the highest ash, moisture and comparatively high per cent of crude fiber. Gupta *et al.* (2001) studied on four horse gram genotypes (ACCK-11, ACCK-210, ACCK-292 and DPL-1) were chemically analysed for proximate principles, protein fractions, methionine and tryptophan content in grain. The chemical analysis revealed showed the presence of 19.71-16% protein, 0.76-1.63 g methionine, and 0.96-2.07 g tryptophan per 100 g protein in grain. The results also indicated that tryptophan was not limiting in these genotypes. Protein was found to be the highest in PHG-62. ACCK-11 had comparatively better distribution of protein fractions in their grain protein compared to other genotypes

The quantitative changes in protein and free amino acid contents and *in vitro* protein digestibility of seeds of high yielding variety PHG 9 during germination were examined at CAZRI (Ismail *et al.*, 2003). Results revealed that there was a progressive increase in free amino acid content in seeds during germination. The profile of protein content changed considerably in the early stage of germination and there was decreasing trend in the protein content during germination. In vitro protein digestibility was significantly increased and decreased at later stages of germination.

Sangita *et al.* (2004) analyzed the protein and oil content for the seeds of the wild horse gram (IC 212722). Seed contains 38.37 ± 1.03 per cent crude proteins. More than 95 per cent of the total nitrogen belongs to protein nitrogen.

The seeds of two varieties of horse gram 'AK-21' and 'AK-42' were assessed for their physicochemical and, nutritional properties The protein content of 'AK-21' and 'AK-42' were 15.10 and 15.32 g per cent (DMB), respectively. The fat content of 'AK-21' was higher (1.8 g per cent) as compared to 'AK-42' (1.29 g per cent). Fibre content of both varieties ranged between 4.57-5.15 g percent. The energy content ranged from 376.12 to 377.21 kcal/100 g and 2.77 to 3.08 g percent respectively on dry matter basis. The amount of iron was 8.71-9.16 mg per cent (DMB) (Shashi *et al.*, 2012).

Mean concentrations of macrominerals (Ca, K, Mg, P, and S) and microminerals (Cu, Fe, Mn, Ni, and Zn) ranged from 1.3-14 mg/g DW, and 1.0-95.0 micro g/g DW, respectively among seven accessions adapted to Griffin, USA (Morris *et al.*, 2013).

Khatun *et al.* (2013) reported that legumes are good source of calcium, iron and zinc, but, are also a source of phytate and other anti-nutritional factors and dietary fibre components that can negatively affect the bio-accessibility of these minerals. Ten horse gram genotypes were studied for estimation of calcium and iron content as well as the bio-accessibility of these two minerals. The effect of processing such as germination, cooking and roasting on the bio-accessibility was also studied. The calcium and iron content of ten horse gram genotypes ranged from 244 to 312 and 5.89 to 7.44 mg/100 g of seed, respectively. In-vitro bio-accessibility of iron and calcium of raw horse gram genotypes ranged from 0.26 to 0.85 and 22.50 to 38.50 mg/100 g of seeds, respectively.

2.6 Qualitative characters studies

Sunil *et al.* (2014) studied on six qualitative traits and reported that variation in early plant vigour, growth habit, growth pattern, stem colour, flower colour and seed colour. And given visual score for each trait, early plant vigour (1-Poor, 2-Good, 3-Very good), growth habit (1-Bushy, 2-Semi-spreadng, 3-Spreading, 4-Trailing), growth pattern (2-Determinate), stem colour (1-Light yellow, 2-Green, 3-purple, 99-Others), flower colour (1-Light yellow, 2-Yellow, 99-others), seed colour (1-Light yellow, Creamy-2, 4-Brown, 99-Others).

Latha *et al.* (2013) reported that out of 13 seed colour categories noticed, three colours such as light brown, motteled cream and cream were the most commonly found ones in the population while motteled greyish cream colour was observed in IC320010. Maximum colour polymorphism was exhibited in IC47135, having 9 colour pattern. Minimum number of seed colour catagories (2) was noticed in IC68591, IC47137 and IC71793A.

Kulkarni and Mogle (2011) studied on qualitative traits like seed size, seed colour and shattering ability. And classified the each traits into seed size (Bold, Medium and Small), seed colour (Faint gray, Brown gray, Gray brown, Yellow gray, Faint brown, Dark brown, Brown, Brown pink), shattering ability (Shattering, Non shattering).

III MATERIAL AND METHODS

A field experiment was conducted to study the genetic diversity within horse gram germplasm collection for yield and yield contributing characters. The details of the material used and techniques adopted for analysis and interpretation are described here under.

3.1 Experimental location

The experiment was carried out at Regional Agricultural Research Station, Vijayapur, (University of Agricultural Sciences, Dharwad) during late *Kharif* 2014-15. The research station is situated in the Northern Dry Zone of Karnataka between 16°49'N latitude, 75°43'E longitude and at an altitude of 593 meters above the mean sea level. The rainfall data is given in the Appendix I.

3.2 Experimental material

Experimental material for the present study was comprised of 111 horse gram germplasm lines. These genotypes included 80 entries that were received from AICRP on Dryland Agriculture of RARS, Vijayapur and 30 local collections. The detailed list of genotypes used in this investigation is given in Table 1a. The local collections (BHGM-1 to BHGM-30) were made from different districts of Karnataka such as Tumkur, Koppal, Haveri, Gadag, Vijayapur, Mandya, Mysore, Davangere, Gulbarga and Hassan. The detailed list of genotypes used in this investigation is given in Table 1b.

Among the lines tested, GPM-6 and Kavalgi local were used as check variety. GPM-6 is a high yielding, variety of U. A. S Dharwad released for north Karnataka. The variety is tolerant to yellow mosaic virus and root rot diseases.

3.3 Methodology

3.3.1 Experimental design and layout

The experimental material was planted in a Randomized Block Design (RBD) with two replications. Each entry planted in two rows of 3 m length and with spacing of 45 cm between rows and 10 cm between plants. Overview of experimental plot laid out is shown in plate 1.



Plate 1. General view of experimental plot of germplasm lines of horse gram

3.3.2 Cultivation practices

The land with good soil fertility and very well prepared soil with fine tilth was taken and the recommended package of practices for cultivation of horse gram was adopted.

Table 1a. List of Horse gram germplasm lines used in the present study

Entry no.	Entry name	Entry no.	Entry name	Entry no.	Entry name
1	GPM-6	38	GPM-37	75	BHL-20
2	BJPL-1	39	GPM-49	76	BHL-154
3	GPM-23	40	VLG-19	77	BHL-48
4	CRHG-9	41	GPM-4-61-4-1	78	BHL-26
5	DS22	42	GPM-36	79	BHL-66
6	IC100938	43	DHG-04	80	BHL-128
7	DEH-1	44	PHG-12	81	BHGM-1
8	PHG-9	45	GPM-28	82	BHGM-2
9	VJPL-2	46	LONE-1	83	BHGM-3
10	IC100935	47	GHI-641	84	BHGM-4
11	KBHG-1	48	GPM-171	85	BHGM-5
12	AK-42	49	GPM-46	86	BHGM-6
13	GPM-30	50	PHG-02	87	BHGM-7
14	BLHG-1	51	PHG-21	88	BHGM-8
15	BGM1183	52	CRHG-07	89	BHGM-9
16	AK-21	53	PS-2-4	90	BHGM-10
17	CRHG-4	54	GPM-58	91	BHGM-11
18	CRHG-6	55	GPM-48	92	BHGM-12
19	CRHG-8	56	GPM-44-2	93	BHGM-13
20	CRHG 19R	57	GPM-12-B	94	BHGM-14
21	CRIDA 18R	58	SHG-317	95	BHGM-15
22	GPM-11	59	VLG-08	96	BHGM-16
23	GPM-23	60	GPM-65	97	BHGM-17
24	RS28-607	61	GPM-66	98	BHGM-18
25	GPM-422	62	8B	99	BHGM-19
26	GPM-62	63	GPM-92	100	BHGM-20
27	GPM-13	64	14GH 5R	101	BHGM-21
28	GPM-51	65	12B	102	BHGM-22
29	AK-44	66	GPM-59	103	BHGM-23
30	AK-22	67	GPM-79	104	BHGM-24

31	GPM-18	68	GPM-32	105	BHGM-26
32	GPM-25	69	CRHG-05	106	BHGM-27
33	GPM-44	70	GPM-22	107	BHGM-28
34	BHG-1	71	BHL-78	108	BHGM-29
35	GPM-63	72	BHL-44	109	BHGM-30
36	GPM-03	73	BHL-15	110	Kavalagi local
37	GPM-4.4-113	74	BHL-60	111	Bailhongal local

Table 1b. Details regarding local collections of horse gram used in the present study

SL NO	Code	Village/place of collection	Taluk	District
1.	BHGM-1	Appasandra	Thurvekere	Tumkur
2.	BHGM-2	Honnudike	Tumkur	Tumkur
3.	BHGM-3	Nitturu Mattigath	Gubbi	Tumkur
4.	BHGM-4	Masigola	Koppala	Koppala
5.	BHGM-5	Koppala	Koppala	Koppala
6.	BHGM-6	Koppala	Koppala	Koppala
7.	BHGM-7	Timkapur	Byadgi	Haveri
8.	BHGM-8	Gadag	Gadag	Gadag
9.	BHGM-9	Jumanal	Vijayapur	Vijayapur
10.	BHGM-10	Hirelingadalli	Haveri	Haveri
11.	BHGM-11	Yellichekanahalli	Mandya	Mandya
12.	BHGM-12	Bhattadapura	Hunsur	Mysore
13.	BHGM-13	Shanthekeslugere	Mandya	Mandya
14.	BHGM-14	Chikhamarali	Pandavapura	Mandya
15.	BHGM-15	Manoor	Sindagi	Bijapur
16.	BHGM-16	Manoor	Sindagi	Bijapur
17.	BHGM-17	Manoor	Sindagi	Bijapur
18.	BHGM-18	Manoor	Sindagi	Bijapur
19.	BHGM-19	Kateveeranahalli	Shira	Tumkur
20.	BHGM-20	Revanal	Gubbi	Tumkur
21.	BHGM-21	Kamdoda	Ranebennur	Haveri
22.	BHGM-22	Magoda	Ranebennur	Haveri
23.	BHGM-23	Kamdoda	Ranebennur	Haveri
24.	BHGM-24	Devagondanakatti	Ranebennur	Haveri

25.	BHGM-25	Gulberga	Kalaburgi	Kalaburgi
26.	BHGM-26	Gulberga	Kalaburgi	Kalaburgi
27.	BHGM-27	Jagloor	Jagaloor	Davanagere
28.	BHGM-28	Hnjihalli	Alur	Hassan
29.	BHGM-29	Benakanahalli	Vijayapur	Vijayapur
30.	BHGM-30	Arasikere	Arasikere	Hassan

3.3.3 Climatic conditions

The monthly meteorological data obtained from Meteorological department from Regional Agricultural Research Station, Vijayapur, with regard to temperature, relative humidity, rainfall and number of rainy days during the course of investigations is presented in Appendix I.

3.3.4 Recording observations

The following observations were recorded on both qualitative and quantitative characters.

3.3.4.1 Quantitative characters

3.3.4.1.1 Days to 50 per cent flowering

The difference between date of sowing and the flowering date at the time of 50 per cent of plants in a plot flowered were recorded.

3.3.4.1.2 Days to maturity

It was recorded as number of days taken from date of sowing to the date when about 80 per cent of pods in a plot reached maturity.

3.3.4.1.3 Plant height (cm)

Height of the plant from ground level to the tip of the plant was measured in centimeters at the time of maturity on five randomly selected plants.

3.3.4.1.4 Number of primary branches

Branches on the main stem of all the five randomly selected plants were recorded by counting the total number of primary branches at the time of harvest.

3.3.4.1.5 Number of pods per plant

Fully developed pods were separated from three randomly selected plants and counted. The average was taken as the number of pods per plant.

3.3.4.1.6 Pod length (cm)

The length of each pod was recorded for five randomly selected pods in each plant and each pod measured using thread and length was recorded in centimeters for all the five pods.

3.3.4.1.7 Pod yield per plant (g)

The total pods obtained from each five randomly selected plants was weighted and expressed in 'g' per plant.

3.3.4.1.8 Number of seeds per pod

The seeds from five representative pods were separated, counted and the average number of seeds per pod was calculated by dividing the number of seeds by the number of pods.

3.3.4.1.9 Seed yield per plant (g)

From each of the five randomly selected plants, dry pods were harvested and threshed separately. Seed weight was recorded in grams after thorough drying.

3.3.4.1.10 Fodder weight per plant (g)

After harvest of five randomly selected plants, dry weight was determined and expressed in 'g' per plant.

3.3.4.1.11 100 seed weight (g)

It was computed by 100 randomly chosen filled seeds from a dried composite sample made by mixing the yield of all the five selected plants in each replication. The weight in grams was recorded.

3.3.4.1.12 Harvest index

It was recorded as ratio of seed yield to total biological yield and expressed in percentage. It was calculated by the formula.

$$\text{Harvest index (\%)} = \frac{\text{Seed yield per plant (g)}}{\text{Biological yield (g)}} \times 100$$

3.3.4.2 Qualitative traits

3.3.4.2.1 Stem colour

Stem colour was recorded at the time of flowering of the crop based on following scale (Sunil *et al.*, 2014); 1 = Red and 2 = Green.

3.3.4.2.2 Seed colour

Observation on seed colour was taken based on visual score. Seeds were categorized as cream, creamy brown, light brown, brown, dark brown, light black and black based on 1-5 scale (Sunil *et al.* 2014; Latha *et al.*, 2013) as follows; 1-Cream, 2- Brown, 3- Dark brown, 4- Light black, 5- Black.

3.3.4.2.3 Seed lustre

Seed lustre evaluated based on following scale. 1= Lustrous (seed with shiny seed coat) and 2= Non Lustrous (seed with dull seed coat)

3.3.4.2.4 Seed size

Seed size was recorded after harvest of the crop was evaluated based on 1-3 scale where in 1 = Bold, 2 = Medium and 3 = Small.

3.3.4.3 Plant and grain nutrient content

A total of 21 genotypes among the germplasm lines were subjected for nutritional quality analysis. These were the entries of multilocation yield trials conducted for two years under AICRP on Dryland Agriculture (Anon., 2012, Anon., 2013). These were screened for grain nutrients (Ca, Fe, Zn) content, and plant nitrogen and protein content. 21 genotypes were screened for grain protein content. Total protein was estimated in selected genotypes using Micro Kjeldhal Distillation Method (A.O.A.C, 1980). About 3-5 gram of plant randomly drawn from each of the genotype were powdered. One gram of powder was accurately weighed using electronic balance and subjected to digestion. Total nitrogen in the plant obtained after titration was multiplied with the factor 6.25 to arrive at protein content and expressed in percentage. Grain micronutrients (calcium, iron and zinc) content of these genotypes was estimated using Atomic Absorption Spectrophotometer (AAS) using mineral solution which was made using diacid mixture.

3.5 Statistical analysis

The data on individual mean for each trait was subjected to statistical analysis. The data was analyzed using WINDOSTAT ver 8.5 software programme. For the analysis of the data, the following statistical methods were employed.

3.5.1 Analysis of variance (ANOVA)

The data on mean values for all the characters were analyzed for the variance following randomized block design as per the outline presented below.

Source of variation	Degrees of freedom	Sum of squares	Mean sum of squares	"F" ratio
Replications	(r-1)	A	P	P/R
Treatments	(t-1)	B	Q	Q/R
Error	(r-1)(t-1)	C	R	
Total	(rt-1)	D	S	

Where,

r = Number of replications

- t = Number of genotypes
 A = Replication sum of squares
 B = Treatment sum of squares
 C = Error sum of squares
 D = Total sum of squares

P, Q, R and S= Mean sum of squares of replications, treatments, error and total, respectively.

The significance of “F” value was tested by comparing the computed value with the table value as given by Fisher. Further, standard error of means ($SEm_{\pm}$), critical difference (CD) and co-efficient of variation (CV) were worked out using appropriate formulae to facilitate the comparison of means of genotypes in ANOVA table.

3.5.2 Genetic diversity analysis

3.5.2.1 Multivariate analysis using D^2 statistics

Mahalanobis (1936) D^2 - statistic was used for assessing of the genetic divergence between genotypes.

The generalized distance between any two populations is defined as,

$$D^2 = Y_{ij}\beta_i\beta_j$$

Where,

Y_{ij} = The reciprocal matrix to the common dispersion matrix

β_i = The difference between the two mean values of the two populations for i^{th} character ($\mu_{i1} - \mu_{i2}$)

β_j = The difference between the mean values of the two populations for the j^{th} character ($\mu_{j1} - \mu_{j2}$)

μ = Vector mean values for all the characters

The formula for the estimation of distance, D^2 from samples

$$D^2 p = d_1 (S-1) d$$

Where,

$D^2 p$ = Square of the distance considering P values.

$$d_1 = (X_{i1} - X_{i2})$$

X = Vector for mean values of all the characters

S - 1 = inverse of variance covariance matrix

Formula for computation of D values, which requires inversion of the matrix, becomes complicated especially when the numbers of variables under consideration are large.

Therefore, the original correlated un-standardized variables (X_i) were transformed to standardized uncorrelated variables (Y_i) so that the computation of D^2 values reduce to simple summation of squares of the differences between values of transformed variables of the two population *i.e.*, $D^2 i$.

From the newly transformed uncorrelated variables, the square of the distance was computed using the following formula.

$$D^2 = (Y_{i1} - Y_{i2})^2$$

Where,

Y_{i1} = Vector of transformed mean values, for first genotype

Y_{i2} = Vector of transformed mean values, for second genotype

The square root of the D^2 values gives the generalized distance (D) between the two populations. The D^2 values were arranged in a matrix form. The significance of D^2 values between any populations was tested using the following formula.

$$F = \frac{(n_1 + n_2 - p - 1)}{(n_1 + n_2 - 2) P} \times \frac{(n_1 n_2) D^2}{(n_1 + n_2)}$$

This computed F values was compared with table F value at 5 per cent and 1 percent levels of significance with P (number of characters) and $(n_1 + n_2 - p - 1)$ degrees of freedom.

3.5.2.2 Clustering of the D^2 values

All the $n(n - 1)/2$ D^2 values were clustered as follows: The two genotypes having the lowest D^2 value between them were selected and a third genotype which had on an average the smallest D^2 value from the first two, was added. Similarly, fourth was chosen which showed, the smallest average D^2 value from the first three. If at any stage increase in D^2 values because of the addition of a new genotype exceeded the average of those already included, then that genotype was taken out. The genotypes that are included already in that group were considered as the first cluster. The procedure is repeated for other genotypes omitting those that are already included in the former clustre.

The average distance of all the genotypes within the cluster (intracluster distance) and average distance between any two clusters (intercluster distance) were calculated.

3.5.3 Identification of superior genotypes

The working collections were assessed for identification of superior genotypes for various traits by comparing with the check varieties included in the study. The following CD values were used for the comparison.

Where CD is calculated using these $SEd \times t$ at 5 % or 1 % level

SEd (between means of a check and test variety) = $EMS (1+1/b+1/c+1/bc)$

3.5.4 Estimation of Genetic parameters

The different genetic parameters should be estimated in order to evaluate and assess the genetic variability among the germplasm lines of horse gram by adopting following formulae.

3.5.4.1 Estimation of variance components

Genotypic and phenotypic components of variance were estimated with the help of following formulae.

$$\text{Genotypic variance } (\sigma^2_g) = \frac{\text{MSS (treatment)} - \text{MSS (error)}}{\text{Number of replications}}$$

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \text{MSS (error)}$$

3.5.4.2 Co-efficient of variability

Both genotypic and phenotypic coefficients were computed for each character as per the method suggested by Burton and De Vane (1953).

$$\text{Genotypic coefficient of variability (GCV)} = \frac{\sigma_g}{\bar{X}} \times 100$$

$$\text{Phenotypic coefficient of variability (PCV)} = \frac{\sigma_p}{\bar{X}} \times 100$$

Where,

σ_g = Genotypic standard deviation

σ_p = Phenotypic standard deviation

$\bar{X}$ = General mean of character

GCV and PCV values were categorized as low, moderate and high values as suggested by Sivasubramanian and Menon (1973), which is as follows:

1-10 per cent : Low

10.1-20 per cent : Moderate

20.1 per cent and above : High

3.5.4.3 Heritability (h^2)

Heritability in broad sense was computed as the ratio of the total phenotypic variance as suggested by Hanson *et al.* (1956) and expressed in terms of percentage.

$$\text{Heritability } (h^2) = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

The heritability percentage was low, moderate and high as given by Robinson *et al.* (1949).

0-30 per cent : Low

30.1-60 per cent : Moderate

60.1 per cent and above: High

3.5.4.4 Genetic advance (GA)

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

$$GA = h^2 k \sigma_p$$

Where,

h^2 = Heritability in broad sense

k = Selection differential which is equal to 2.06 at 5 % intensity of selection (Lush, 1940)

σ_p = Phenotypic standard deviation

3.5.4.5 Genetic advance as per cent of mean (GAM)

$$GAM = \frac{GA}{\bar{X}} \times 100$$

Where,

GA = Genetic advance

$\bar{X}$ = General mean of the character

Genetic advance as per cent mean was categorized as low, moderate and high as given by Johnson *et al.* (1955).

It is as follows,

0-10 per cent : Low

10.1-20 per cent : Moderate

20.1 per cent and above : High

3.5.5 Association study

3.5.5.1 Correlation analysis

The correlation coefficients were worked out to determine the degree of association of a character with yield and also among the yield components.

Genotypic and phenotypic correlations were computed by using the formula given by Weber and Morthy (1952).

$$r = \frac{\text{Cov}(xy)_p}{\sigma p_x \times \sigma p_y} \times 100$$

$$r = \frac{\text{Cov}(xy)_g}{\sigma g_x \times \sigma g_y} \times 100$$

Where,

r = Correlation coefficient

$\text{Cov}(xy)$ = Covariance between the characters 'x' and 'y'

σp_x and σp_y = Phenotypic variance of the character 'x' and 'y' respectively

σg_x and σg_y = Genotypic variance of the character 'x' and 'y' respectively

Correlation coefficients were compared against 'r' values given in Fisher and Yates (1963) table at (n-2) degrees of freedom at the probability levels of 0.05 and 0.01 to test their significance.

3.5.5.2 Path analysis

Path analysis was carried out by using both phenotypic and genotypic correlation coefficients to know the direct and indirect effects of the components on yield as suggested by Wright (1921) and illustrated by Dewey and Lu (1959).

Path coefficients were obtained by solving the simultaneous equations, which express the basic relationship between correlations and path coefficients. The equations are as follows:

$$r_{1y} = a + r_{12}b + r_{13}c + \dots + r_{1l}l_i$$

$$r_{2y} = r_{21}a + b + r_{23}c + \dots + r_{2l}l_i$$

$$r_{3y} = r_{31}a + r_{32}b + c + \dots + r_{3l}l_i$$

$$r_{ly} = r_{l1}a + r_{l2}b + r_{l3}c + \dots + l_i$$

Where,

r_{1y} to r_{ly} = Coefficient of correlation between causal factors 1 to l with dependent characters y.

r_{12} to r_{ll} = Coefficient of correlation among causal factors.

a, b, c...l = Direct effects of characters 'a' to 'l' on the dependent characters 'y'

Residual effect is computed as follows,

$$\text{Residual effect (R)} = 1 - \sqrt{a^2 + b^2 + c^2 + \dots + l^2 + 2abr_{12} + 2acr_{13} + \dots}$$

IV EXPERIMENTAL RESULTS

The present study was conducted at the Regional Agricultural Research Station, Vijayapur during the late *Kharif* season of 2014-15, to assess genetic diversity and variability, degree of association and relative importance of various metric traits upon seed yield within germplasm collection of 111 genotypes of Horse gram. The observations were recorded on days to 50 per cent flowering, days to maturity, plant height (cm), number of primary branches, number of pods per plant, pod length (cm), pod yield per plant (g), number of seeds per pod, seed yield per plant (g), fodder weight (g), 100 seed weight (g), harvest index, seed colour, seed lustre, seed size and stem colour. A total of 21 genotypes were screened for plant protein content and grain nutrient contents (protein, iron & calcium). The results pertaining to analysis of variances (ANOVA), genetic parameters, genetic diversity, correlation, path analysis and evaluation of selected genotypes for plant and grain nutrient contents are presented under the following headings.

4.1 Analysis of variance

4.2 Genetic diversity

4.3 Genetic variability parameters

4.4 Correlation Coefficient

4.5 Path coefficient analysis

4.6 Evaluation of selected genotypes for quality traits

4.1 ANALYSIS OF VARIANCE

Analysis of variance is an important tool for breeder to dissect out the total variability into known and unknown. Significant differences between the treatments indicate the presence of wide variability among the treatments. An effort was made to assess the variability among 111 Horse gram accessions in the present investigation. The analysis of variance for yield and yield attributing characters of these genotypes and their mean sum of squares were highly significant for all the characters studied in germplasm lines of Horse gram. The results obtained were presented in Table 2.

Table 2. Analysis of variance for yield and yield attributing characters in horse gram germplasm lines

Source of variation	Degrees of freedom	Days to 50% Flowering	Days to Maturity	Plant height (cm)	No. Primary Branches	No. Pods/plant	Pod Weight/plant (g)	Pod length (cm)	No. seeds/pod	Seed Weight/plant (g)	Fodder Weight/Plant (g)	100 Seed weight	Harvest index (%)	Seed yield (Kg/ha)
Replication	1	23.35	47.79	32.39	0.99	32.7	8.65	1.14	0.36	1.42	3.15	0.33	136.53	907790.3
Treatment	110	138.15**	178.78**	211.3**	0.83**	191.9**	5.41**	0.95**	0.43**	1.60**	7.29**	0.12**	128.42**	158113.6**
Error	110	6.32	0.82	130.30	0.51	51.15	1.61	0.10	0.36	0.64	1.12	0.06	47.99	49478.34
S.Em.±	-	1.77	0.64	8.03	0.50	5.03	0.89	0.23	0.42	0.56	0.74	0.17	4.87	156.57
CV (%)	-	4.44	0.83	19.22	23.65	22.28	24.67	7.09	11.74	23.67	23.72	6.41	18.68	24.06
CD 5%	-	4.98	1.80	22.62	1.41	14.17	2.51	0.65	1.19	1.58	2.10	0.49	13.72	440.82
CD 1%	-	6.59	2.38	29.92	1.86	18.74	3.33	0.86	1.57	2.09	2.78	0.64	18.15	583.06

* -Significant at 5 % probability

** -Significant at 1 % probability

4.2 GENETIC DIVERSITY

The genetic diversity among 111 genotypes for 13 characters was measured by employing Mahalanobis's generalized distance (D^2) statistic. The correlated unstandardized mean values (X) for all the genotypes for 13 quantitative characters were transferred in to the uncorrelated standardized values (Y). The results pertaining to genetic diversity is presented below.

4.2.1 Group constellations

A method suggested by Tocher (Rao, 1952) was used the accessions into different clusters based on D^2 values. The 111 accessions were grouped in to sixteen clusters.

The distribution pattern into various clusters is given in Table 3 and depicted in Fig. 1. Among sixteen clusters, Cluster II was the biggest comprising of 51 accessions followed by Cluster I with 21 accessions, Cluster III with 19 accessions and Cluster XII comprising of 8 accessions, while remaining clusters were solitary comprising of one genotype each.

4.2.2 Genetic distance of intra and inter clusters

The average D^2 values of intra and inter cluster distances are given in Table 4. Only in clusters I, II, III and XII, high intra cluster distance was observed. Maximum intra cluster distance was shown by cluster XII (6.69) followed by cluster III (5.65), cluster II (5.12) and cluster I (4.75).

Among 111 horse gram accessions, inter cluster distance varied from 3.77 to 24.89. The maximum inter cluster distance observed between Cluster-III and IX (24.89) followed by cluster III and VII (24.66). The lowest inter cluster distance (3.62) was noticed between cluster X and IV. Cluster III and IX were most diverse clusters intercluster distance of 24.89. Cluster XVI was most distant cluster with as many cluster showed maximum inter cluster distance with it.

Cluster I (with intracluster distance of 4.75) which comprised of 21 accessions. The cluster was closely related to V, XI, XIV, XIII, XVI, III and XII with D^2 values of 5.87, 6.18, 6.32, 6.56, 8.13, 8.20 and 9.24, respectively. Whereas, it was diverse from clusters VI, II, XV, IV, VIII, X, VII and IX with D^2 values of 10.21, 12.81, 13.16, 16.44, 16.56, 18.05, 18.48 and 18.63, respectively.

Table 3. Clustering pattern of germplasm lines of horse gram based on D² analysis

Cluster No.	Number of genotypes	Name of the genotypes
I	21	BHGM-20, BHGM-22, BHGM-21, BHL-26, BHL-154, BHGM-23, BHGM-11, BHGM-8, BHGM-27, BHGM-7, BHGM-19, GPM-171, LONE-1, BHGM-10, AK-44, IC100935, IC100938, BHGM-6, BHGM-4, BHGM-5 and PHG-9
II	51	GPM-37, VLG-08, GPM-4-61-4-1, GPM-44, GPM-4.4-113, KBHG-1, RS28-607, GPM-422, PHG-12, GPM-23, BHGM-13, GPM-79, DHG-04, AK-42, BHGM-30, GPM-46, PS-2-4, GPM-62, GPM-49, GPM-36, BHL-48, PHG-21, GPM-25, BHL-78, BHL-128, GHI-641, CRHG-07, GPM-32, VLG-19, 14GH 5R, BHGM-24, GPM-18, GPM-92, BHGM-2, GPM-11, GPM-44-2, 8B, GPM-51, SHG-317, Bailhongal local, BHGM-1, BHG-1, BHGM-3, PHG-02, Kavalgi local, BJPL-1, GPM-12-B, AK-22, BHL-44, GPM-28 and GPM-13
III	19	DS22, BHGM-18, AK-21, BHGM-15, BHGM-29, BHGM-16, Bijapur local, BGM1183, DEH-1, BLHG-1, BHGM-17, CRIDA 18R, GPM-66, CRHG-9, CRHG-05, GPM-48, BHGM-9, BHGM-14 and BHL-60
IV	1	GPM-59
V	1	GPM-23
VI	1	GPM-6
VII	1	BHL-20
VIII	1	GPM-03
IX	1	GPM-58
X	1	12B
XI	1	BHGM-28
XII	8	GPM-30, CRHG-8, CRHG-4, CRHG-6, BHGM-12, CRHG 19R, BHL-66 and GPM-63
XIII	1	BHL-15
XIV	1	GPM-65
XV	1	GPM-22
XVI	1	BHGM-26

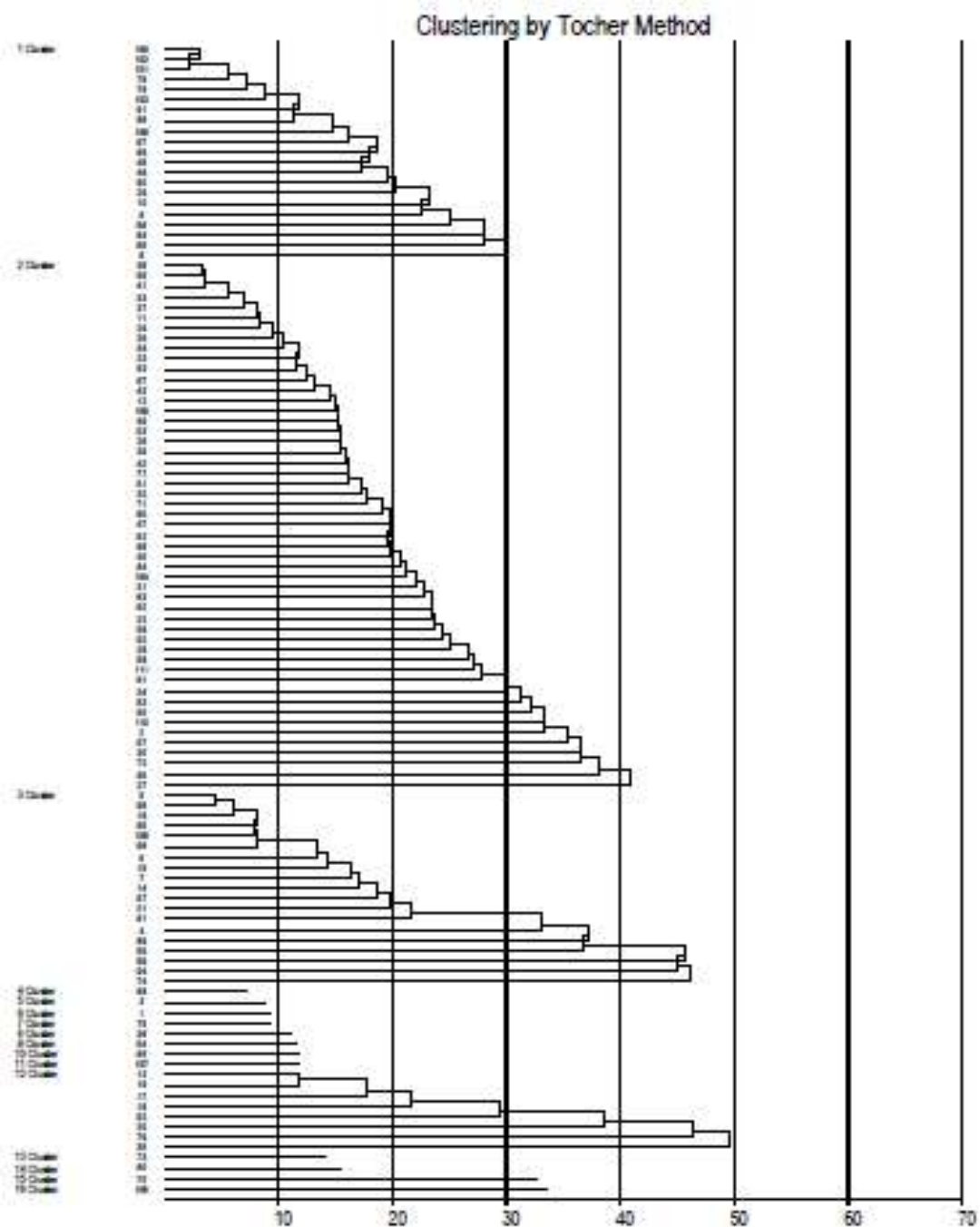


Fig. 1 Clustering pattern of 111 horse gram germplasm lines into different cluster

Cluster II (5.12) is the biggest one comprising of 51 accessions. The cluster II was closely related to IV, VIII, VI, X, XV, IX and XII with D^2 values of 6.59, 7.20, 7.24, 7.46, 7.64, 7.92 and 8.30, respectively, whereas, it was diverse from other clusters like I, V, XIV, XVI, XI, XIII and III with D^2 values of 12.81, 13.31, 15.07, 15.80, 15.99, 16.39 and 18.73, respectively.

Cluster III (5.65) including 19 accessions (DS22, BHGM-18, AK-21, BHGM-15, BHGM-29, BHGM-16, VJPL-2, BGM1183, DEH-1, BLHG-1, BHGM-17, CRIDA 18R, GPM-66, CRHG-9, CRHG-05, GPM-48, BHGM-9, BHGM-14 and BHL-60). The cluster III was closely related to XIII, XI, V, XVI, I and XIV with D^2 values of 7.55, 7.78, 8.03, 8.05, 8.2 and 8.38, respectively. Whereas, cluster II diverse from XII, VI, II, XV, VIII, IV, X, VII and IX with D^2 values of 14.12, 15.09, 18.73, 19.05, 22.38, 22.66, 24.22, 24.66 and 24.89, respectively.

Cluster IV formed a solitary cluster with a single accession (GPM-59) and was closely related to IX, X, VIII, VII, II, XV and VI with D^2 values of 3.39, 3.62, 4.79, 5.51, 6.59, 8.10 and 10.82, respectively. Whereas, it was diverse from XII, I, V, XIV, XI, XIII, XVI and III with D^2 values of 12.04, 16.44, 17.60, 17.78, 19.28, 19.46, 19.78 and 22.66, respectively.

Cluster V formed a solitary cluster with single accession (GPM-23) was closely related to I, XVI, III, XIII, XIV, XII, VI and XI with D^2 values of 5.87, 7.79, 8.03, 8.30, 8.72, 9.00, 9.02 and 9.06, respectively. Whereas it was diverse from II, XV, VIII, IV, VII, X and IX with D^2 values of 13.31, 14.19, 16.88, 17.60, 18.86, 18.88 and 19.41, respectively.

Cluster VI formed a solitary cluster with single accession (GPM-6) and was closely related to XII, VI, V, XV, VIII, with D^2 values of 5.95, 7.24, 9.02, 9.14 and 9.52, respectively. Whereas, it was diverse from I, IV, VII, X, IX, XVI, XIV, XIII, XI and VI with D^2 values of 10.21, 10.82, 11.60, 11.73, 12.31, 12.33, 12.89, 13.73, 14.20 and 15.09, respectively.

Cluster VII formed a solitary cluster with single accession (BHL-20) and was closely related to X, IX, IV, VIII, II, and XV with D^2 values of 3.65, 4.03, 5.51, 6.87, 7.54 and 9.64, respectively. Whereas, it was diverse from VI, XII, I, V, XIV, XVI, XI, XIII and III with D^2 values of 11.60, 12.94, 18.48, 18.86, 20.76, 21.54, 21.62, 22.04 and 24.66, respectively.

Cluster VIII formed a solitary cluster with single accession (GPM-03) and was closely related to IV, IX, X, VII, II, XV and VI with D^2 values of 4.79, 5.74, 6.09, 6.87, 7.2, 9.39 and 9.52, respectively. Whereas, it diverse from XII, I, V, XIV, XVI, XIII, XI and III with D^2 values of 11.87, 16.56, 16.88, 17.95, 19.29, 19.71, 20.07 and 22.38, respectively.

Cluster IX formed a solitary cluster with single accession (GPM-58) and was closely related to IV, X, VII, VIII, II and XV with D^2 values of 3.39, 3.77, 4.03, 5.74, 7.92, and 9.70 respectively. Whereas, it diverse from VI, XII, I, V, XIV, XI, XVI, XIII and III with D^2 values of 12.31, 13.56, 18.63, 19.41, 20.41, 21.66, 21.90 21.92 and 24.89 respectively.

Cluster X formed a solitary cluster having single accession (12B) and it was closely related to IV, VII, IX, VIII, II and XV with D^2 value of 3.62, 3.65, 3.77, 6.09, 7.46 and 8.71, respectively. Whereas, it was diverse from the VI, XII, I, V, XIV, XVI, XI, XIII and III with D^2 values of 11.73, 13.13, 18.05, 18.88, 19.55, 21.10, 21.14, 21.15 and 24.22, respectively.

Cluster XI formed a solitary cluster having single genotype (BHGM-28) and it was closely related to XIII, I, XIV, III, V and XVI with D^2 value of 6.05, 6.18, 6.74, 7.78, 9.06 and 9.58, respectively. Whereas, it was diverse from XII, VI, XV, II, IV, VIII, X, VII and IX with D^2 values 12.42, 14.20, 15.97, 15.99, 19.28, 20.07, 21.14, 21.62 and 21.66, respectively.

Cluster XII (6.69) comprising of eight accessions (GPM-30, CRHG-8, CRHG-4, CRHG-6, BHGM-12, CRHG 19R, BHL-66 and GPM-63) were closely related to VI, II, V, I and XV with D^2 value of 5.95, 8.30, 9.0, 9.24 and 10.54, respectively. Whereas, it was diverse from XVI, VIII, IV, XIV, XI, VII, X, XIII, IX and III with D^2 values of 11.28, 11.87, 12.04, 12.26, 12.42, 12.94, 13.13 13.15, 13.56 and 14.12, respectively.

Cluster XIII formed a solitary cluster (BHL-15) and it was closely related to XIV, XI, I, III and V with D^2 value of 3.92, 6.05, 6.56, 7.55 and 8.30, respectively. Whereas, it was diverse from XVI, XII, VI, XV, II, IV, VIII, X, IX and VII with D^2 value of 11.10, 13.15, 13.73, 14.75, 16.39, 19.46, 19.71, 21.15, 21.92 and 22.04, respectively.

Cluster XIV formed a solitary cluster (GPM-65) and it was in close proximity with cluster XIII, I, XI, III, V and XVI with D^2 value 3.92, 6.32, 6.74, 8.38, 8.72 and 9.88, respectively. Whereas, it was diverse from clusters XII, VI, XV, II, IV, VIII, X, IX and VII with D^2 value 12.26, 12.89, 14.25, 15.07, 17.78, 17.95, 19.55, 20.41 and 20.76, respectively.

Cluster XV also formed a solitary cluster with a single accession (GPM-22). It was close to clusters II, IV, X, VI, VIII, VII and IX having D^2 values of 7.64, 8.10, 8.71, 9.14, 9.39, 9.64 and 9.70, respectively. Whereas, it was found to be diverse from the clusters XII, I, V, XIV, XIII, XI, XVI and III having the D^2 value 10.54, 13.16, 14.19, 14.25, 14.75, 15.97, 18.22 and 19.05, respectively. Cluster XVI also formed a solitary cluster with a single accession (BHGM-26). It was in close proximity to clusters V, III, I, XI and XIV comprising of D^2 value 7.79, 8.05, 8.13, 9.58 and 9.88, respectively. Whereas, it was far from clusters XIII, XII, VI, II, XV, VIII, IV, X, VII and IX with D^2 values 11.10, 11.28, 12.33, 15.80, 18.22, 19.29, 19.78, 21.10, 21.54 and 21.90, respectively.

4.2.3 Contribution of different characters towards divergence

Out of 13 characters studied in germplasm accessions of horse gram, the trait days to maturity contributes highest (71.20 %) towards the genetic divergence, followed by days to 50% flowering (16.56 %), fodder weight per plant (4.96 %), number of pods per plant (1.65 %), seed yield (1.59 %), seed yield per plant (1.03 %), pods weight per plant (0.82 %), 100 seed weight (0.59 %), harvest index (0.44 %), number of branches per plant (0.43 %), number of seeds per pod (0.36 %), plant height (0.21 %) and pod length (0.15). The results are presented in Table 5 and plate 2.

4.2.4 Cluster mean analysis

Comparison of cluster means for different characters is provided in Table 6. The results indicated substantial variation present among clusters grouped according to D^2 analysis. Based on the range of means, it was possible to know the characters influencing divergence. Among the accessions of the present study, low days to 50% flowering was recorded in the clusters VI, XVI, V, XII (below 50 days) and clusters IV, XI, XIV, X, XV and IX had highest days to 50% flowering (above 65 days), while remaining clusters had moderate days to 50% flowering indicating the wide range of genetic diversity available in the accessions. Minimum number of days to 50% flowering was observed in cluster VI (42.50) and greater number of days to 50% flowering observed in IV cluster (67.50).

Table 5. Per cent contribution of characters towards total divergence in horse gram germplasm lines

Sl. No.	Source	Contribution (%)
1	Days to maturity	71.20
2	Days to 50 per cent flowering	16.56
3	Fodder weight per plant (g)	4.96
4	Number of pods per plant	1.65
5	Seed yield (Kg/ha)	1.59
6	Seed yield per plant (g)	1.03
7	Pod weight per plant (g)	0.82
8	100 seed weight (g)	0.59
9	Harvest index (%)	0.44
10	Number of branches per plant	0.43
11	Number of seeds per pod	0.36
12	Plant height (cm)	0.21
13	Pod length (cm)	0.15
	Total	100

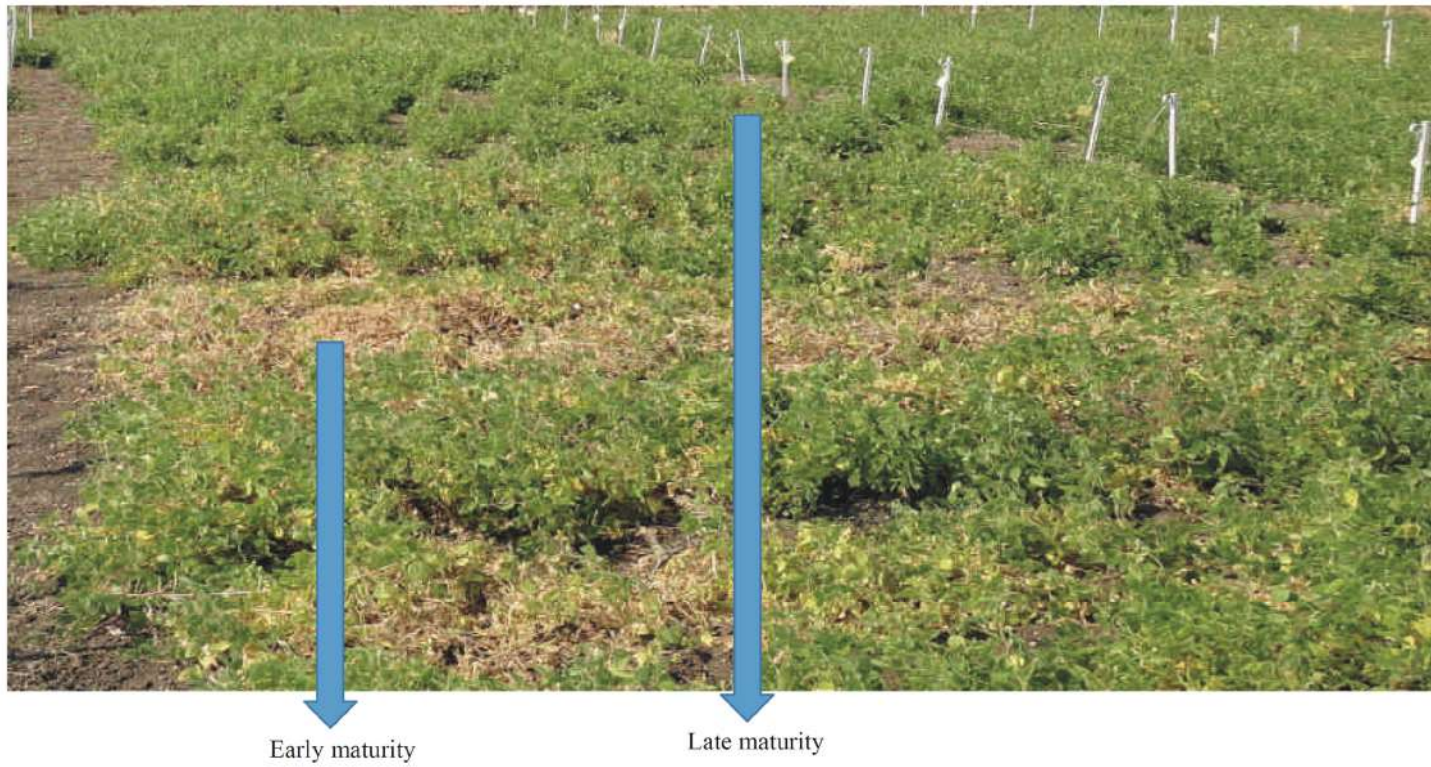


Plate 2. General view and varietal differences for maturity early vs late among germplasm lines of horse gram

Days to maturity was very low in the clusters III, XIII, XI, XIV and XVI (below 100 days) whereas, the highest days to maturity was occurred in the clusters VII, X, IX and IV (above 120 days), while remaining clusters were moderate in days to maturity. Highest mean for plant height (cm) was showed by clusters X (75.10), VIII (74.90) and VII (74.2) whereas lowest plant height was observed in clusters XI (30.90) and XII (50.56), while other clusters were moderate in plant height. Thus indicating a wide range of diversity existed for these traits.

The cluster mean for number of primary branches was recorded highest in clusters XVI (3.9), XIV (3.80) and XII (3.35), whereas lowest primary branches observed in the clusters IV (2.20) and V (2.40). The remaining clusters were moderate in bearing primary branches indicating that this trait is also having the wide range of diversity.

Highest number of pods per plant was observed in the cluster XVI (68.00) and the lowest recorded in the cluster V (16.20). Whereas other clusters having the moderate number of pods. Thus indicated highest diversity also present in this trait.

The cluster means for pod weight per plant was recorded highest in cluster XIV (8.30) and the lowest was occurred in the cluster V (2.80). Remaining clusters showed moderate in pod weight per plant. Pod length shows highest cluster mean in the cluster VIII (5.22), whereas lowest was recorded in the cluster XV (4.27), and remaining clusters showed moderate in pod length indicating that these traits shows higher diversity.

Number of seeds per pod was highest in the cluster IV (6.00) whereas lowest mean for the trait was recorded in the cluster XV and XVI (4.80). While other remaining clusters having the moderate in number of seeds per pod indicated presence of diversity for this trait.

The cluster mean for seed weight per plant was recorded highest in clusters, XV (6.60) followed by XIII (5.35) and XIV (5.20), whereas lowest mean observed in the clusters V (2.15) followed by XI (2.45). Remaining clusters were moderate in seed weight per plant. Thus indicating that wide range of diversity existed among genotypes for this trait also.

Fodder weight per plant was highest in the cluster VIII (9.5) followed by IV (8.85) whereas lowest was recorded in the cluster XI (1.80) followed by V (2.95), while other

Table 6. Cluster means of germplasm lines of horse gram for yield and yield related traits

Cluster	No. of entries /cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	No. Primary branches	No. pods/ plant	Pod weight/p lant(g)	Pod length (cm)	No. seeds/p od	Seed weight/p lant (g)	Fodder weight/p lant(g)	100 seed weight (g)	Harvest index (%)	Seed yield(Kg/ha)	overall score	Rank
I	21	58.55 (8)	101.88 (7)	56.63(11)	3.07 (5)	31.15 (7)	4.81 (11)	4.60 (9)	5.15 (10)	3.33 (9)	3.81 (10)	3.79 (13)	39.71 (7)	823.18 (13)	120	11
II	51	58.34 (7)	116.32 (11)	63.12 (7)	2.89 (8)	30.92 (8)	5.11 (9)	4.67 (5)	5.22 (7)	3.33 (10)	5.01(9)	3.92 (8)	34.08 (11)	887.95 (11)	111	9
III	19	50.87 (5)	94.37 (1)	53.82 (14)	3.26 (4)	36.38 (6)	5.45 (8)	4.66 (6)	4.89 (12)	3.29 (12)	3.32 (13)	3.72 (14)	40.38 (6)	1093.23 (8)	109	8
IV	1	67.50 (16)	120.50 (13)	68.4 (5)	2.20 (16)	39.70 (4)	7.15 (4)	4.71 (3)	6.00 (1)	4.35 (5)	8.85 (2)	4.00 (5)	27.15 (14)	846.30 (12)	100	6
V	1	47.00 (3)	101.50 (6)	64.30 (6)	2.40 (15)	16.20 (16)	2.80 (16)	4.71 (4)	5.20 (8)	2.15 (16)	2.95 (15)	4.50 (1)	38.55 (8)	1268.52 (6)	120	12
VI	1	42.50 (1)	111.00(9)	61.50 (10)	2.50 (11)	27.10 (12)	4.79 (12)	4.55 (10)	5.10 (11)	4.35 (6)	5.60 (8)	3.95 (7)	41.45 (5)	1374.07 (3)	105	7
VII	1	62.50 (9)	124.5 (16)	74.20 (3)	2.70 (9)	20.60 (15)	3.40 (15)	4.45 (12)	5.20 (9)	3.15 (13)	3.75 (11)	3.90 (9)	44.10 (3)	906.5 (10)	134	15
VIII	1	57.00 (6)	119.5 (12)	74.90 (2)	2.90 (6)	39.20 (5)	4.35 (13)	5.22 (1)	6.00 (2)	3.30 (11)	9.85 (1)	4.05 (4)	23.40 (16)	1338.89 (5)	84	2
IX	1	66.00 (12)	123.5 (14)	72.90 (4)	2.50 (12)	30.80 (9)	5.50 (7)	4.32 (14)	5.30 (5)	3.35 (8)	8.75 (3)	4.20 (3)	23.60 (15)	521.30 (15)	121	13
X	1	66.50 (13)	123.5 (15)	75.10 (1)	2.90 (7)	40.80 (3)	7.70 (3)	4.32 (15)	5.40 (4)	5.00 (4)	6.30 (5)	4.00 (6)	35.65 (9)	1372.25 (4)	89	3
XI	1	67.00 (15)	98.50 (3)	30.90 (16)	2.50 (13)	23.30 (13)	3.50 (14)	4.61 (8)	5.50 (3)	2.45 (15)	1.80 (16)	3.20 (16)	47.30 (1)	351.85 (16)	149	16
XII	8	49.00 (4)	109.81 (8)	50.56 (15)	3.35 (3)	29.78 (10)	4.95 (10)	4.64 (7)	4.85 (13)	3.44 (7)	3.51 (12)	3.83 (12)	43.87 (4)	793.75 (14)	119	10
XIII	1	65.00 (10)	97.50 (2)	62.00 (8)	2.70 (10)	28.30 (11)	6.15 (5)	4.46 (11)	5.30 (6)	5.35 (2)	5.75 (6)	3.90 (10)	35.05 (10)	1105.55 (7)	98	5
XIV	1	67.00 (14)	99.50 (4)	61.70 (9)	3.80 (2)	44.90 (2)	8.30 (1)	4.83 (2)	4.80 (14)	5.20 (3)	7.30 (4)	3.85 (11)	33.75 (12)	1411.10 (1)	79	1
XV	1	65.50 (11)	115.00 (10)	54.4 (13)	2.50 (14)	22.90 (14)	5.65 (6)	4.27 (16)	4.80 (15)	6.60 (1)	5.65 (7)	4.25 (2)	30.85 (13)	1000.00 (9)	131	14
XVI	1	45.00 (2)	99.50 (5)	56.4 (12)	3.90 (1)	68.00 (1)	8.10 (2)	4.45 (13)	4.80 (16)	2.65 (14)	3.20 (14)	3.50 (15)	45.15 (2)	1410.20 (2)	99	4

remaining clusters had moderate values. The cluster mean for 100 seed weight was recorded highest in clusters, V (4.50), XV (4.25) and IX (4.20), whereas lower seed weight per plant observed in the clusters XI (3.20) and XVI (3.50) and remaining clusters were moderate in 100 seed weight. Thus indicating the wide range of diversity present among genotypes for both the traits.

Cluster mean for harvest index was highest in the cluster XI (47.30) whereas lowest was recorded in the cluster VIII (23.40) followed by IX (23.60), while other remaining clusters were recorded moderate harvest index. The cluster mean for seed yield (kg/ha) was recorded highest in clusters XIV (1411.10) followed by XVI (1410.20), VI (1374.07), whereas lowest means for the traits were observed in the clusters XI (351.85) followed by IX (521.30) and remaining clusters were moderate in plot yield. Thus indicating wide range of diversity is present for this trait also.

4.3 GENETIC VARIABILITY PARAMETERS

Assessment of variability was done among the 111 germplasm accessions of horse gram. The mean values obtained for various traits of all accessions are given in Appendix II. The results pertaining to genetic parameters *viz* range, mean, genotypic variance, phenotypic variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2), genetic advance (GA) and genetic advance as per cent of mean (GAM) were calculated to estimate the extent of genetic variability for 13 characters. The results are presented in the Table 7.

4.3.1 Days to 50 per cent flowering

The analysis of variance showed that the entries differed significantly for this character (Table 2). The early flowering entry (BGM1183) took 40.5 days to 50% flower. The late flowering was observed in the entry SHG-317 which took 69.00 days. On an average all the entries flowered by 56.59 days after sowing. This is an indication of wide variability existed. The estimated GCV and PCV of this character were 14.34 and 15.01 per cent respectively. The heritability recorded by this trait was 91.25 per cent, while the genotypic and phenotypic variance was 65.91 and 72.23 respectively, genetic advance was 15.97 and genetic advance as per cent of mean was 28.22. These estimates indicated moderate GCV and PCV, while it has high heritability and genetic advance as percent mean.

4.3.2 Days to maturity

This character exhibited highly significant varietal differences (Table 2). The days to maturity ranged from 91.50 (BHGM-15) to 124.50 (BHL-20) days with the mean value of 108.80 days. The lower values of GCV of 8.66 per cent and PCV of 8.70 per cent indicating lower variation for this trait. Marginal difference between GCV and PCV indicated negligible environmental influence on this character. The genotypic and phenotypic variance estimates were 88.97 and 89.80, respectively. This trait recorded high heritability (99.08 per cent), while the genetic advance was 19.34 and genetic advance as per cent of mean was 17.77.

4.3.3 Plant height (cm)

The differences among the genotypes with respect to plant height were found to be highly significant (Table 2). The plant height was ranged from 30.90 (BHGM-28) to 89.80 cm (DHG-04) with a mean value of 59.38 cm. The GCV and PCV values were 10.71 and 22.00 per cent, respectively for the trait and it was moderate in variation. The genotypic and phenotypic variance values were 40.51 and 170.81, respectively. Heritability estimate of 23.72 per cent was recorded for this trait was moderate in nature, with the genetic advance of 6.38 and genetic advance as per cent of mean of 10.75.

4.3.4 Number of primary branches

This character exhibited highly significant varietal differences (Table 2). The minimum number of branches was found in the genotype DEH-1 (1.80) while, maximum number of branches were found in GPM-48 (5.20) with a mean of 3.01. The GCV of 13.42 per cent and PCV of 27.20 per cent were registered for this trait. The genotypic variance was 0.16 and phenotypic variance was 0.67. Moderate heritability recorded for the trait was 24.35 per cent with the genetic advance 0.41 and high genetic advance over the mean of 13.64 percent was noticed for the character.

4.3.5 Number of pods per plant

The differences among the genotypes with respect to number of pods per plant were found to be highly significant (Table 2). The number of pods per plant was ranged from 15.10 (KBHG-1) to 68.00 (BHGM-26) with an average of 32.09. The high GCV and PCV estimates recorded were 26.14 and 34.35, per cent respectively, indicating higher variation observed for the trait. The genotypic and phenotypic variance recorded was

70.37 and 121.53 respectively, while the genetic advance was 13.15 and the higher genetic advance as per cent of mean of 40.97 per cent with high heritability estimate of 57.91 per cent was observed.

4.3.6 Pod weight per plant (g)

This character exhibited highly significant varietal differences (Table 2). The pod weight per plant (g) recorded for the genotypes was ranged from 2.50 (GPM-30) to 10.70 (CRHG-05) with a mean value of 5.15. The higher GCV and PCV recorded for the trait were 26.73 and 36.37, per cent respectively with high heritability of 53.99 per cent with genetic advance of 2.08 and high genetic advance as per cent of mean of 40.46, and the genotypic and phenotypic variance observed was 1.89 and 3.51, respectively.

4.3.7 Pod length (cm)

The differences among the genotypes with respect to pod length were found to be significant (Table 2). The pod length was ranged from 4.07 cm (GPM-44-2) to 5.22 cm (GPM-03) with an average pod length of 4.64 cm. The lower GCV of 1.09 per cent and PCV of 7.01 per cent with low heritability of -2.46 per cent, the genetic advance -0.01 and the genetic advance as per cent of mean -0.35 per cent were recorded for this trait, and also very low genotypic variance and phenotypic variance recorded were -0.002 and 0.10, respectively for the character.

4.2.8 Number of seeds per pod

This character exhibited highly significant varietal differences (Table 2). The number of seeds per pod was ranged from 3.90 (CRHG-6) to 6.20 (BHL-44) with a mean value of 5.13. The lower GCV and moderate PCV for number of seeds per pod recorded were 3.75 and 12.33 per cent, respectively. The low heritability estimates of 9.29 per cent, low genetic advance and genetic advance as per cent of mean of 0.12 and 2.35, respectively. The genotypic and phenotypic variance estimates recorded for the trait were 0.03 and 0.40, respectively.

4.3.9 Seed weight per plant (g)

The differences among the genotypes with respect to seed weight per plant were found to be highly significant (Table 2). The average yield per plant recorded was 3.38 g and the yield per plant was ranged from 1.85 g (GPM-30) to 6.60 g (CRHG-05). The

higher GCV and PCV recorded were 20.48 and 31.30 per cent, respectively. While, low genetic advance and high genetic advance over the mean were observed with values 0.93 and 27.61, respectively. With high heritability of 44.82 per cent.

4.3.10 Fodder weight per plant (g)

The differences among the genotypes with respect to fodder weight per plant were found to be highly significant (Table 2). The average fodder weight per plant recorded was 4.47 g and the fodder weight per plant was ranged from 1.20 g (BHGM-8) to 9.85 g (GPM-03). The higher GCV and PCV recorded were 39.26 and 45.87 per cent, respectively. While, low genetic advance and high genetic advance over the mean were 3.09 and 69.22, with high heritability of 73.25 per cent. The estimates of genotypic and phenotypic variances were 3.08 and 4.20, respectively.

4.3.11 100 seed weight (g)

This character exhibited highly significant varietal differences (Table 2). The average 100 seed weight recorded was 3.85 g and it ranged from 3.15 (BHGM-29) to 4.50 g (GPM-23). The lower GCV and PCV values were 4.75 and 7.98 per cent, respectively. Lower genetic advance and genetic advance as per cent of mean were recorded (0.22 and 5.83, respectively) with high heritability of 35.49 per cent. The estimates of genotypic and phenotypic variance recorded were 0.03 and 0.09, respectively.

4.3.12 Harvest index (%)

This character exhibited highly significant varietal differences (Table 2). The average harvest index recorded was 37.08 per cent and the minimum and maximum harvest index was found in the accessions GPM-03 (23.42) to CRHG 19R (63.33) per cent. The moderate GCV and high PCV values were 17.10 and 25.32, per cent respectively. While, low genetic advance and high genetic advance as per cent of mean were 8.82 and 23.78 with high heritability of 45.59 per cent were observed for the trait. The higher genotypic and phenotypic variance were observed (40.21 and 88.20, respectively).

4.3.13 Seed yield (Kg/ha)

This character exhibited highly significant varietal differences (Table 2). The average yield recorded was 924.32 kg/ha and the minimum to maximum yield (kg/ha) was found in the accessions BHGM-28 (351.85) to VJPL-2 (1673.15). The higher GCV and

Table 7. Estimates of range, mean, variability, heritability and genetic advance for different characters among horse gram germplasm lines

Variability parameters	Range		Mean	Variance		Co-efficient of variation (%)		h ² bs (%)	GA (%)	GAM (%)
	Min.	Max		Genotypic	Phenotypic	Genotypic	Phenotypic			
Days to 50 % flowering	40.50 (BHGM1183)	69.00 (SHG-317)	56.59	65.91	72.23	14.34	15.01	91.25	15.97	28.22
Days to maturity	91.50 (BHGM-15)	124.50 (BHL-20)	108.80	88.97	89.80	8.66	8.70	99.08	19.34	17.77
Plant height (cm)	30.90 (BHGM-28)	89.80 (DHG-04)	59.38	40.51	170.81	10.71	22.00	23.72	6.38	10.75
Number of primary branches	1.80 (DEH-1)	5.20 (GPM-48)	3.01	0.16	0.67	13.42	27.20	24.35	0.41	13.64
Number of pods per plant	15.10 (KBHG-1)	68.00 (BHGM-26)	32.09	70.37	121.53	26.14	34.35	57.91	13.15	40.97
Pod weight per plant (g)	2.50 (GPM-30)	10.70 (CRHG-05)	5.15	1.89	3.51	26.73	36.37	53.99	2.08	40.46
Pod length (cm)	4.07 (GPM-44-2)	5.22 (GPM-03)	4.64	-0.002	0.10	1.09	7.01	-2.46	-0.01	-0.35
Number of seeds per pod	3.90 (CRHG-6)	6.20 (BHL-44)	5.13	0.03	0.40	3.75	12.33	9.29	0.12	2.35
Seed weight per plant (g)	1.85 (GPM-30)	6.60 (CRHG-05).	3.38	0.48	1.12	20.48	31.30	44.82	0.93	27.61
Fodder weight per plant (g)	1.20 (BHGM-8)	9.85 (GPM-03)	4.47	3.08	4.20	39.26	45.87	73.25	3.09	69.22
100 seed weight (g)	3.15 (BHGM-29)	4.50 (GPM-23)	3.85	0.03	0.09	4.75	7.98	35.49	0.22	5.83
Harvest index (%)	23.42 (GPM-03)	63.33 (CRHG 19R)	37.08	40.21	88.20	17.10	25.32	45.59	8.82	23.78
Seedyield (Kg/ha)	351.85 (BHGM-28)	1673.1 (VJPL-2)	924.32	54317.65	103796.00	25.21	34.85	52.33	347.31	37.57

PCV values were 25.21 and 34.85, per cent respectively were recorded. Higher genetic advance and genetic advance as per cent of mean were 347.31 and 37.57, respectively with high heritability of 52.33 per cent were observed for the trait. The higher genetic and phenotypic variance estimates were observed (54317.65 and 103796.00, respectively).

4.4 CORRELATION COEFFICIENTS

Improvement in the seed yield is an important activity of crop breeding, the ultimate seed yield is a complex process that will be affected by many genetic and non-genetic factors. In order to know the magnitude of the association between the seed yield with other yield influencing traits, correlation analysis is an effective tool. The correlation studies give us an idea about how the traits are associated with each other as well as with the seed yield. The results of the association studies are presented hereunder.

Phenotypic correlations were calculated among 13 characters to know the nature of association existing among them and presented in the Table 8.

4.4 Phenotypic correlation coefficients between seed yield and its components

4.4.1 Days to 50 per cent flowering

The days to maturity exhibited highest positive significant association with days to 50 per cent flowering ($r=0.484$) at phenotypic level followed by number of seeds per pod (0.442), 100 seed weight (0.381), pod length (0.337), seed weight per plant (0.295), fodder weight per plant (0.294), number of primary branches (0.283), pod weight per plant (0.233) and plant height (0.200). It had positive non-significant association with number of pods per plant (0.079) and harvest index (0.0009). The seed yield (kg/ha) showed negative significant association with days to 50 per cent flowering (-0.203).

4.4.2 Days to maturity

The trait had highest positive and significant association with 100 seed weight (0.674) at phenotypic level followed by number of seeds per pod (0.612), pod length (0.603), fodder weight (0.517), days to 50% flowering (0.484), plant height (0.442), seed weight per plant (0.418), number of primary branches (0.359) and pod weight per plant (0.256). Whereas, the trait exhibited positive non-significant association with number of pods per plant (0.033). It exerts negative non-significant association with harvest index (-0.014) and seed yield per hectare (-0.018).

4.4.3 Plant height (cm)

The plant height had positive significant correlation with seed yield per hectare (0.168) and fodder weight (0.649), followed by number of seeds per pod (0.462), days to maturity (0.442), seed weight per plant (0.360), 100 seed weight (0.345), pod weight per plant (0.326), pod length (0.279), number of primary branches (0.213), days to 50% flowering (0.200) and number of pods per plant (0.154), It had negative non-significant correlation with harvest index (-0.283).

4.4.4 Number of primary branches

The primary branches exhibited positive significant correlation with seed yield per hectare (0.201) at phenotypic level. The higher positive significant association of primary branches exhibited with pod length (0.627) followed by 100 seed weight (0.612), number of seeds per pod (0.591), seed weight per plant (0.525), number of pods per plant (0.384), days to maturity (0.359), harvest index (0.337), days to 50% flowering (0.283), fodder weight (0.223) and plant height (0.213).

4.4.5 Number of pods per plant

It showed positive significant association with seed yield per hectare (0.185) and highest positive correlation was occurred with pod weight per plant (0.775), followed by seed weight per plant (0.552), number of primary branches (0.384), fodder weight per plant (0.265), pod length (0.260), number of seeds per pod (0.259), 100 seed weight (0.213) and plant height (0.154).

4.4.6 Pod weight per plant (g)

The pod weight per plant had positive and significant association with seed yield per hectare (0.263) and highest positive correlation was exhibited with seed weight per plant (0.821) at phenotypic level followed by number of pods per plant (0.775), fodder weight per plant (0.520), number of seeds per pod (0.487), number of primary branches (0.468), 100 seed weight (0.452), pod length (0.426), plant height (0.326), days to maturity (0.256) and days to 50% flowering (0.233). Pod weight per plant showed positive non-significant correlation with harvest index (0.036).

4.4.7 Pod length (cm)

The pod length exhibited positive and significant association with seed yield per hectare (0.205), while highest association of pod length was occurred with 100 seed weight (0.914) followed by number of seeds per pod (0.793), number of primary branches (0.627), days to maturity (0.603), seed weight per plant (0.580), pod weight per plant (0.426), fodder weight per plant (0.371), days to 50% flowering (0.337), harvest index (0.317), plant height (0.279) and number of pods per plant (0.260) at phenotypic level.

4.4.8 Number of seeds per pod

The number of seeds per plant had positive and significant association with seed yield per hectare (0.139) and highest positive correlation was exhibited with pod length (0.793), 100 seed weight (0.782) at phenotypic level followed by seed weight per plant (0.642), days to maturity (0.612), number of primary branches (0.591), fodder weight per plant (0.505), pod weight per plant (0.487), plant height (0.462), days to maturity (0.442), number of pods per plant (0.259) and harvest index (0.233).

4.4.9 Seed weight per plant (g)

It showed positive significant association with seed yield per hectare (0.235) and highest positive correlation was occurred with pod weight per plant (0.821), followed by number of seeds per pod (0.642), 100 seed weight (0.622), pod length (0.580), number of pods per plant (0.552), fodder weight per plant (0.542), number of primary branches (0.525), days to maturity (0.418), plant height (0.360), days to 50% flowering (0.295) and harvest index (0.247).

4.4.10 Fodder weight per plant (g)

Fodder weight per plant exhibited positive significant association with seed yield per hectare (0.153) while highest positive significant correlation occurred with plant height (0.649), followed by seed weight per plant (0.542), pod weight per plant (0.520), days to maturity (0.517), number of seeds per pod (0.505), 100 seed weight (0.467), pod length (0.371), days to 50% flowering (0.294), number of pods per plant (0.265) and number of primary branches (0.223) at phenotypic level. However, fodder weight per plant showed negative significant correlation with harvest index (0.483).

Table 8. Phenotypic correlation co-efficient between different traits in germplasm lines of horse gram

Character	Days to 50% flowering	Days to maturity	Plant height (cm)	No. primary branches	No. pods/plant	Pod weight/Plant (g)	Pod length (cm)	No. seeds/pod	Seed weight/plant (g)	Fodder weight/Plant (g)	100 seed weight (g)	Harvest index (%)	Seed yield (Kg/ha)
Days to 50% flowering	1.00	0.484**	0.200**	0.283**	0.079	0.233**	0.337**	0.442**	0.295**	0.294**	0.381**	0.0009	-0.203**
Days to maturity		1.00	0.442**	0.359**	0.033	0.256**	0.603**	0.612**	0.418**	0.517**	0.674**	-0.014	-0.018
Plant height (cm)			1.00	0.213*	0.154*	0.326**	0.279**	0.462**	0.360**	0.649**	0.345**	-0.283**	0.168*
No. primary branches				1.00	0.384**	0.468**	0.627**	0.591**	0.525**	0.223**	0.612**	0.337**	0.201**
No. pods/plant					1.00	0.775**	0.260**	0.259**	0.552**	0.265**	0.213**	0.126	0.185**
Pod weight/Plant (cm)						1.00	0.426**	0.487**	0.821**	0.520**	0.452**	0.036	0.263**
Pods length (cm)							1.00	0.793**	0.580**	0.371**	0.914**	0.317**	0.205**
No. seeds/ pod								1.00	0.642**	0.505**	0.782**	0.233**	0.139*
Seed weight/Plant (g)									1.00	0.542**	0.622**	0.247**	0.235**
Fodder weight/Plant (g)										1.00	0.467**	-0.483**	0.153*
100 seed weight (g)											1.00	0.225**	0.225**
Harvest index (%)												1.00	0.018
Seed yield (Kg/ha)													1.00

* -Significant at 5 % probability, ** -Significant at 1 % probability

4.4.11 100 seed weight (g)

100 seed weight recorded positive significant correlation with seed yield per hectare (0.225), whereas it showed highest association with pod length (0.914), number of seeds per pod (0.782), days to maturity (0.674), seed weight per plant (0.622), number of primary branches (0.612), fodder weight per plant (0.467), pod weight per plant (0.452), days to 50% flowering (0.381), plant height (0.345), harvest index (0.2252) and number of pods per plant (0.213) at phenotypic level.

4.4.12 Harvest index (%)

Harvest index showed positive and non-significant correlation with seed yield per hectare at phenotypic level (0.018), while the highest positive significant correlation was occurred with number of primary branches (0.337), pod length (0.317), seed weight per plant (0.247), number of seeds per pod (0.233) and 100 seed weight (0.225). However, harvest index showed negative significant association with fodder weight per plant (0.483) and plant height (0.283).

4.5 PATH COEFFICIENT ANALYSIS

The path analysis was done to partition the correlation coefficient into direct and indirect effects. The phenotypic correlation coefficients of various characters which showed significant association with seed yield were subjected to path analysis to estimate the direct and indirect effects of component traits. Seed yield considered as dependent variable in the analysis. The direct and indirect effects of various traits with respect to seed yield at phenotypic level are presented in Table 9.

4.5. Path analysis at phenotypic level

4.5.1 Direct effects

Out of 12 characters, six characters had positive direct effect on seed yield per hectare at phenotypic level. The highest positive effect on seed yield was observed in 100 seed weight (0.3482) followed by pod weight per plant (0.2336), plant height (0.1537), number of primary branches (0.0893), pod length (0.0386) and seed weight per plant (0.0187), whereas, other six characters showed negative direct effect. The highest negative direct effect was observed by days to 50% flowering (-0.2999) followed by days

to maturity (-0.2247), number of seeds per pod (-0.0942), number of pods per plant (-0.0779), harvest index (-0.0573) and fodder weight per plant (-0.0296) at phenotypic level.

4.5.2 Indirect effects

Indirect effect on seed yield considering each character is described below.

4.5.2.1 Days to 50% flowering

Days to 50% flowering exhibited negative correlation and negative direct effect on seed yield. It also showed indirect and negative effect through days to maturity (-0.1452) followed by number of seeds per pod (-0.1328), 100 seed weight (-0.1145), pod length (-0.1012), seed weight per plant (-0.0885), fodder weight per plant (-0.0883), number of primary branches per plant (-0.0849), pod weight per plant (-0.0701), number of pods per plant (-0.0238) and harvest index (-0.0003). Whereas, there was no positive indirect effect on seed yield through days to 50% flowering.

4.5.2.2 Days to maturity

Days to maturity had negative correlation and negative direct effect on seed yield. It also had negative indirect effect on seed yield through 100 seed weight (-0.1515) followed by number of seeds per pod (-0.1376), pod length (-0.1355), fodder weight per plant (-0.1163), days to 50% flowering (-0.1088), plant height (-0.0995), seed weight per plant (-0.0941), number of primary branches per plant (-0.0809), pod weight per plant (-0.0576) and number of pods per plant (-0.0075). It also showed positive indirect effect through harvest index (0.0033) on seed yield at phenotypic level.

4.5.2.3 Plant height

Plant height exhibited positive correlation and also positive direct effect on seed yield. It had highest positive indirect effect on seed yield through fodder weight per plant (0.0999) followed by number of seeds per pod (0.07122), days to maturity (0.0681), seed weight per plant (0.0554), 100 seed weight (0.0532), pod weight per plant (0.0502), pod length (0.0430), number of primary branches per plant (0.0328), days to 50% flowering (0.0307) and number of pods per plant (0.0237) at phenotypic level. It also showed negative indirect effect on seed yield through harvest index (-0.0435).

4.5.2.4 Number of primary branches

Number of primary branches per plant showed positive correlation and also positive direct effect on seed yield. It had highest positive indirect effect on seed yield through pod length (0.0561) followed by 100 seed weight (0.0547), number of seeds per pod (0.0528), seed weight per plant (0.0469), pod weight per plant (0.0418), number of pods per plant (0.0343), days to maturity (0.0321), harvest index (0.0301), days to 50% flowering (0.0253) fodder weight per plant (0.0200) and plant height (0.0190) at phenotypic level.

4.5.2.5 Number of pods per plant

Number of pods per plant expressed positive correlation and negative direct effect on seed yield. Whereas it exhibited highest negative indirect effect on seed yield through pod weight per plant (-0.0605) followed by seed weight per plant (-0.0430), number of primary branches per plant (-0.0299), fodder weight per plant (-0.0207), pod length (-0.0203), number of seeds per pod (-0.0203), 100 seed weight (-0.0167), plant height (-0.0120), harvest index (-0.0098), days 50% flowering (-0.0062) and days to maturity (-0.0026) at phenotypic level.

4.5.2.6 Pods weight per plant

Pod weight per plant had correlation and positive direct effect on seed yield. Whereas it exhibited highest positive indirect effect on seed yield through seed weight per plant (0.1918) followed by number of pods per plant (0.1812), fodder weight per plant (0.1215), number of seeds per pod (0.1138), number of primary branches per plant (0.1093), 100 seed weight (0.1057), pod length (0.0995), plant height (0.0762), days to maturity (0.0599), days to 50% flowering (0.0546) and harvest index (0.0085) at phenotypic level.

4.5.2.7 Pods length

Pod length exhibited positive correlation and positive direct effect on seed yield at phenotypic level. Whereas it also showed highest positive indirect effect on seed yield through 100 seed weight (0.0353) followed by number of seeds per pod (0.0306), number of primary branches per plant (0.0242), days to maturity (0.0233), seed weight per plant (0.0224), pod weight per plant (0.0164), fodder weight per plant (0.0143), days to 50%

flowering (0.0130), harvest index (0.0123), plant height (0.0108) and number of pods per plant (0.0100).

4.5.2.8 Number of seeds per pod

Number of seeds per pod had positive correlation and negative direct effect on seed yield at phenotypic level. However, it had highest negative indirect effect on seed yield through pod length (-0.0747) followed by 100 seed weight (-0.0737), seed weight per plant (-0.0605), days to maturity (-0.0577), number of primary branches per plant (-0.0557), fodder weight per plant (-0.0476), pod weight per plant (-0.0459), plant height (-0.0436), days to 50% flowering (-0.0417), number of pods per plant (-0.0245) and harvest index (-0.0220)..

4.5.2.9 Seed weight per plant

Seed weight per plant exhibited positive correlation and positive direct effect on seed yield. While it also had highest positive indirect effect on seed yield through pod weight per plant (0.0154) followed by number of seeds per pod (0.0120), 100 seed weight (0.0117), pod length (0.0109), number of pods per plant (0.0103), fodder weight per plant (0.0102), number of primary branches (0.0098), days to maturity (0.0078), plant height (0.0068), days to 50% flowering (0.0055) and harvest index (0.0046) at phenotypic level.

4.5.2.10 Fodder weight per plant

Fodder weight per plant showed positive correlation and negative direct effect on seed yield at phenotypic level. However, it had highest negative indirect effect on seed yield through plant height (-0.0192) followed by seed weight per plant (-0.0161), pod weight per plant (-0.0154), days to maturity (-0.0153), number of seeds per pod (-0.0150), 100 seed weight (-0.0138), pod length (-0.0110), days to 50% flowering (-0.0087), number of pods per plant (-0.0078) and number of primary branches (-0.0066), while it had positive indirect effect on seed yield through harvest index (0.0143) at phenotypic level.

4.5.2.11 100 seed weight

100 seed weight exhibited positive correlation and positive direct effect on seed yield. Whereas it had highest positive indirect effect on seed yield through pod length (0.3184) followed by number of seeds per pod (0.2725), days to maturity (0.2348), seed weight per plant (0.2186), number of primary branches per plant (0.2134), fodder weight

Table 9. Direct and indirect effects on seed yield at phenotypic level in germplasm lines of horse gram

Character	Days to 50% flowering	Days to maturity	Plant height (cm)	No. primary branches	No. pods/plant	Pod weight/Plant (g)	Pod length (cm)	No. seeds/pod	Seed weight/Plant (g)	Fodder weight/Plant (g)	100 seed weight (g)	Harvest index (%)
Days to 50% flowering	-0.2999	-0.1452	-0.0600	-0.0849	-0.0238	-0.0701	-0.1012	-0.1328	-0.0885	-0.0883	-0.1145	-0.0003
Days to maturity	-0.1088	-0.2247	-0.0995	-0.0809	-0.0075	-0.0576	-0.1355	-0.1376	-0.0941	-0.1163	-0.1515	0.0033
Plant height (cm)	0.0307	0.0681	0.1537	0.0328	0.0237	0.0502	0.0430	0.07122	0.0554	0.0999	0.0532	-0.0435
No. primary branches	0.0253	0.0321	0.0190	0.0893	0.0343	0.0418	0.0561	0.0528	0.0469	0.0200	0.0547	0.0301
No. pods/plant	-0.0062	-0.0026	-0.0120	-0.0299	-0.0779	-0.0605	-0.0203	-0.0203	-0.0430	-0.0207	-0.0167	-0.0098
Pod weight/plant (g)	0.0546	0.0599	0.0762	0.1093	0.1812	0.2336	0.0995	0.1138	0.1918	0.1215	0.1057	0.0085
Pod length (cm)	0.0130	0.0233	0.0108	0.0242	0.0100	0.0164	0.0386	0.0306	0.0224	0.0143	0.0353	0.0123
No. seeds/pod	-0.0417	-0.0577	-0.0436	-0.0557	-0.0245	-0.0459	-0.0747	-0.0942	-0.0605	-0.0476	-0.0737	-0.0220
Seed weight/plant (g)	0.0055	0.0078	0.0068	0.0098	0.0103	0.0154	0.0109	0.0120	0.0187	0.0102	0.0117	0.0046
Fodder weight/plant (g)	-0.0087	-0.0153	-0.0192	-0.0066	-0.0078	-0.0154	-0.0110	-0.0150	-0.0161	-0.0296	-0.0138	0.0143
100 seed weight (g)	0.1329	0.2348	0.1204	0.2134	0.0744	0.1575	0.3184	0.2725	0.2168	0.1626	0.3482	0.0784
Harvest index (%)	-0.0001	0.0008	0.0162	-0.0193	-0.0072	-0.0021	-0.0182	-0.0134	-0.0142	0.0277	-0.0129	-0.0573
Correlation with seed yield (Kg/ha)	-0.2033**	-0.0186	0.1689*	0.2015**	0.1853**	0.2634**	0.2056**	0.1397*	0.2358**	0.1536*	0.2255**	0.0186

per plant (0.1626), pod weight per plant (0.1575), days to 50% flowering (0.1329), plant height (0.1204), harvest index (0.0784) and number pods per plant (0.0744) at phenotypic level.

4.5.2.12 Harvest index

Harvest index had positive correlation and negative direct effect on seed yield. Whereas it showed positive indirect effect on seed yield through fodder weight per plant (0.0277) followed by plant height (0.0162) and days to maturity (0.0008), while, it also had negative indirect effect on seed yield through number of primary branches per plant (-0.0193), pod length (-0.0182), plant height (-0.0162), seed weight per plant (-0.0142), number of seeds per pod (-0.0134), 100 seed weight (-0.0129), number of pods per plant (-0.0072), pod weight per plant (-0.0021) and day to 50% flowering (-0.0001) at phenotypic level.

4.6 EVALUATION OF SELECTED GENOTYPES FOR QUALITY TRAITS

4.6.1 Nutritional quality traits

A set of 21 genotypes were screened for nutritional quality traits like grain micronutrients (Ca, Fe and Zn), protein, plant nitrogen and plant protein content. The result are given in Table 10.

Wide range of variability was observed for grain protein and micro nutrients content. Grain protein content among 21 genotypes was ranged from 17.21 to 25.63 %. The protein content (%) recorded was 23.06, 25.63, 24.37, 23.00, 22.04, 22.04, 22.92 and 23.41 in the genotypes GPM-6, BJPL-1, GPM-23, CRHG-9, DS22, IC100938, DEH-1 and PHG-9, respectively. Among micronutrients, the range of values for Calcium, iron and zinc were 38.43-104.812 mg/100g, 0.39-7.083 mg/100g and 0.966-5.467 mg/100g, respectively. The highest Ca content was observed in CRHG-9 and lowest in PHG-9. With respect to Fe content, highest values were recorded by genotypes CRIDA18R and lowest by CRHG-6. Regarding Zn content, the genotype IC100938 recorded highest and GPM-30 recorded the lowest value. The plant nitrogen and protein content value were ranged from 0.69 to 1.33 per cent and 4.31 to 8.31 per cent respectively.

Table 10. Evaluation of horse gram genotypes for grain protein, micronutrients contents, plant nitrogen and plant protein content

Sl. No	Genotypes	Grain protein (%)	Zn (mg/100g)	Fe (mg/100g)	Ca (mg/100g)	Plant N Content (%)	Plant protein content (%)
1	GPM-6	23.06	3.533	3.803	100.665	1.00	6.25
2	BJPL-1	25.63	3.866	4.280	54.799	0.95	5.94
3	GPM-23	24.37	4.866	5.437	68.232	0.84	5.25
4	CRHG-9	23.00	4.533	5.407	104.81	1.04	6.5
5	DS22	22.04	3.533	1.230	59.199	0.95	5.94
6	IC100938	22.04	4.467	0.927	55.432	1.06	6.63
7	DEH-1	22.92	4.200	3.957	86.965	1.17	7.31
8	PHG-9	23.41	1.467	1.963	38.432	1.09	6.81
9	VJPL-2	21.58	2.667	4.923	49.432	0.78	4.88
10	IC100935	23.56	5.467	4.813	91.465	0.75	4.69
11	KBHG-1	22.57	3.100	2.220	82.832	0.76	4.75
12	AK-42	22.16	1.533	0.627	53.266	0.69	4.31
13	GPM-30	22.30	0.966	2.257	41.032	0.92	5.75
14	BLHG-1	21.61	1.799	2.860	42.199	0.80	5.00
15	BGM1183	20.70	3.733	3.773	45.532	0.90	5.63
16	AK-21	21.49	2.199	0.990	47.832	1.33	8.31
17	CRHG-4	19.89	2.033	1.163	61.666	1.14	7.13
18	CRHG-6	19.68	1.033	0.390	59.966	0.70	4.38
19	CRHG-8	17.24	1.666	1.903	87.299	0.88	5.50
20	CRHG 19R	17.21	2.733	1.200	79.599	0.94	5.88
21	CRIDA 18R	18.58	1.599	7.083	78.232	0.97	6.06
	Mean	21.66	2.904	2.915	66.138	0.94	5.85
	C.V.	9.00	2.57	2.88	4.48	2.58	2.61
	S.Em	1.38	0.171	0.192	0.677	1.62	1.66
	C.D.	4.07	0.48	0.538	1.896	4.54	4.64

4.6.2 Qualitative traits

All the genotypes were screened for stem colour and seed quality traits like seed colour, seed lustre and seed size and number of genotypes categorised into different qualitative trait presented in the Table 11. The plants in each entry were scored for stem pigmentation at flowering stage. Among the genotypes, 75 lines were observed with purple pigmentation and 36 were with normal green colour. With respect to seed colour, genotypes were categorised as cream (44 lines), brown (64 lines), dark brown (1), light black (1) and black (1). All the genotypes were recorded as lustrous grains. Regarding seed size, the genotypes were categorised as bold (16), medium (87) and small (8). The details on their observation are given in Appendix III.

Table 11. Grouping of genotypes under different category for seed quality traits among horse gram germplasm lines

Characters	Catagary and genotypes				-	-	-
Stem colour	Catagary	Purple	Green		-	-	-
	No. genotypes	75	36		-	-	-
Seed colour	Catagary	Cream	Brown		Dark brown	Light black	Black
	No. genotypes	44	64		GPM-46	GPM-62	CRHG-4
Seed luster	Catagary	Luster	Non-Luster		-	-	-
	No. genotypes	111	-		-	-	-
Seed size	Catagary	Bold	Medium	Small	-	-	-
	No. genotypes	16	87	8	-	-	-

V DISCUSSION

Horse gram (*Macrotyloma uniflorum* (Lam.) Verdc) is one among arid legumes that form important source of food and nutrients, rich in protein for human beings especially in dryland regions. It is an important component in the dryland crop production system, due to its ability to withstand drought with minimum management. Like other pulses it plays role as food & fodder, as green manure crop, as cover crop in controlling soil erosion, enhancing soil fertility and having ability of fixing atmospheric nitrogen into the soil. Grains serve as excellent source of protein, minerals (iron, calcium) and polyphenols which have high antioxidant capacity, and hemagglutinin which is a substance found in antibodies and autoimmune functions. Horse gram is having highest calcium content among all the established pulses and arid legumes. Recent studies have confirmed that horse gram is having anti-hyperglycemic and plays role in life style diseases like diabetics. Apart from its good nutritional composition, it has many therapeutic uses (to treat renal stones, piles, edema etc.), which makes it as potential food source for future.

The present crop distribution at global level shows that its cultivation is concentrated in Southern India, with highest area and production in Karnataka (Anon., 2007-12). At present large acreages under horse gram in Karnataka are found in Southern districts (Mysore, Tumkur, Mandya and Chamrajnagar), and in northern dryzone of Karnataka, area under horse gram is high in Koppal followed by Bijapur, Bellary, Belgaum & Haveri districts) (Anon., 2009-10). In these areas, most of the farmers are growing local genotypes.

Crop improvement work in horse gram was initiated by the State Department of Agriculture and through ICAR sponsored schemes during 1940s and 1950s. Single plant selection was made from locally available stocks. Subsequently improvement began under All India Co-ordinated Pulse Improvement Project (AICPIP) in late 1960s and 1970s with the objective of developing shorter-duration and high yielding varieties. Since then number of cultivars were released by different states for cultivation. However, the varieties released so far are the result of pure line selection and none by hybridization, and in addition they are region specific and do not hold promise for commercial agriculture as the plant types contain many weedy traits such as twining and indeterminate growth habit, asynchronous and delayed maturity and photosensitivity, and the genetic improvement of horse gram has been undertaken at just a few institutions in India, but no improvement programme is in place at the global level (Mohar Singh *et al.*, 2013). Therefore, the genetic improvement

programme needs to be strengthened in horse gram by cross hybridization and mutation breeding. The selection of genetically diverse parents for hybridization programme is most crucial for generating genetic variability in the crop. Hence, it needs to be assessed genetic diversity, the nature and magnitude of variability in the available horse gram genotypes. It is also desired to screen the available high yielding varieties for plant and grain nutrition to identify desired genotypes for value addition.

The precise information on the nature and degree of genetic variability, heritability, genetic advance, correlation among various traits that contribute towards seed yield and genetic divergence would help the breeder in identifying the appropriate genotype. Path analysis has been used by plant breeders to assist in identifying useful traits during selection. Partitioning of the correlation coefficient into its components, one component being the path coefficient that measures the direct effect of a predictor variable upon its response variable; the second component being the indirect effects of a predictor variable on the response variable through another predictor variable is the advantage of path analysis.

Considering the importance of the crop and the above indicated facts, the present study was carried out to assess the genetic variability and genetic diversity among the available germplasm involving released varieties, single plant selection derivatives, local collections and other germplasm collections for various qualitative and quantitative traits; to characterize the selected genotypes for grain nutrients content and plant nitrogen content; and to study the association between various traits.

A total of 111 germplasm lines (involving released varieties, single plant selection derivatives, local collections) formed the experimental material. Among these 30 were local collections made from different horse gram districts of Karnataka. These lines were evaluated during late *kharif* 14-15 in a replicated trial in RBD design at RARS Bijapur for yield and yield traits. The observations were recorded on days to 50% flowering, days to maturity, plant height (cm), number of primary branches, number of pods per plant, pod weight per plant (g), pod length (cm), number of seeds per pod, seed weight per plant (g), fodder weight per plant (g), 100 seed weight (g), harvest index (%) and seed yield (kg/hectare). Also a total of 21 selected genotypes were evaluated for plant nitrogen content, and grain nutrients content (protein, iron and calcium).

The data recorded on various traits were subjected to Mahalanobis's D^2 statistical analysis, variability analysis, correlation coefficient analysis and path coefficient analysis. The results obtained are discussed below in the light of available literature under following headings.

5.1 Analysis of variance

5.2 Genetic diversity

5.3 Genetic variability parameters

5.4 Correlation studies

5.5 Path co-efficient analysis

5.6 Screening genotypes for quality traits

5.7 Phenotypic performance of genotypes over check

5.1 ANALYSIS OF VARIANCE

The analysis of variance for all the germplasm lines of horse gram for yield and yield traits revealed that all the genotypes displayed considerable amount of differences in their mean performance with respect to all the characters studied (Table 2). This indicates the presence of variability among treatments.

5.2 GENETIC DIVERSITY ANALYSIS

Genetic divergence analysis in general helps in assessing nature of diversity in order to identify specific parents for realizing useful recombinants in breeding programme of self pollinating crops like horse gram. Several methods have been advocated by various workers to estimate the genetic divergence in crop plants (Murthy and Quadri, 1966; Bhatt, 1970 and Hussaini, 1973). Of the several methods available, Mahalanobis generalized distance estimated by D^2 statistic (Rao, 1952) is a unique tool for discriminating population considering a set of parameters together rather than infusing from indices based on morphological similarities and phylogenetic relationships. Several workers have followed Mahalanobis's D^2 statistic on a wide range of crop species to measure the genetic distance among the available breeding material and to identify characters responsible for such divergence. In the present study, D^2 analysis has been applied to assess the diversity available among available germplasm lines for 13 quantitative traits. Genetic divergence

analysis helps in assessing nature of diversity in order to identify the genetically diverse lines which can be used to create new variability through hybridization.

5.2.1 Genetic diversity

Based on D^2 values, a total of 111 germplasm accessions were grouped into sixteen clusters. Among these clusters, Cluster II was the largest comprising of 51 accessions followed by Cluster I with 21 accessions, Cluster III with 19 accessions and cluster XII comprising with 8 accessions. Whereas 12 solitary clusters were formed. The genotypes of the solitary clusters may be very unique and useful in breeding. In the present study the genotypes identified in solitary clusters are GPM-59 (cluster IV), GPM-23 (cluster V), GPM-6 (cluster VI), BHL-20 (cluster VII), GPM-03 (cluster VIII), GPM-58 (cluster IX), 12B (cluster X), BHGM-28 (cluster XI), BHL-15 (cluster XIII), GPM-65 (cluster XIV), GPM-22 (cluster XV) and BHGM-26 (XVI).

The formation of such clusters may be due to total isolation preventing the gene flow or intensive natural/human selection for diverse adaptive complexes. All the clusters other than solitary clusters viz., Cluster I, II, III and XII recorded intra cluster distance of more than 0. Among these, maximum intra cluster distance was shown by cluster XII (6.69) followed by cluster III (5.65), cluster II (5.12) and cluster I (4.75). The maximum intra cluster distance in cluster XII indicated the genotypes in this cluster were relatively more diverse than the genotypes within other clusters.

Inter cluster distances were ranged from 3.77 to 24.89. High inter cluster distance was obtained between Cluster III and IX were most diverse clusters (with distance of 24.89) followed by cluster III and VII (24.66), cluster-III and X (24.22), cluster III and IV (22.66), cluster III and VIII (22.38), cluster VII and XIII (22.04), cluster IX and XIII (21.92), cluster IX and XVI (21.90), cluster IX and XI (21.66), cluster VII and XI (21.62) and cluster VII and XVI (21.54) indicating high diversity among the genotypes. It is desirable to select genotypes from clusters showing high inter cluster distances. Hence, genotypes of cluster III may be crossed with the genotypes of to clusters IV, VII, VIII, & IX to obtain high heterotic response and desirable segregants. The cluster III having 19 genotypes may form good combination for hybridization with genotypes of solitary clusters viz., GPM-58 (IX), BHL-20 (VII), 12B (X), GPM-59 (IV) and GPM-03 (VIII). Similarly BHL 20 (VII) and GPM-58 (IX) may form good combination with BHL-15 (XIII), BHGM-26 (XVI) and BHGM-28 (XI) for hybridization to use in horse gram crop improvement.

The genotype GPM-6, a high yielding variety tolerant to yellow mosaic disease and root rot disease, has been released for North Karnataka in recent years. This variety in the present study grouped in solitary cluster VI which has also recorded with high intercluster distance with cluster III (15.09) and cluster XI (14.2). Hence, GPM-6 may crossed with genotypes of cluster III and cluster XI (BHGM-28). The genotype BHGM-28 is a local collection from Gulbarga.

Prakash *et al.* (2010) reported that the 100 germplasm accessions were grouped into eighteen different non-overlapping clusters. Cluster I, having 19 genotypes, emerged with highest number of entries; cluster III (14), cluster V (13), cluster VI and VII (8), VIII and XI (6), cluster II and IX (5), XIII (3), cluster X and XII (2), while cluster XIV, XVI, XVII and XVIII were solitary clusters had single genotype in each cluster. Kalia and Dogra (2006) reported nine clusters. Diversity analysis by Singhal *et al.* (2010) classified 88 genotypes into ten clusters and it was suggested that varieties belong to clusters VIII and IX having great statistical distance may be selected for hybridization programme. Five clusters were in 20 genotypes were recorded by Sunil *et al.* (2009). The greatest inter-cluster distance separated clusters II and V, followed by clusters IV, and V, III and IV. Entries in clusters V and II were suggested to be suitable as parents for use in horse gram improvement.

Geetha *et al.* (2011) studied on genetic divergence among 100 germplasm accessions and were grouped into sixteen different clusters. The cluster VI was the largest with 43 genotypes followed by cluster I (14) and cluster XV (11). The intra and inter cluster divergence among the genotypes was varying in magnitude. Further it implies that the intra-cluster distance was maximum in cluster I followed by clusters II and XV. The widest inter cluster distance was noted between cluster I and XIII. The distance between clusters X and XII was minimum. Hence, it was suggested that genotypes of cluster I may be crossed with the genotypes of to cluster XIII and cluster X genotypes crossed with the genotypes of to XII to obtain high heterotic response and desirable segregants.

5.2.2 Contribution of characters towards divergence

Among 13 characters studied in germplasm accessions of horse gram, the days maturity contributes highest (71.20 %) towards the genetic divergence, followed by days to 50% flowering (16.56 %), fodder weight per plant (4.96 %), number of pods per plant (1.65 %), seed yield (1.59 %), seed yield per plant (1.03 %), pods weight per plant (0.82 %), 100 seed weight (0.59 %), harvest index (0.44 %), number of branches per plant (0.43 %),

number of seeds per pod (0.36 %), plant height (0.21 %) and pod length (0.15) (Table 5, Fig 2). Ganeshaiah (1979) also reported that days taken for flowering, days to maturity, number of pods per plant and hundred seed weight were the contributions towards the discrimination of the entries to total divergence.

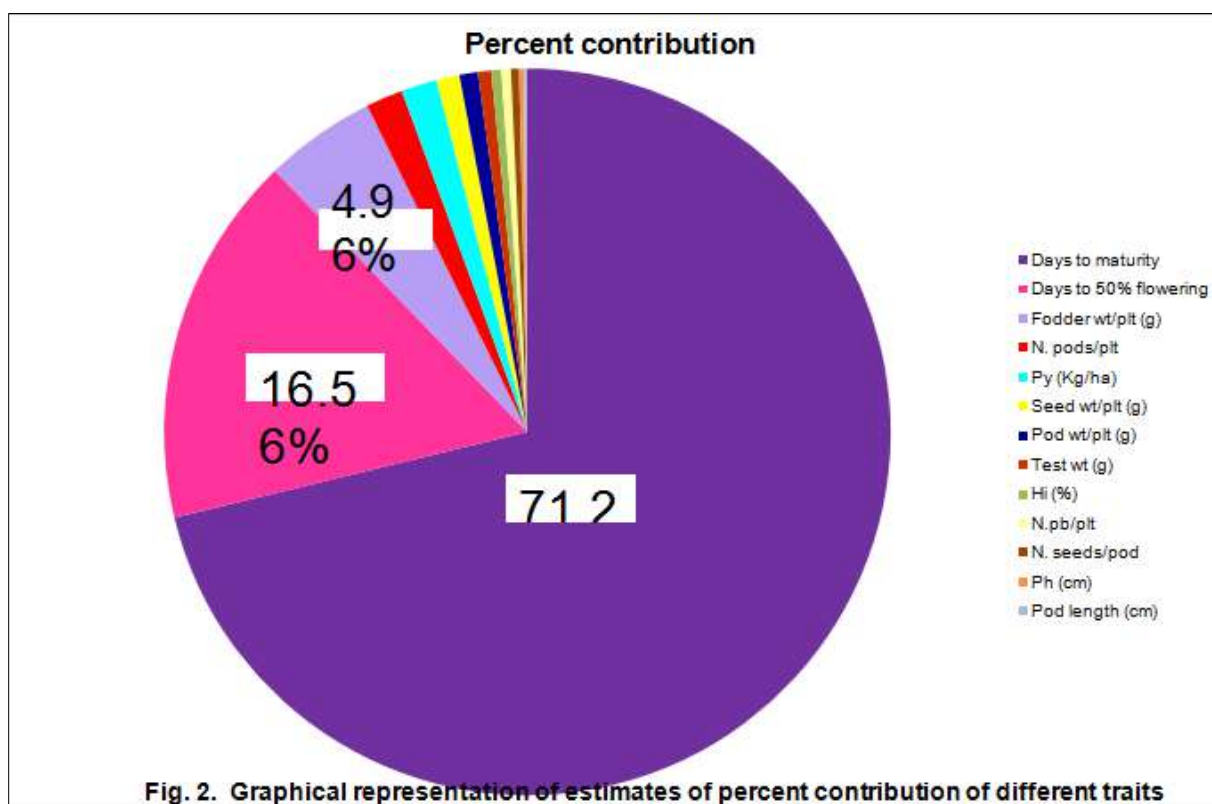
However, Prakash *et al.* (2010) reported that character contribution in cluster divergence revealed that the maximum contribution in cluster formation was attributed by seed yield (94.93) followed by number of pods per plant (3.17), plant height (1.21) and number of seeds per pod (0.65), whereas, remaining traits played minor role in cluster divergence. In contrast, Kalia and Dogra (2006) reported that plant height, number of days to 50% flowering, number of days to maturity, number of primary branches per plant, number of pods per plant, seed yield per plant, biological yield per plant, and harvest index were important characters contributing to maximum genetic divergence. Ramkrishnan *et al.* (1978) reported that hundred seed weight and dry weight of nodular tissue are chief contribution to total divergence in horse gram.

5.2.3 Analysis of cluster means

All the genotypes were spread over sixteen clusters and means were scored across the clusters for all the thirteen characters (Table 5).

The highest cluster mean was given the first rank and the clusters possessing next best means were given second, third and so on up to sixteenth rank for all the traits except for days to 50 per cent flowering and days to maturity, for all these the lowest mean was given the first rank. Accordingly, cluster XIV (GPM 65) with overall score of 79 across the thirteen characters secured first rank followed by cluster VIII (GPM-03), cluster X (12B), cluster XVI (BHGM-26) and cluster XIII (BHL-15) indicating the presence of most promising genotypes in them and can be extensively used for further breeding programme to generate new material.

Among clusters of germplasm accessions of horse gram, the maximum cluster means for days to 50% flowering was recorded in cluster IV (67.50) that comprised of late flowering genotypes, followed by cluster XI (67.00). While, minimum mean was recorded in cluster VI (42.50) followed by XVI (45.00) that comprised of early flowering genotypes. Hence, the early maturing genotypes viz., GPM-6 and BHGM-26 are suitable for use in hybridization programme to derive early maturing and high yielding genotypes.



Maximum mean values for days to maturity was observed in cluster VII (124.50) that comprised of late maturing genotypes, followed by cluster IX (123.50) and X (123.50). While, minimum mean was reported in cluster III (94.37) followed by XIII (97.50), XI (98.50), XIV and XVI (99.50) that comprised of early maturing genotypes. The means indicated that for the development of early maturing genotypes and these lines may be selected from clusters III (19 genotypes), XIII (BHL-15), XI (BHGM-28), XIV (GPM-65) along with consideration of high seed yield.

Highest cluster mean for number of pods per plant was recorded in cluster XVI (68.00), followed by cluster XIV (44.90), for pod weight in clusters XIV (8.30) and XVI (8.10), for number of seeds per pod in cluster IV and VIII (6.00), followed by cluster XI (5.50), for seed weight per plant recorded in cluster XV (6.60) followed by XII (5.35), for fodder weight per plant in cluster VIII (9.85) followed by IV (8.85), for 100 seed weight in cluster V (4.50), followed by cluster XV (4.25), for harvest index observed in cluster XI (47.30) followed by XVI (45.15) for yield per hectare recorded in cluster XIII (1411.10) and cluster XVI (1410.20).

The cluster XIV (GPM-65) showed high mean values for plant height, no. of primary branches, number of pods per plant, pod weight per plant, pod length, seed weight per plant, fodder weight per plant and seed yield per hectare. Similarly, the cluster XVI (BHGM-26) is early maturing, recorded high mean values for number of primary branches, no. of pods per plant, pod weight per per plant, harvest index and seed yield per hectare. Therefore, it is desired to use these genotypes in hybridization programme for development of high yielding genotypes.

Prakash *et al.* (2010) reported that Cluster XII showed the maximum mean value for seed yield. Kanaka (2014) gave the characteristic of cluster V was showed a considerably higher mean value for leaf width, the numbers of primary branches per plant and secondary branches per plant, seed yield per plant, test weight and seedling length. Geetha *et al.* (2011) reported that the cluster XIV showed the maximum mean value for seed yield followed by cluster VII. The high mean in cluster XIII and XVI indicating that those characters were directly contributes to the seed yield and the selection of genotypes by considering these characters may be desirable in the hybridization programme for the development of high yielding varieties.

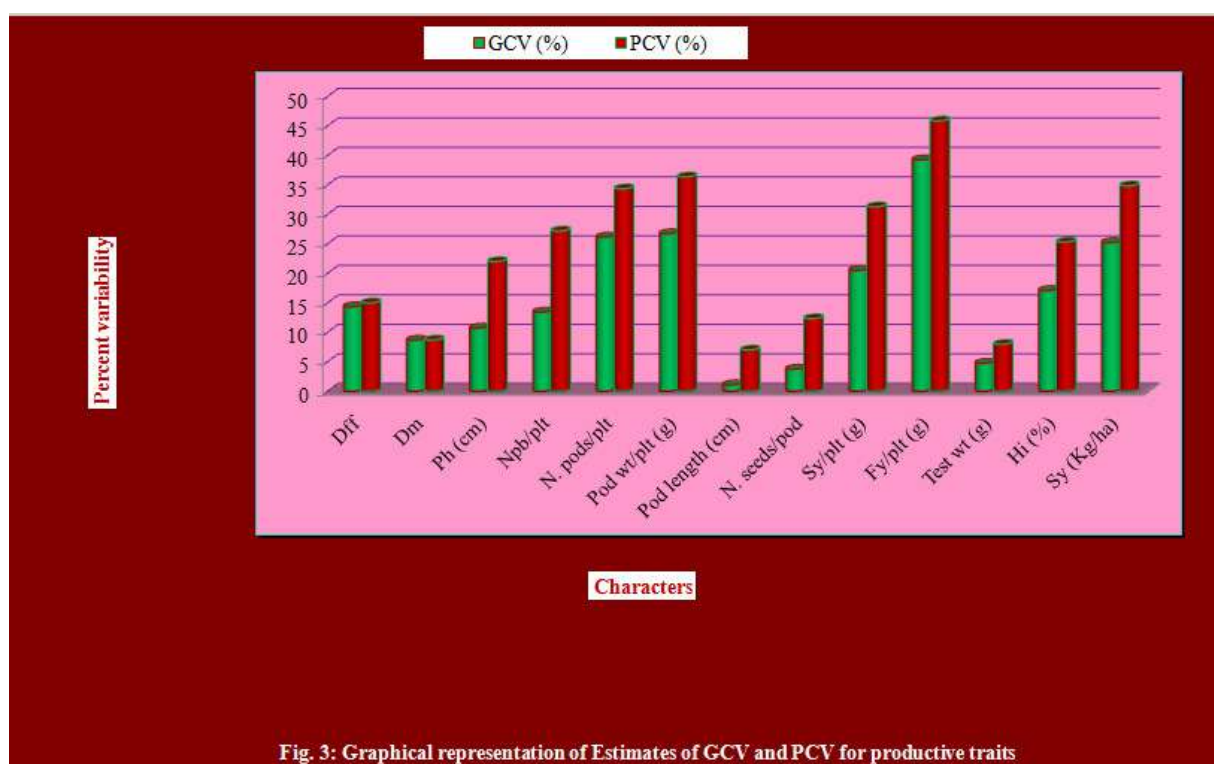
5.3 GENETIC VARIABILITY PARAMETERS

Effectiveness of selection depends on the magnitude of genetic variability for a particular character. The phenotypic variance measures the magnitude of variance arising out of difference in phenotypic character. While the genotypic variance measures the magnitude of variance arising out of genotypic values. The absolute values of phenotypic and genotypic variance can be used for comparing the magnitude of variability for different characters since the mean and units of measurement of the characters may differ. Hence the co-efficient of variation expressed in percentage at phenotypic and genotypic levels have been used to compare the variability observed among the different characters.

It is not just the magnitude of variation but the extent of heritable variation, which matters most for advancing gains in selection program. The coefficient of variation indicates only the extent of the variability present for a character and does not discriminate the variability into heritable and non-heritable portion. The heritability worked out in broad sense would suggest how far the variation is heritable and selection is effective. Though heritability estimates are the true indicators of genetic potentiality of the genotypes as a tool for selection (Johnson *et al*, 1955), but the changes in the level of heritability due to fluctuation of the environmental factors detracted from total dependence on such estimates. However, heritability estimates when considered in conjunction with the predicted genetic gain form a reliable tool in selection. They indicate the expected genetic advance of a character in response to the certain selection pressure imposed on them.

The genotypes showed a wide range of variation for all the characters. Wide range of variation provides ample scope for selection of superior and desired genotypes by the plant breeders for further improvement in these characters. The results obtained are presented in Table 7. Diagrammatic representation of GCV and PCV are presented in Fig. 3. Whereas, heritability estimates and genetic advance on per cent of mean were presented in Fig. 4.

In the present investigation, high heritability coupled with high genetic advance as per cent of mean was observed for days to 50% flowering, days to maturity, pods per plant, pod weight per plant, seed weight per plant, fodder weight per plant, harvest index and seed yield. These findings are in accordance with earlier reports of Yarguntappa (1987), Sood *et al.* (1994), Aggarwal and Kang (1976), Sahoo *et al.* (2010), Latha *et al.* (2013),



Balan *et al.* (1991), Patil and deshमुख (1982), Venkateswarlu (2000), Shivashankar *et al.* (1977), Ganeshiah (1982), Suraiya *et al.* (1988) and Dobhal and Rana (1994). These results indicated that traits are controlled by additive gene action and hence these traits can be fixed by selection.

High heritability coupled with low genetic advance was recorded for 100 seed weight. These findings were in accordance with earlier reports of Sood *et al.* (1994). Moderate GCV, moderate heritability and high genetic advance were noticed for the traits plant height and number of primary branches. These findings are in accordance with earlier reports of Rao and Chandrakar (1994), Raina *et al.* (2007), Ramkrishan *et al.* (1978), Suraiya *et al.* (1988) and Sahoo *et al.* (2010). Whereas, low heritability with low genetic advance estimates were observed for pod length and number of seeds per pod. These findings are in accordance with earlier reports of Birari *et al.* (1987), Khulbe *et al.* (2013), Sahoo *et al.* (2010) and Nehru *et al.* (2000).

Based on estimates obtained, variability and heritability studied for yield and each of its component traits are discussed under following sections.

5.3.1 Days to 50% flowering

In the present study, the variability analysis among germplasm accessions of horse gram revealed that moderate phenotypic and genotypic co-efficient of variation, high heritability and high genetic advance were exhibited by days to 50% flowering. These results were in agreement with the earlier observations by Suraiya *et al.* (1988), Kabir and Sen (1990), Savithramma (1994), Dobhal and Rana (1994) and Sood *et al.* (1994). Only high heritability was observed by Ganeshiah *et al.* (1982), Yarguntappa (1987), Singh (1990) and Khulbe *et al.* (2013) for days to 50% flowering.

5.3.2 Days to maturity

The variability study showed that low estimates of phenotypic and genotypic coefficients of variation and high heritability and genetic advance were observed for the trait days to maturity. Similar results of low GCV and PCV estimates were reported by Shivashankar *et al.* (1977). High heritability and genetic advance were reported by Ganeshiah (1979) and Suraiya *et al.* (1988). Similar results for high heritability were reported by Kallesh (1981) and Birari *et al.* (1987). Yarguntappa (1987), Aggarwal and Kang (1976) and Sood *et al.* (1994) reported low GCV and PCV with high heritability. High

heritability with high genetic advance for days to maturity indicating the major role of additive component of genetic variance and selection may be effective.

5.3.3 Plant height

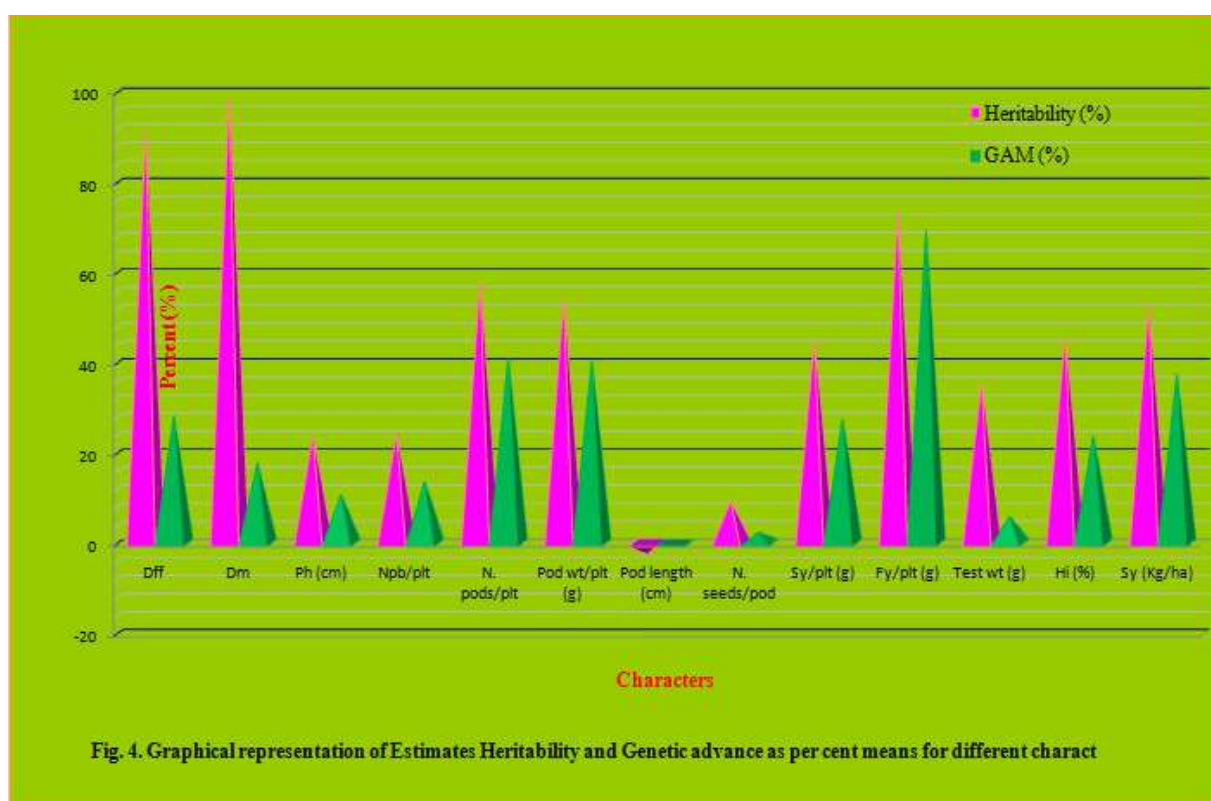
Moderate variability at both genotypic and phenotypic levels and moderate heritability with high genetic advance were observed for plant height. Similar results were reported by Ganeshiah (1979), Yarguntappa (1987) and Savithramma (1994). Raina *et al.* (2007), Ramkrishan *et al.* (1978), Suraiya *et al.* (1988) and Sahoo *et al.* (2010) reported high genetic advance for the trait. Rao and Chandrakar (1994) also observed moderate heritability for plant height.

5.3.4 Number of primary branches per plant

Number of primary branches per plant showed moderate GCV and high PCV values with moderate heritability and high genetic advance. Similar results of moderate GCV and heritability for the trait were reported by Savithramma (1994). Ganeshiah (1979) reported moderate GCV with high GA. Ramkrishan *et al.* (1978), Patil and Deshmukh (1982), Senapati *et al.* (1998), Shivashankar *et al.* (1977), Aggarwal and Kang (1976), Nehru *et al.* (2000) were reported high GA. Suraiya *et al.* (1988), Ram *et al.* (2003) Sahoo *et al.* (2010) reported high PCV with high GA.

5.3.5 Number of pods per plant

High variability in terms of GCV and PCV, high heritability and high genetic advance estimates were observed for the trait. Similar results were given by Ganeshiah (1979), Kallesh (1981), Yarguntappa (1987) and Sahoo *et al.* (2010). Balan *et al.* (1991) reported high GCV, heritability and GA. Sreekantharadya *et al.* (1975) reported high GCV, PCV and heritability. Raina *et al.* (2007), Patil and Deshmukh (1982), Latha *et al.* (2013) and Aggarwal and Kang (1976) observed high heritability with GA for the trait. Samal and Senapati (1998) reported high heritability, whereas Khulbe *et al.* (2013) recorded high GCV, PCV, with high GA and only high PCV observed by Kalia and Dogra (2007). Venkateswarlu (2000) observed high GCV, heritability and high GA. The high heritability indicates that the character is least influenced by the environmental effects, and hence the selection for improvement of such character may be useful. But high PCV, GCV and genetic advance showed that character was governed by additive genes and selection will be rewarding for improvement of such trait.



5.3.6 Pod weight per plant

Pod weight per plant in present study recorded high estimates of GCV, PCV, heritability and high genetic advance. These results are in conformity with reports by Balan *et al.* (1991) and Sahoo *et al.* (2010). High GCV, PCV, heritability coupled with high genetic advance over mean indicating that most likely the heritability was due to trait governed by additive gene effects and selection may be effective.

5.3.7 Pod length

Pod length exhibited low estimates of GCV, PCV, heritability and genetic advance in the present investigation. Similar results were observed by Sahoo *et al.* (2010) and Nehru *et al.* (2000).

5.3.8 Number of seeds per pod

For number of seeds per pod, low values of GCV, heritability and GA, and moderate values of PCV were recorded in present study. These results are in conformity with reports by Shivashankar *et al.* (1977). Yarguntappa (1987), Ganeshiah (1980), Savithramma (1994) reported low GCV. Sreekantharadya *et al.* (1975) recorded moderate PCV, Samal and Senapati (1997); Sahoo *et al.* (2010) noticed low heritability, Birari *et al.* (1987) and Nehru *et al.* (2000) reported low heritability with low GA, Khulbe *et al.* (2013) reported low GCV, heritability and GA. The low estimates of heritability, genetic advance and low genetic variability observed impede trait improvement through selection.

5.3.9 Seed yield per plant

This trait had higher GCV, PCV, heritability and GA in present study. These results are in conformity with reports of Rao and Chandrakar (1994), Kalia and Dorga (2007) who reported high GCV and PCV estimates. Samal and Senapati (1998) and Khulbe *et al.* (2013) noticed high GCV, PCV with high heritability. Birari *et al.* (1987) reported only high heritability, Latha *et al.* (2013), Balan *et al.* (1991), Sahoo *et al.* (2010) reported high heritability and GA. High GCV, PCV, heritability coupled with high genetic advance over mean indicates the trait governed by additive gene effects and selection may be effective.

5.3.10 Fodder weight per plant

Fodder weight per plant recorded higher GCV, PCV, heritability and GA in the present investigation. Similar results were noticed by Yarguntappa (1987), Sahoo *et al.* (2010). Nehru *et al.* (2000) reported high GCV, heritability with high GA. High GCV, PCV, heritability coupled with high genetic advance over mean indicating that most likely the heritability was due to additive gene effects and selection may be effective.

5.3.11 100 seed weight

100 seed weight recorded lower GCV, PCV and GA with higher heritability in present investigation. Sood *et al.* (1994) reported similar results. Suraiya (1980), Ganeshiah (1980), Savithramma (1994) reported narrow GCV and PCV. Ram *et al.* (2003) reported high heritability, while Raina *et al.* (2007), Yarguntappa (1987), Kabir and Sen (1990), Latha *et al.* (2013), Singh (1990) confirmed that 100 seed weight was highly heritable. Low to moderate PCV and GCV, high heritability coupled with moderate genetic advance over mean indicating that the character showing less variability, least influenced by environmental effects and more or less character is governed by non-additive genes and improvement of character through heterosis breeding.

5.3.12 Harvest index

It was observed high PCV with moderate GCV and high heritability and GA for the trait. Similar results on moderate GCV for the trait were reported by Savithramma (1994), and high PCV with moderate GCV by Kalia and Dogra (2007). High PCV, heritability coupled with high genetic advance over mean with moderate GCV indicating that most likely the heritability was due to additive gene effects and selection may be effective.

5.3.13 Seed yield per hectare

Seed yield per hectare shown high GCV, PCV, heritability and GA estimates. Similar results were obtained by Yarguntappa (1987) and Sood *et al.* (1994). Sharma (1995) reported high GCV, PCV and heritability. Rao and Chandrakar (1994), reported high GCV, PCV with high GA. Ram *et al.* (2003), Patil and deshमुख (1982), Aggarwal and Kang (1976) and Ramkrishnan *et al.* (1978) reported high heritability with high GA, Birari *et al.* (1987) and Nehru *et al.* (2000) reported high heritability, Rao and Nanda (1994) reported only high GA for the trait. High GCV, PCV, heritability coupled with high genetic advance

over mean indicating that most likely the heritability due to trait governed by additive gene effects and selection may be effective.

5.4 CORRELATION COEFFICIENTS

Yield is the result of combined effects of several component characters. Amelioration of yield is the ultimate aim of the plant breeder in any crop improvement programme and this has to be achieved through gaining insight into the behaviour of component characters that are associated with grain yield. Correlation studies provide information on the nature and extent of association between any two pairs of metric characters. Hence, it would be possible to bring genetic up gradation in one character by selection of related characters. Grafius (1959) opined that there may not be any gene for yield as such, but operates only through its components. Obviously, knowledge about character association will surely help to identify the character to make selection for higher yield with a view to determine the extent and nature of relationship among the yield contributing characters. Correlation coefficients not only denote the total association existing between a pair of characters which themselves are the result of the interaction between various features of the plant but also it measures the relationship existing between pair of characters. A dependent character is the result of interaction of many mutually associated component characters and change in any one component will disturb the whole network of cause and effect system.

In the present study, correlation coefficients estimated between yield and its component traits, and among the component traits are discussed below.

5.4.1 Correlation of seed yield with component traits

In general, all the component traits were significantly positively associated with both seed yield per plant and seed yield per hectare except for the significant and negative association of days to 50% flowering, positive and non-significant association of harvest index, and negative non-significant association of days to maturity with seed yield per hectare was observed.

5.4.1.1 Days to 50% flowering

Days to 50 per cent flowering showed significant negative correlation with seed yield per hectare (Table 8) which in agreement with earlier findings of Singh (1990) and Sood *et al.* (1994). Negative correlation was desirable for this trait as less number of days to

flowering reduces the crop duration, it helps the crop to escape terminal drought, hence, selection can be practiced for early flowering genotypes with high seed yield to suit for scanty rainfall areas. However, days to 50% flowering was significantly positively correlated with seed yield per plant. Ghorpade (1985) also reported positive correlation with seed yield per plant.

5.4.1.2 Days to maturity

The association of days to maturity was negative and non-significant with seed yield at phenotypic level. The supportive evidences were given by Singh (1990), Rao and Nanda (1994) and Sood *et al.* (1994) who reported negative but significant association. This negative correlation helps to select the early maturing genotypes with high seed yield. However, days to maturity was found to be significantly positively correlated with seed yield per plant. Ganeshiah (1979) and Yarguntappa (1987) also reported positive association of days to maturity with seed yield per plant.

5.4.1.3 Plant height

Positive significant association of plant height observed with both the seed yield per hectare and seed yield per plant. The supportive evidences of positive and significant association with seed yield were given by Kabir and sen (1989), Aggarwal and Kang (1976), Shivashankar *et al.* (1977), Kallesh (1981), Yarguntappa (1987), Roopadevi *et al.* (2002), and Rao and Chandrakar (1994).

5.4.1.4 Number of primary branches

Positive significant correlation with seed yield per plant and seed yield hectare was observed. Results are in line with earlier findings given by Aggarwal and Kang (1976), Ganeshiah (1979), Dabhos *et al.* (1990), Paliwal *et al.* (2005), Roopadevi *et al.* (2002), Rao and Chandrakar (1994), and Dobhol and Rana, 1994.

5.4.1.5 Number of pods per plant

Significant positive association with seed yield per plant followed by seed yield per hectare was observed. Similar results of significant positive association with seed yield were reported by Aggarwal and Kang (1976), Shivashankar *et al.* (1977), Ganeshiah (1979), Kallesh (1981), Patil and Deshmukh (1982a), Patil *et al.* (1983), Yarguntappa (1987), Kabir and Sen (1989), Roopadevi *et al.* (2002), Singh (1990), Savithramma (1994),

Rao and Chandrakar (1994), Sunil *et al.* (2014), Lad *et al.*, (1999), Rama *et al.* (2007) and Sharma (1995). In contrast to this, Ghorpade (1985) reported negative correlation with seed yield per plant.

5.4.1.6 Pod weight per plant (g)

Positive and significant association of this trait with seed yield per hectare and seed yield per plant was observed. These results are in conformity with reports by Dabhos *et al.* (1990), Savithramma (1994) and Lad *et al.*, (1999).

5.4.1.7 Pod length (cm)

Positive significant correlation of this trait with seed yield per hectare and seed yield per plant was observed. Similar results are reported by Kabir and sen (1989), Roopadevi *et al.* (2002) and Lad *et al.*, (1999). In contrast Sharma (1995) reported negative association.

5.4.1.8 Number of seeds per pod

Positive and significant association of this trait with seed yield per hectare and seed yield per plant was observed. The supportive evidences are given by Shivashankar *et al.* (1977), Kallesh (1981), Yarguntappa (1987), Kabir and Sen (1989), Dabhos *et al.* (1990), Roopadevi *et al.* (2002), Lad *et al.* (1999) and Rama *et al.* (2007). In contrast Sharma (1995) reported negative association.

5.4.1.9 Seed weight per plant (g)

Positive significant association of seed yield per plant with seed yield per hectare was observed. These findings are in agreement with the Rao and Chandrakar (1994).

5.4.1.10 Fodder weight per plant (g)

Positive significant association of fodder yield per plant was observed with seed yield per plant and seed yield per hectare. These findings are in agreement with Savithramma (1994) and Rama *et al.* (2007).

5.4.1.11 100 seed weight (g)

Positive significant correlation of this trait with seed yield per plant and seed yield per hectare was observed. These findings are in agreement with Latha *et al.* (2013), Patil and Deshmukh (1982a), Patil *et al.* (1983), Yarguntappa (1987), Sharma (1995),

Roopadevi *et al.* (2002) and Sarkar *et al.* (2005) who reported positive and significant association.

5.4.1.12 Harvest index (%)

The association of this trait was positive and significant with seed yield per plant but positive and non-significant with seed yield per hectare.

5.4.2 Correlation among yield component traits

The association among all component traits was positive and significant except positive non-significant association observed between no. of pods per plant and days to 50% flowering, days to maturity & harvest index, and between pod weight per plant and harvest index, significant negative association of harvest index with plant height and fodder weight per plant, and negative non-significant association of harvest index with days to maturity. Among the traits pod weight per plant, test weight and pod length may be used as indirect selection criteria for seed yield.

5.5 PATH CO-EFFICIENT ANALYSIS

The path co-efficient analysis is a statistical method developed by Wright (1921). The analysis takes into account the cause and effect relation between the variables and is unique in partitioning the association into direct and indirect effect through other independent variables. The path co-efficient analysis also measures the relative importance of casual factors involved. The results of correlation and path co-efficient analysis obtained are discussed below. The results are presented in Table 9 graphically depicted in Fig. 5.

5.5.1 Days to 50% flowering

Days to 50% flowering had negative direct effect on seed yield. This observation is in line with report by Sood *et al.* (1994). In contrast to this, Pandya *et al.* (2002), Aggarwal and Kang (1976) and Ganeshaiah (1979) reported direct positive effect. Days to 50% flowering had negative indirect effect on seed yield through days to maturity followed by number of seeds per pod, 100 seed weight, pod length, seed weight per plant, fodder weight per plant, number of primary branches per plant, pod weight per plant. In contrast to this, Yarguntappa (1987) reported positive indirect effect on seed yield.

5.5.2 Days to maturity

It was observed that this trait had negative direct effect on seed yield. This finding is in line with Sood *et al.* (1994). In contrast to this, Pandya *et al.* (2002) reported direct positive effect. The trait had negative indirect effect on seed yield through 100 seed weight followed by number of seeds per pod, pod length, fodder weight per plant, days to 50% flowering, plant height, seed weight per plant, number of primary branches per plant. This observation is in line with Yarguntappa (1987).

5.5.3 Plant height (cm)

It was observed that this trait had positive direct effect on seed yield. This finding is in line with report of Pandya *et al.* (2002). In contrast to this finding, Khulbe *et al.* (2013) reported that plant height exhibited negative direct effect on seed yield per plant. In the present study, it was observed positive indirect effect on seed yield through fodder weight per plant followed by number of seeds per pod, days to maturity, seed weight per plant, 100 seed weight, pod weight per plant, pod length, number of primary branches per plant, days to 50% flowering and number of pods per plant. It also shows negative indirect effect on seed yield through harvest index. This finding was in line with Yarguntappa (1987). In contrast to this, Aggarwal and Kang (1976) and Ganeshaiah (1979) reported that it had low negative effect on yield.

5.5.4 Number of primary branches

Number of primary branches had positive direct effect in present study. This is in agreement with Pandya *et al.* (2002) and Paliwal (2005). Positive indirect effect on seed yield was observed through pod length followed by 100 seed weight, number of seeds per pod, seed weight per plant, pod weight per plant, number of pods per plant, days to maturity, harvest index, days to 50% flowering, fodder weight per plant and plant height.

5.5.5 Number of pods per plant

Number of pods per plant had negative direct effect on seed yield. In contrast to this, Aggarwal and Kang (1976), Ganeshaiah (1979), Paliwal (2005), Yarguntappa (1987), Singh (1990) and Khulbe *et al.* (2013) revealed that it showed high positive direct effect on yield. In contrast to this Kabir and Sen (1989) reported high positive direct effect on pod yield. It had negative indirect effect on seed yield through pod weight per plant followed by seed weight per plant, number of primary branches per plant, fodder weight per plant, pod length, number of seeds per pod, 100 seed weight, plant height, harvest index, days 50%

flowering and days to maturity. This finding was in line with Raina *et al.* (2007). In contrast to this, Kallesh (1981) and Yarguntappa (1987) reported that it had positive indirect effect.

5.5.6 Pods weight per plant

It had positive direct effect on seed yield. This finding is in line with reports by Balan *et al.* (1991a), Savithramma (1994) and Balan *et al.* (1994). Indirect effect on seed yield was observed through seed weight per plant followed by number of pods per plant, fodder weight per plant, number of seeds per pod, number of primary branches per plant, 100 seed weight, pod length, plant height, days to maturity, days to 50% flowering and harvest index.

5.5.7 Pods length

It had positive direct effect on seed yield. This observation is in line with results of Singh (1990) and Kabir and Sen (1989). Indirect effect on seed yield was observed through 100 seed weight followed by number of seeds per pod, number of primary branches per plant, days to maturity, seed weight per plant, pod weight per plant, fodder weight per plant, days to 50% flowering, harvest index, plant height and number of pods per plant.

5.5.8 Number of seeds per pod

It had negative direct effect on seed yield. This finding was in line with report by Singh (1990). In contrast to this finding, Yarguntappa (1987) and Kabir and Sen (1989) reported positive direct effect on pod yield. It had negative indirect effect on seed yield through pod length followed by 100 seed weight, seed weight per plant, days to maturity, number of primary branches per plant, fodder weight per plant, pod weight per plant, plant height, days to 50% flowering, number of pods per plant and harvest index. This observation is in agreement with Rama *et al.* (2007).

5.5.9 Seed weight per plant

It was observed its positive direct effect on seed yield. This finding confirmed the results reported by Savithramma (1994). The trait had indirect effect on seed yield through pod weight per plant followed by number of seeds per pod, 100 seed weight, pod length, number of pods per plant, fodder weight per plant, number of primary branches, days to maturity, plant height, days to 50% flowering and harvest index.

5.5.10 Fodder weight per plant

The trait had negative direct effect on seed yield. In contrast to this, Rama *et al.* (2007) and Savithramma (1994) reported that the trait exhibited positive direct effect on

seed yield per plant. It had negative indirect effect on seed yield through plant height followed by seed weight per plant, pod weight per plant, days to maturity, number of seeds per pod, 100 seed weight, pod length, days to 50% flowering, number of pods per plant and number of primary branches. This finding is in agreement with Raina *et al.* (2007) and Rama *et al.* (2007).

5.5.11 100 seed weight

It had positive direct effect on seed yield. This finding is in line with reports of Aggarwal and Kang (1976), Ganeshaiah (1979), Paliwal *et al.* (2005) and Khulbe *et al.* (2013). In contrast to this finding, Kabir and Sen (1989) and Singh (1990) reported negative direct effect on pod yield. It had positive indirect effect on seed yield through pod length followed by number of seeds per pod, days to maturity, seed weight per plant, number of primary branches per plant, fodder weight per plant, pod weight per plant, days to 50% flowering, plant height harvest index and number pods per plant. This observation is in line with reports of Raina *et al.* (2007) and Sood *et al.* (1994).

5.5.12 Harvest index

It had negative direct effect on seed yield. In contrast to this, Rama *et al.* (2007) and Savithramma (1994) reported that it had positive direct effect on seed yield per plant. Whereas it shows positive indirect effect on seed yield through fodder weight per plant followed by plant height and days to maturity. While it also had negative indirect effect on seed yield through number of primary branches per plant, pod length, plant height, seed weight per plant, number of seeds per pod, 100 seed weight, number of pods per plant, pod weight per plant and day to 50% flowering.

5.5.2 Residual effect

In plant breeding, it is very difficult to have complete knowledge of all component traits of yield. The residual effect, permits precise explanation about the pattern of interaction of other possible components of yield. In other words, residual effect measures the role of other possible independent variables which were not included in the study on the dependent variables. The residual effect is estimated with the help of direct effects and simple correlation coefficients. In the present study the residual effect in germplasm lines of horse gram for direct and indirect effects were 0.8789. The residual effect is high indicates that besides the characters studied, there are some other attributes which contributes for yield.

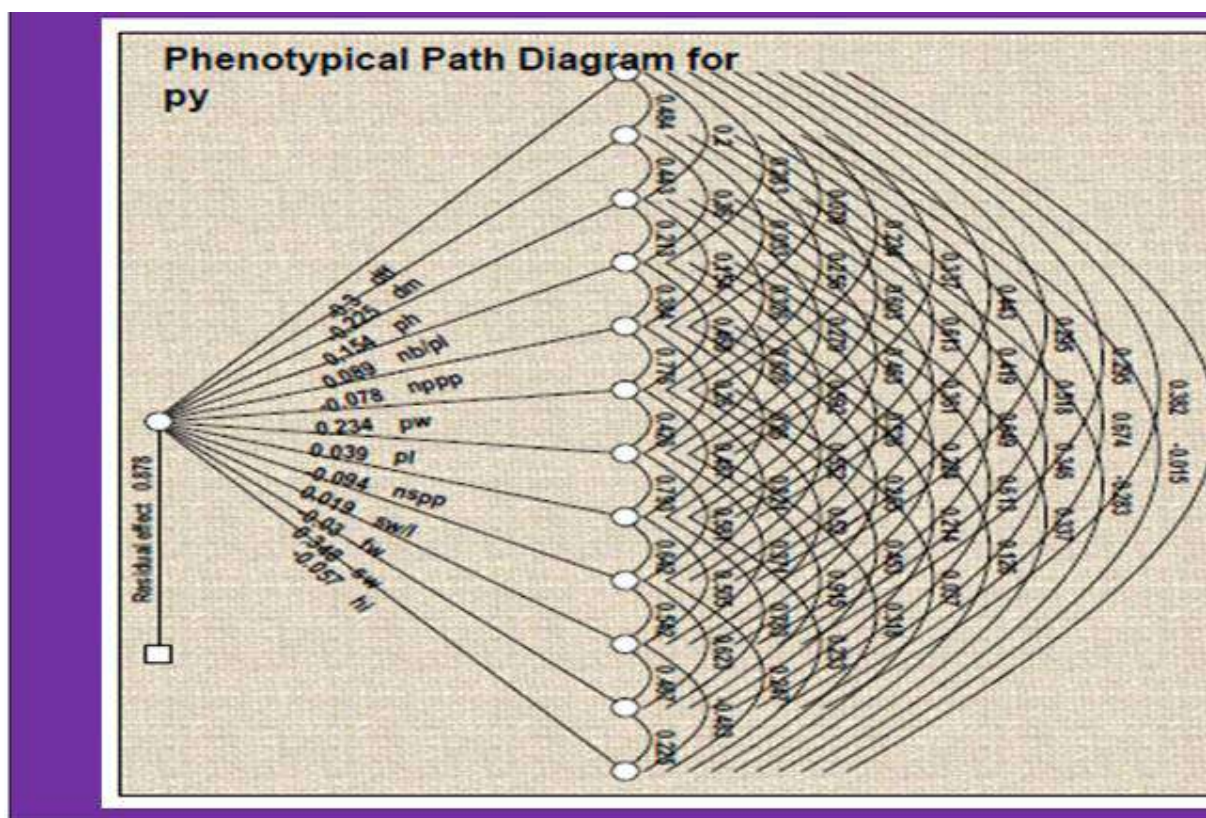


Fig. 5 Phenotypic path diagram for yield and its related traits in horse gram germplasm lines

5.6 SCREENING GENOTYPES FOR QUALITY TRAITS

5.6.1 Nutritional quality

Wide range of variability was observed for grain micro nutrients content among 21 entries. The range of values for calcium, iron and zinc were 3.843-104.812 mg/100g, 0.39-7.083 mg/100g and 0.966-5.467 mg/100g, respectively. The highest Ca content was observed in CRHG-9 and lowest in PHG-9. With respect to Fe content, highest values were recorded by genotypes CRIDA18R and lowest by CRHG-6. Regarding Zn content, the genotype IC100938 recorded highest and GPM-30 recorded the lowest value. The plant nitrogen and protein content value were ranged from 0.69 to 1.33 per cent and 4.31 to 8.31 per cent respectively. Grain protein content among 21 genotypes was ranged from 17.21 to 25.63 %. Highest protein content (%) was recorded in BJPL-1 (25.63 %) followed by GPM-23 (24.37) and PHG-9 (23.41) and GPM-6 (23.06) and lowest in CRHG19R (17.21).

Although horse gram is having nutritionally rich grains and fodder but its potentiality has not been exploited completely. Its low productivity compared to other pulse crops might have made horse gram less attractive to formers for its increased cultivation (Sajjanar *et al.*, 2013). However, there is great scope for increasing the yield of grains and fodder of this pulse crop by adopting improved technologies including use of high yielding varieties. Presently majority formers are growing local genotypes although, several varieties have been released for its cultivation in different states. In addition to yield parameters, varietal differences for nutritional quality parameters (like minerals composition, protein content, fatty acid profile, flavonals etc.,) have been reported by several workers. High yielding varieties with superiority for nutritional quality will fetch high remunerative prices for formers provided value added to the crop (Sajjanar *et al.*, 2013) according to Khatun *et al.* (2013) that legumes are good source of calcium, iron and zinc. Therefore to study varietal differences for these grain micronutrients content and plant nitrogen and protein content, a total of 21 in the present study varieties of horse gram were evaluated. The genotypes were selected based on yield data of two years (2012 and 2013). The results of nutritional quality analysis are presented in Table 11.

Among the genotypes, the calcium content was ranged from 384.30 to 1048.12 ppm. Highest calcium content was observed in genotypes CRHG-9 and GPM-6 followed by IC100935, CRHG-8, DEH-1, KBHG-11, CRHG-19R, CRIDA18R and GPM-23. The iron content was ranged from 3.9 to 70.83 ppm. Highest Fe content was found in CRIDA18R

followed by GPM-23, CRHG-9, VJPL-2, IC100935, BJPL-1, DEH-1, GPM-6 and BGM1183. With respect to zinc content, the values were ranged between 9.66 to 54.67 ppm. Highest Zn content was recorded in the genotype IC100938 followed by GPM-23, IC100935, DEH-1, BJPL-1, BGM1183 and GPM-6. Studies on varietal differences for grain micronutrients content were also made by number of workers. Khatun *et al.* (2013) reported that calcium content of ten horse gram genotypes was ranged from 244 to 312 mg/100 g of seed. Shashi *et al.* (2012) reported that iron content of 8.71 - 9.16 mg/100 g seed, among two varieties. Whereas Khatun *et al.* (2013) reported that iron content of ten horse gram genotypes ranged from 5.89 to 7.44 mg/100 g of seed.

With respect to plant nitrogen content and protein content, the values ranged between 0.69 to 1.33 per cent and 4.31 to 8.31 per cent among the genotypes. Highest contents were observed in genotypes AK-21 and DEH-1.

Considering high yield, micronutrients content (Ca, Fe and Zn), plant nitrogen content and plant protein content, the promising genotypes identified were GPM-6, GPM-23 CRHG-9 and DEH-1. All these genotypes were early maturing except GPM-6. These genotypes can further be tested for nutritional quality and utilized for value addition.

5.6.2 Qualitative traits

The plants in each entry were scored for stem pigmentation at flowering stage. Among the genotypes, 75 lines were observed with purple pigmentation and 36 were with normal green colour. With respect to seed colour, genotypes were categorized as cream (44 lines), brown (64 lines), dark brown (1), light black (1) and black (1). All the genotypes were recorded as lustrous grains. Regarding seed size, the genotypes were categorized as bold (16), medium (87) and small (8). The genotype GPM-46 is having the dark brown colour seeds, GPM-62 with light black colour seeds and CRHG-4 with black colour seeds. The score given for these qualitative traits in accordance with the Sunil *et al.* (2014), Ganesh and Umesh (2011) and Latha *et al.* (2013). Differences in stem colour, seed colour and seed size is given in plate 3 and 4.

5.7 PERFORMANCE OF GENOTYPES OVER CHECK

The top 10 performing genotypes for each of the traits and range of values among these genotypes is given in Table 12a. The genotypes DS22 and BHGM-18 were early flowering and early maturing entries. The promising genotypes identified for various traits

CREAM



BROWN



DARK BROWN



LIGHT BLACK



BLACK



SMALL



MEDIUM



BOLD



Flower with purple spot



Pods



Plate 3: Difference in seed colour and seed size of germplasm lines of horse gram



RED STEM



GREEN STEM

Plate 4. Difference in stem colour of germplasm lines of horse gram

Table 12a. Top ten genotypes identified for different traits among 111 germplasm lines of horsegram

Sl.no.	Trait	Genotypes	Range among top 10 performing lines
1	Days to 50% flowering	BGM1183, DS22, CRHG-6, GPM-6, GPM-28, BHGM-18, VJPL-2, CRHG-8, CRHG-9 and BHGM-17	40.50-44.00
2	Days to maturity	BHGM-15, DS22, AK-21, VJPL-2, BHGM-18, BHGM-29, DEH-1, BHGM-16, GPM-48 and BLHG-1	91.50- 94.00
3	Plant height (cm)	DHG-04, GPM-63, BJPL-1, 12B, BHL-60, GPM-03, BHL-20, BHL-48, GPM-58 and GPM-4-61-4-1	89.80-72.70
4	No. primary branches	GPM-48, GPM-11, CRHG-4, PHG-02, CRHG-05, CRIDA 18R, BHGM-11, AK-44, BHGM-6 and BHGM-16	5.20-4
5	No. pods/plant	BHGM-26, CRHG-05, CRHG-4, BHL-60, BHGM-4, VJPL-2, DEH-1, GPM-46, GPM-32 and BHGM-6	68.00-47.70
6	Pod weight/plant (g)	CRHG-05, CRHG-4, BHL-60, DEH-1, 8B, GPM-65, BHL-44, BHGM-26, BHGM-4 and GPM-48	10.70-7.75
7	Pod length (cm)	GPM-03, VLG-19, 8B, GPM-422, BHGM-15, GPM-46, BHL-26, GPM-92, LONE-1 and BHL-78	5.74-5.40
8	No. seeds/pod	BHL-44, GPM-11, GPM-03, GPM-4-61-4-1, GPM-59, BHL-26, GHI-641, 8B, BHGM-24 and PHG-12	6.20-5.8
9	Seed weight/plant (g)	CRHG-05, DEH-1, 8B, CRHG-4, BHL-44, BHL-60, GPM-65, 12B, BHL-78 and BHGM-16	6.60-4.5
10	Fodder weight/plant (g)	GPM-03, GPM-12-B, GPM-63, GPM-59, GPM-58, Bailhongal local, GHI-641, AK-44, GPM-4-61-4-1 and GPM-65	9.85-7.3
11	100 seed weight (g)	GPM-23, GPM-49, AK-42, CRHG 19R, GPM-12-B, GPM-22, DEH-1, GPM-30, GPM-58 and Kavalgi local	4.50-4.20
12	Harvest index (%)	CRHG 19R, BHGM-8, CRHG-6, BHG-1, BHGM-6, BHGM-16, BHGM-11, BHGM-15, CRIDA 18R and BHGM-9	63.33-47.53
13	Seed yield (Kg/ha)	VJPL-2, CRHG-9, BHGM-29, GPM-65, BHGM-26, CRHG-05, GPM-6, 12B, GPM-03 and BHGM-9	1673.15-1307.40

are DEH1, 12B, CRHG-4, 8B, BHGM-16, BHGM-26, GPM-03 and GPM-65. These genotypes also showed significant superiority over GPM 6 for various traits like number of primaries (CRHG-4, BHGM-16), number of pods per plant (CRHG-4, BHGM-16, BHGM-26, GPM-65, 12B), pod length (GPM-03, DEH1 & 8B) and fodder weight (GPM 65, GPM-03) (Table 12b). However, considering high cluster distance with GPM-6 (cluster VI), the genotypes viz., BHGM-16, BHGM-26, DEH1, GPM 65 and 12B may be used for improvement of GPM 6 (a high yielding variety tolerant to yellow mosaic disease and root rot disease, released for North Karnataka) for various component traits.

6. Future line of work

- The genotypes of cluster III may be crossed with the genotypes of clusters IV, VII, VIII, & IX to obtain high heterotic response and desirable segregants. The cluster III having 19 genotypes may form good combination for hybridization with genotypes of solitary clusters viz., GPM-58 (IX), BHL-20 (VII), 12B (X), GPM-59 (IV) and GPM-03 (VIII). Similarly, BHL 20 (VII) and GPM-58 (IX) can be crossed with BHL-15 (XIII), BHGM-26 (XVI) and BHGM-28 (XI) to get desirable segregants in horse gram crop improvement.
- The genotypes of clusters which secured overall high ranking across thirteen characters viz., GPM 65 (cluster XIV), GPM-03 (cluster VIII), 12B (cluster X), BHGM-26 (cluster XVI) and BHL-15 (cluster XIII) are considered most promising genotypes and can be extensively used for further breeding programme to generate new material.
- The early maturing genotypes viz., GPM-6, BHGM-26 may be used in hybridization programme to derive early flowering and high yielding genotypes.
- GPM-6, a high yielding variety tolerant to yellow mosaic disease and root rot disease, released for North Karnataka may be crossed with genotypes of distant cluster III viz., DS22, BHGM-18, AK-21, BHGM-15, BHGM-29, BHGM-16, VJPL-2, BGM1183, DEH-1, BLHG-1, BHGM-17, CRIDA 18R, GPM-66, CRHG-9, CRHG-05, GPM-48, BHGM-9, BHGM-14 and BHL-60, and a local collection BHGM-28 to create variability.
- GPM 6 may be improved for various traits by hybridization with genotypes belonging to distant clusters which have shown significantly superior performance for the traits over GPM 6 viz., BHGM-16 (number of primary branches, number of pods), BHGM 26 (number of pods & pod weight per plant), DEH1 (no. of pods/plant & pod length), GPM

Table 12b. List of genotypes showing significantly better performance over check GPM-6 for various traits

Sl.no.	Trait	Genotypes	Mean value of GPM-6
1	Days to 50% flowering (earliness)	None	42.5
3	Plant height (cm)	DHG-04	61.5
4	No. primary branches	GPM-48, GPM-11, PHG-02, CRHG-4, CRHG-05, CRIDA 18R, BHGM-11, AK-44, BHGM-16, BHGM-6	2.50
5	No. pods/plant	BHGM-26, CRHG-05, CRHG-4, BHL-60, BHGM-4, VJPL-2, DEH-1, GPM-46, GPM-32, BHGM-6, GPM-12-B, GPM-48, BHGM-16, GPM-65, BHGM-27, 8B, BHGM-3, GPM-422, BGM1183, LONE	27.10
6	Pod weight/plant (g)	CRHG-05, CRHG-4, BHL-60, DEH-1, 8B, GPM-65, BHL-44, BHGM-26, BHGM-4, GPM-48, 12B, GPM-32, GPM-12-B, LONE-1	4.79
7	Pod length (cm)	GPM-03, GPM-92, DEH-1, GPM-46, GPM-79, IC100935, PHG-21	4.65
8	No. seeds/pod	BHL-44, GPM-03, GPM-59, GPM-11, BHL-26, GPM-4-61-4-1	5.10
9	Seed weight/plant (g)	GPM-22	4.35
10	Fodder weight/plant (g)	GPM-03, GPM-12-B, GPM-63, GPM-59, GPM-58, Bailhongal local, GHI-641, AK-44, GPM-4-61-4-1, GPM-65	5.60
11	100 seed weight (g)	GPM-23	3.95
12	Harvest index (%)	CRHG 19R, BHGM-8, CRHG-6	41.48
13	Seed yield (Kg/ha)*	CRHG-9, VJPL-2 and GPM-65.	1374.07

*The genotypes are numerically superior over GPM -6

65 (no. of pods, pod weight/plant, fodder weight/plant & seed weight per plant), 12B (pod weight per plant).

- The high grain and fodder yielding genotypes including local collections identified in the present study may be tested in multilocation yield trials.
- The promised genotypes of identified based on yield and nutritional parameters viz., GPM-6, CRHG-9, GPM-23 and DEH-1 may further be tested for detailed nutritional quality and utilized in value addition.

VI SUMMARY

Horse gram (*Macrotyloma uniflorum* (Lam) Verdec), an arid legume, forms an important component in the dryland crop production system, due to its ability to withstand drought with minimum management, plays role as food & fodder, as green manure crop and as good cover crop. It forms potential source for future due to its superior grain nutrients composition (as excellent source of protein, iron, calcium and antioxidants), anti-hyperglycemic properties and many therapeutic uses.

The present crop distribution at global level shows that its cultivation is concentrated in Southern India, with highest area and production in Karnataka (Anon., 2007-12). It is being grown across different states of the country. Although, several varieties have been released by different states for cultivation since inception of AICRP (pulses). However, the varieties released so far are the result of pure line selection and none by hybridization. Genetic improvement of horse gram has been undertaken at only few institutions in India (Mohar Singh *et al.*, 2013). Therefore, the genetic improvement programme needs to be strengthened in horse gram by cross hybridization and mutation breeding. The selection of genetically diverse parents for hybridization programme is most crucial for generating genetic variability in the crop.

Hence, the present study was under taken to assess genetic diversity, the nature and magnitude of genetic variability in the available horse gram genotypes, to characterize the selected genotypes for grain nutrients content and plant nitrogen content; and to study the association between various traits.

A total of 111 germplasm lines (involving released varieties, single plant selection derivatives & 30 local collections) formed the experimental material. These lines were planted during late *kharif* 14-15 in a replicated trial in RBD design at RARS Bijapur. The observations were recorded on days to 50% flowering, days to maturity, plant height (cm), number of primary branches, number of pods per plant, pod weight per plant (g), pod length (cm), number of seeds per pod, seed weight per plant (g), fodder weight per plant (g), 100 seed weight (g), harvest index (%) and seed yield (kg/hectare). Also a total of 21 genotypes were evaluated for plant nitrogen content, and grain nutrients content (protein, iron and calcium).

The data recorded on various traits were subjected to Mahalanobis's D^2 statistical analysis, variability analysis, correlation coefficient analysis and path coefficient analysis. The results obtained are summarized below.

- The analysis of variance revealed significant differences for all the characters studied among accessions. Thus indicating that choice of genotypes and characters under study were genetically diverse and appropriately chosen.
- Based on D^2 values, 111 genotypes were grouped into 16 clusters. Cluster II was the largest comprising of 51 genotypes, followed by cluster I (21 genotypes), Cluster III (19 genotypes) and cluster XII (8 genotypes). The 12 clusters (IV, V, VI, VII, VIII, IX, X, XI, XIII, XIV, XV and XVI) had solitary entries consisting of GPM-59, GPM-23, GPM-6, BHL-20, GPM-03, GPM-58, 12B, BHGM-28, BHL-15, GPM-65, GPM-22 and BHGM-26, respectively. Formation of more clusters in general and solitary clusters in particular is an indicative of existence of enormous amounts of diversity among the set of genotypes. The genotypes that fall into solitary clusters more often had unique characters which make them divergent. Hence, use of these unique entries as choice of parent for hybridization would result in heterotic hybrids.
- Inter cluster distances were ranged from 3.77 to 24.89. High inter cluster distance was obtained between Cluster III and IX were most diverse clusters (with distance of 24.89) followed by cluster III and VII (24.66), cluster-III and X (24.22), cluster III and IV (22.66), cluster III and VIII (22.38), cluster VII and XIII (22.04), cluster IX and XIII (21.92), cluster IX and XVI (21.90), cluster IX and XI (21.66), cluster VII and XI (21.62) and cluster VII and XVI (21.54) indicating high diversity among the genotypes. Hence, genotypes of cluster III may be crossed with the genotypes of to clusters IV, VII, VIII, & IX to obtain high heterotic response and desirable segregants.
- Among 13 characters studied in germplasm accessions of horse gram, the days maturity contributes highest (71.20 %) towards the genetic divergence, followed by days to 50% flowering (16.56 %), fodder weight per plant (4.96 %).
- The genotypes of clusters which secured overall high ranking across thirteen characters viz., GPM 65 (cluster XIV), GPM-03 (cluster VIII), 12B (cluster X),

BHGM-26 (cluster XVI) and BHL-15 (cluster XIII) are considered most promising genotypes and can be extensively used for further breeding programme to generate new material.

- Genetic variability analysis revealed that high PCV was observed for plant height, number of primary branches per plant, number of pods per plant, pod weight per plant, seed weight per plant, fodder weight per plant, harvest index and seed yield, moderate PCV was observed for days to 50% flowering and number of seeds per pod. High GCV observed for the traits number of pods per plant, pod weight, seed weight per plant, fodder weight per plant and seed yield. Moderate GCV observed for days to 50% flowering, plant height, number of primary branches and harvest index. Characters having high PCV and GCV coupled with high heritability were number of pods per plant, pod weight per plant and fodder weight per plant. Moderate PCV and GCV coupled with high heritability was observed for days to 50% flowering and days to maturity indicating a little improvement in yield can be achieved through selection for these traits.
- All the component traits studied were significantly positively associated with both seed yield per plant and seed yield per hectare except for the significant and negative association of days to 50% flowering, positive and non-significant association of harvest index, and negative non-significant association of days to maturity with seed yield per hectare was observed.
- The association among all component traits was positive and significant except for positive non-significant association observed between no. of pods per plant and days to 50% flowering, days to maturity & harvest index, and between pod weight per plant and harvest index, significant negative association of harvest index with plant height and fodder weight per plant, and negative non-significant association of harvest index with days to maturity.
- Path co-efficient analysis revealed that 100 seed weight had the highest positive direct effect on seed yield followed by plant height. Hence, it would be rewarding to lay stress on these characters in selection programme for increasing the seed yield.

- Performance of genotypes for various traits viz., BHGM-18 (early flowering and early maturity), CRHG-05 and CRHG-4 (number of primary branches, number of pods per plant, pod weight per plant) and GPM-58 (Seed weight per plant, fodder weight and 100 seed weight) may be used for improvement of GPM 6 for various component traits through hybridization.
- The range of values among 21 entries for grain micronutrients Calcium, iron and zinc were 38.43-104.812 mg/100g, 0.39-7.083 mg/100g and 0.966-5.467 mg/100g, respectively. The plant nitrogen and protein content value were ranged from 0.69 to 1.33 per cent and 4.31 to 8.31 per cent respectively. Grain protein content among 21 genotypes was ranged from 17.21 to 25.63%. Promised genotypes identified for nutritional parameters viz., GPM-6, CRHG-9, GPM-23 and DEH-1 Hence, it would be rewarding for improving the nutrient contents of horse gram.
- Based on *per se* performance over check variety GPM-6, the promising genotypes identified for various traits were DEH1, 12B, CRHG-4, 8B, BHGM-16, BHGM-26, GPM-03 and GPM-65. However, considering high cluster distance with GPM-6 (cluster VI), the genotypes viz., BHGM-16, BHGM-26, DEH1, GPM 65 and 12B may be used for improvement of GPM 6 for various component traits.

VII REFFERENCES

- A. O. A. C., 1980. Official Methods of Analysis. Association of Officials Analytical Chemists, Washington D. C., 20044.
- Aggarwal, V. D. and M. S. Kang., 1976, Genetic variability, correlation and path analysis studies in horse gram (*Dolichos biflorus* L.). *Tropical Agric.*, 331:310-315.
- Anonymous, 2012, Annu. Rep. (2012-13), AICRP on Dryland Agriculture, Pulse Improvement Project., *UAS Dharwad*, p.130.
- Anonymous, 2013, Annu. Rep. (2013-14), AICRP on Dryland Agriculture, Pulse Improvement Project., *UAS Dharwad*, p.168.
- Anonymous, 2007-2012, Directorate of Economics and statistics, Department of Agriculture and co-operation, Ministry of Agriculture, Govt. of India. agricoop.nic.in/agristatistics.htm.
- Anonymous, 2009-10. www.Districtsofindia.com
- Arun Gupta, Anuradha Bhartiya, Gyanendra Singh, Vinay Mahajan and Bhatt, J. C., 2010 Altitudinal diversity in horse gram (*Macrotyloma uniflorum* (Lam.) Verdc.) landraces collected from Himalayan hill region. *Pl. Genet. Resou. Char. Utiliz.*, 8(3): 214-216.
- Balan, A. and Das, L. D., 1994, Variability in different genotypes of horse gram (*Macrotyloma uniflorum* (Lam). Vardec). *Orissa J. Agric. Res.*, 5(3/4): 235-237.
- Balan, A., Ramasamy, P., Sivasamy, N., 1991, Correlation and path coefficient analysis in horsegram (*Macrotyloma uniflorum* (L.) Verdec)., *Orissa J. Agric. Res.*, 4(1/2): 6-10.
- Bhatt G. M., 1970, Multivariate analysis approach to selection of parents for hybridization aiming at yield improvement in self-pollinated crops, *Australian J. Agr. Res.*, 21(1):1-7.
- Bhave, S.G., Joshi, S. N., Sawant, S.S., Bendale, V.W. and Desai, S. S., 2007, Analysis of genetic parameters for yield and certain yield contributing traits in horse gram. *J. Maha. Agric.Uni.*, 32(2): 239-241.

- Birari, S. P., Deorukhakar, N. V. and Jamadagni, B. M., 1987, Genetic parameters and character association in horse gram [*Dolichos biflorus* L.]. *Indian J. Agric. Res.*, 21(1):55-58.
- Burton, G. W. and De Vane, E. H., 1953, Estimating heritability in talliFeschue (*Festuca arundinances*) from replicated clones material. *Agron. J.*, 45: 478-481.
- Dabhos, B. S., Thomas, T. A. and Sapra, R. L., 1990, factor analysis in kulthi [*Macrotyloma uniflorum*]. *International J. Tropical Agric.*, 8(1):14-18.
- Dasgupta, T., Mukherjee, K., Roychoudhury, B. and Nath, D., 2005, Genetic diversity of horse gram germplasms. *Leg. Res.*, 28(3): 166-171.
- Dewey, D. R. and Lu, K. N., 1959, A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron. J.*, 51: 515-518.
- Dobhal, V.K. and Rana, J.C., 1994a, Genetic analysis for yield and its components in horse gram (*Macrotyloma uniflorum*). *Legume Res*, 17(3/4): 179-182.
- Dobhal, V.K. and Rana, J.C., 1994b, Multivariate analysis in horse gram. *Legume Res.*, 17(3):157-161.
- Durga, K. K., 2012, Variability and divergence in horse gram (*Dolichos uniflorus*). *J. Arid Land.*, 4(1): 71-76.
- East, E. M., 1916, studies on size inheritance in Nicotiana. *Genetics*, 1:164-176.
- Fisher, R. A., Immer, F. R. and Tendin, O., 1932, The genetical interpretation of statistics of the third degree in the study of quantitative inheritance. *Genetics*, 17:107-124.
- Fisher, R. A. and Yates, F., 1963, Statistical tables for biological, agricultural and metrical research, Oliver and Boyd, Edinburgh. pp. 145-149.
- Ganesh Kulkarni, B. and Umesh Mogle, P., 2011, Characterization and evaluation of horse gram [*Macrotyloma uniflorum* L. Verdec] genotypes. *Sci. Research Reporter.*, 1(3):122-125.

- Ganeshaiah, K. N., 1979, Multivariate analysis for yield and its contributing characters in Horse gram [*Dolichos biflorus* L.], *M.Sc., (Agri) Thesis*, U.A.S., Bangalore.
- Ganeshaiah, K. N., Shivashankar, G. and Hiremath, S. R., 1982, Genetic variability for yield and other characters in the germplasm of horse gram. *Mysore J. Agric. Sci.*, 16(4):400-403.
- Geetha, K., Mani, A. K., Hepziba, M. J., Latha, R. and Shanthi, P., 2011, Studies on genetic diversity among germplasm accessions of horse gram [*Macrotylom auniflorum* (Lam) Verde]. *Legume Res.*, 34(1): 14-19.
- Ghorpade. D. S., 1985, Metroglyph analysis of morphological variations in horse gram [*Dolichos biflorus*L.]. *Curr. Res. Reporter*, Mahatma Pule Agril. Univ., 1(1):56-60.
- Grafius, J. E., 1959, Heterosis in barley. *Agron. J.*, 51: 551-554.
- Gupta, D. N., Parab, A. A., Mehta, H. R. and Goyal, R., 2001, Evaluation of nutritive value of promising genotypes of Pigeonpea and horse gram in Konkan. *J. Phytol. Res*, 14(2): 143-146.
- Hanson, C. H., Robinson, H. F. and Comstock, R. E., 1956, biometrical studies of yield in segregating population of Korean Lespodzoa. *Agron. J.*, 48: 314- 318.
- Hussaini, S. H., 1973, Multivariate analysis and group distribution in the world collection of *Eleusine coracana* Gaertn, *NCSI Publications*, p. 81.
- Ismail, S., Wankhede, D.B., Syed, H.M., Kulkarni, A.S. and Fayazuddin, M., 2003. The effect of germination on the changes in protein, free amino acid and in-vitro protein digestibility of moth bean and horse gram. *Advances in Arid legumes Research*, 315-317.
- Jayashri Hiremath, Sunanda Sharan and Vishwanath, K. P., 2001, Chemical composition and functional properties of some important genotypes of horse gram [*Macrotyloma uniflorum* L.Verdec]. *Karnataka J. Agric. Sci.*, 14(4): 943-946.
- Johannsen, W. L. 1909, Elements for der exateteuerblichkeitslehre. Jena: Gustav Fiscer.

- Johnson, H. W., Robinson, H. F. and Comstock, R. E., 1955, Estimation of genetics and environmental variability in soybean. *Agron. J.*, 47: 477-483.
- Joshi, S. N., Bhave, S. G., Bendale, V. W., Jadhav, B. B. and Sawant, S. S., 2000, Analysis of genetic variability and correlation in horse gram [*Macrotyloma uniflorum* (Lam) Verdc.]. *Research on Crops*, 8(3): 632-635.
- Kabir, J. and Sen, S., 1989, Correlation and path analysis in *Lablab niger* Medik., *Dolichos biflorus* Lam and their F₁. *Tropical Agric.*, 66(3): 281-283.
- Kalia, R. and Dogra, P., 2006, Genetic divergence for yield and quality traits in horse gram. *Crop Res.*, 32(3): 438-441.
- Kalia, R. and Dogra, P., 2007, Genetic variability for yield and quality traits in horse gram, *Annals of Bio.*, 23(2): 133-136.
- Kallesh, H. G., 1981, Path analysis and selection indices in three F₂ populations of horse gram [*Macrotyloma uniflorum* (Lam) Verdec.], *M.Sc. (Agri). Thesis*, U.A.S., Bangalore.
- Kanak Durga, K. Sandeep Varma, V., Ankaiah, R. and Ganesh., 2014, Seed storability studies in Horse gram. *WebPub J. Agric. Res.* 2(3):47-54.
- Khatun, A. A., SunandaSharan., Viswanatha, K. P. and Veena, B., 2013, Effect of processing techniques on the bio-accessibility of micronutrients in selected genotypes of horsegram (*Macrotyloma uniflorum*)., *Mysore J. Agric. Sci.*, 47(1): 54-57.
- Khulbe, R. K., Pant, D. P. and Singh, D. V., 2013, Genetic studies in horse gram from NW Himalayan regions of Uttarakhand, India. *Crop Res.*, Hisar, 43(1/2/3): 194-196.
- Kulkarni, G. B. and Mogle, U. P., 2011, Characterization and evaluation of horse gram (*Macrotyloma uniflorum* (Lam)) Verdcourt) genotypes. *Science Research Reporter*, 1(3): 122-125.
- Lad, D.B., Chavan, S.A. and Dumbre, A. D., 1998, Genetic variability and correlation studies in horse gram. *J. Maha. Agric.Uni.*, 23(3): 268-271.

- Lad, D.B., Chavan, S.A. and Dumbre, A. D., 1999, Path coefficient analysis in horse gram. *J. Maha. Agric.Uni.*, 24(1): 102-103.
- Latha, M., Suma, A., Asha, K. I., Dwivedi, N. K., Mani, S. and Indiradevi, A., 2013, Seed polymorphism in South Indian horse gram [*Macrotyloma uniflorum* L.Verdec]: A comprehensive study. *J. Appl. Biol. Biotech.*, 1(04): 001-006.
- Lush, J. L., 1940, Inter-size correlation regression of offspring on dams as a method of estimating heritability of character. *Proc. American Soc. Animal Prod.*, 33: 293- 301.
- Lush, J. L., 1949, Heritability of quantitative characters in farm animals. 8th Congr. *Genet, Hereditas* (Suppl.), 356-375.
- Mahalanobis, P.C., 1936, On the generalized distance in statistics, *Proceed. National Institute of Sci.*, (India), 2(1): 49-55.
- Maloo, S. R., 1999, Components of productivity and plant type concept in Cicer and Vigns species-a review. *Legume Res.*, 22:1-9.
- Mather, K., 1949, Biometrical genetics, Methuen and Co., London.
- Mohar Singh, Upadhyaya, H.D., and Bisht, I.S., 2013, Genetic and Genomic resources of grain legume improvement. Newnes, 18-Jul-2013-Science-332 pages.
- Morris, J. B., Wang, M. L., Grusak, M. A. and Tonniss, B., 2013, Fatty acid, flavonol, and mineral composition variability among seven *Macrotyloma uniflorum* (Lam.) Verdc. Accessions. *Agriculture*, 3(1): 157-169.
- Murthy, B. R. and Quadri, M. I., 1966, Analysis of divergence in some self-compatible forms of *Brassica compestris* L. var. Brown Sarson. *India J. Genet.*, 20: 45-48.
- Nagraja, N., 1997, Genetic variability and association studies involving seed yield, agromorphological and seed characters in horse gram [*Macrotyloma uniflorum* L.Verdec]. *M.Sc., (Agri) Thesis*, U.A.S., Bangalore.

- Nagraja, N., Nehru, S. D. and Manjunath, A., 1999, Plant type for high yield in horse gram as evidence by path coefficients and selection indices. *Karnataka J. Agric. Sci.*, 12(1-4 combined): 32-37.
- Nehru, S. D., Manjunath, A. and Nagaraja, N., 2000, Identification of traits to be selected in breeding for yield in horse gram [*Macrotyloma uniflorum* (Lam.) Verdec.]. *Karnataka J. Agric. Sci.*, 13(1): 11-15.
- Nilson Ehle, H., 1909, Kreuzung UnterSchuxgen and Hafer and Weizen. Tunds Univ. Arsster, N. F. Afd., 2:Ed.5.
- Niveditha Nandi and Jagapathi Tha., 2014, Growth variability and correlation studies in *Dolichus biflorous* L. at two locations. *International J. Bio-res. Stress Mgt.*, 5(21): 275-279.
- Paliwal, R. V., Sodani, S. N. and Jain, L. K., 2005, Correlation and path analysis in horse gram [*Macrotyloma uniflorum* (Lam) Verdc.]. *J. Arid Leg.*, 2(2): 309-310.
- Pandya, R., Ram, B., Vaid, B. and Sharma, L.K., 2002, Correlation and path analysis for yield in horse gram under two rainfall regimes. *Advances in Arid Legumes Res.*, 123-125.
- Patil, H. S., Deshmukh, R. B. and Deokar, A. B. 1983, Variability studies in some quantitative characters of mung bean. *J. Mharashtra Agric. Univ.*, 3(1): 28-29.
- Patil, J. V. and Deshmukh, R. B., 1982, Genetic variability in horsegram. *J. Mharashtra Agric. Univ.*, 7(3):139-1140.
- Patil, J. V. and Deshmukh, R. B., 1982a, Protein contents in horsegram. *J. Maharashtra Agric. Univ.*, 7(3): 271.
- Patil, J. V. and Deshmukh, R. B., 1982b, Association analysis in horsegram. *J. Mharashtra Agric. Univ.*, 8(2):120-121.
- Patil, J. V. and Deshmukh, R. B., 1985, Varietal differences for protein content in horse gram. *Current Research Reporter*, 1(1): 99-100.

- Pense, V. G., 1940, The application of genetics to plant breeding. II. The inheritance quantitative characters and plant breeding. *J. Genet.*, 40: 283-302.
- Powers, L., 1942, The nature of the series of environmental variance and estimation of the genetic variance and the geometric means of crosses involving species of *Lycopersicon*. *Genetics*, 27:561-575.
- Prabha, S. S., Rajendra Prasad and Sambhoo Prasad., 2010, Study on genetic and seed quality parameters in horse gram genotypes under mid hills of north western Himalaya. *Trends in Biosci.*, 3(2): 187-189.
- Prakash, B.G., Hiremath, C.P., Devarnavadgi, S.B. and Salimath, P. M., 2010, Assessment of genetic diversity among germplasm lines of horse gram (*Macrotyloma uniflorum*) at Bijapur. *Electronic J. Plt. Breed.*, 1(4): 414-419.
- Raina, S. K., Dogra, R. K. and Kapila, R. K., 2007, Variation and character association in horse gram (*Macrotyloma uniflorum* (Lam.) Verdc.) germplasm of North Western Himalayas. *Crop Improvement*, 34(2): 197-201.
- Ram, B., Pandya, R., Sharma, L. K. and Vaid, B., 2003, Genetical study of variability parameters in horse gram. *Advances in Arid Legumes Research*, 120-122.
- Rama Kalia, Puneet Dogra and Pandey, D. P., 2007, Correlation and path analysis for yield and its components in horse gram (*Macrotyloma uniflorum* (Lam.) Verdc.). *Research on Crops*, 8(2): 485-491.
- Ramesh, C. K., Abdul Rehman, Prabhakar, B. T., Vijay, A. B. R. and Rao, S. J. A., 2011, Antioxidant potentials in sprouts vs. seeds of *Vigna radiata* and *Macrotyloma uniflorum*. *J. Appl. Pharma. Sci.*, 1(7): 99-103.
- Ramkrishnan, A. Muthukrishnan, P., Ranganathan, C. R. and Srinivasasamy, N. S., 1978, Genetic variability in horse gram [*Dolichos biflorus* L.]. *Madras Agric. J.*, 65(5):281-283.
- Rao, C. R., 1952, Advanced statistical methods in biometrical research. John Wiley and Sons, New York.

- Rao, S. S. and Chandrakar, B. S., 1994, Genetic variability and correlation studies in horse gram. *Curr. Res.*, 159-161.
- Rao, S. S. and Nanda, H. C., 1994, Genetic variability and correlation studies for grain yield and its components in horse gram. *Indian J. Pulse Res.*, 7(1):59-61.
- Robinson, H. F., Compstock, R. E. and Harey, P. H., 1949, Estimates of heritability and degrees of dominance in corn. *Agron. J.*, 43: 353-359.
- Roopadevi, V. D., Vishwanath, A. P., Shivakumar, H. K. and Devkumar, N., 2002, Correlation and regression studies in horse gram (*Macrotyloma uniflorum* Lam. Verde.). *Mysore J. Agric.Sci.*, 36(3): 208-211.
- Sahane, D.V., Dhonukshe, B.L. and Navale, P. A., 1995, Association of physiological parameters with grain yield of horse gram. *J. Maharashtra Agric. Univ.*, 20(1): 149-150.
- Sahoo, J. L., Nayak, B. K., Baisakh, B. and Nayak, A., 2010, Genetic variability in horse gram (*Macrotyloma uniflorum* Lam.). *Environment and Ecology*, 28(2A): 1119-1121.
- Sajjanar, G. M., Kalaghatagi, S. B., Surakod, V. S. and Kallesh, D. T., 2013, Horse gram (*Macrotyloma uniflorum*)-A nutritious dryland pulse crop, AICRP on Dryland Agriculture, Regional Agricultural Research Station, Vijayapur, 586 101, Karnataka. Technical bulletin, 52 pages.
- Sangita Yadav., Negi, K. S. and Mandal, S., 2004. Protein and oil rich wild horse gram. *Genetic Resources and Crop Evolution*, 51(6): 629-633.
- Sarkar, G., Mahato, P., Panda, S. and Senapati, B. K., 2005, Yield relationship among different characters in horse gram [*Macrotyloma uniflorum* (Lam)]. *Journal of Arid Legumes*, 2(2): 410-411.
- Savithramma, D. L., 1994, Genetic divergence studies in horse gram [*Macrotyloma uniflorum* L.Verdec]: An approach to identify morphological and physiological traits for higher production, Ph.D. Thesis, U.A.S., Bangalore.
- Savithramma, D. L., 2002, Character association and path coefficient studies for yield and its components in horse gram. *Mysore J. Agric. Sci.*, 36(1): 1-7.

- Senapati, N., Samal, K. M. and Dhal, A., 1998, Genetic variability and performance of promising horsegram (*Macrotyloma uniflorum* Lam. Verd.) lines under the North Central Plateau agro-climatic zone of Orissa, India. *ACIAR Food Legume Newsletter.*, (27): 9-10.
- Sharma, R. K., 1995, Nature of variation and association among grain yield and yield components in horse gram. *Crop Imp.*, 22(1): 73-76.
- Shashi Jain, Vishakha Singh, Shipra Chelawat, 2012, Chemical and physicochemical properties of horse gram (*Macrotyloma uniflorum*) and its product formulation. *Journal of Dairying Foods and Home Sciences*, 31(3): 184-190.
- Shivashankar, G., Jaillkop, S. H., Chikkadevaiah and Shetter, B. I., 1977, Heritability and correlation studies in horse gram. *Mysore J. Agric. Sci.*, 11:211-216.
- Singh, D. N., 1990, Genetic variability, correlation and path analysis for grain yield and its components in horse gram. *Indian J. Pulse Res.*, 3(1):25-30.
- Singhal, H. C., Tomar, S. S., Baraiya, B. R., Sikarwar, R. S. and Tomar, I. S., 2010, Study of genetic divergence in horse gram (*Macrotyloma uniflorum* L.). *Legume Research*, 33(2): 119-123.
- Sivasubramanian, S. and Menon, M., 1973, Heterosis and inbreeding in rice. *Madras Agril. J.*, 60: 1139.
- Smartt, J., 1990. Grain Legumes: Evaluation and Genetic Resources. Cambridge: Cambridge University Press.
- Sood, B. C., Gartan, S. L. and Kalia, N. R., 1994, Variability, correlation and path studies in horse gram. *Indian J. Res.*, 7(1):68-6.
- Sreekantharadya, R., Shetter, B. I., Chandrappa, H. M. and Shivashankar, G., 1975, Genetic variability in horse gram. *Mysore J. Agric. Sci.*, 9(3):361-363.
- Sudha, N., Musthari Begum, J., Shambulingappa, K. G. and Babu, C. K., 1995, Nutrients and some anti-nutrients in horse gram (*Dolichus biflorus* (Lam.)Verdc). *Food and Nutrition Bulletin*. 16(1):81-83.

- Sunil, N., Sivaraj, N., Pandravada, S.R., Kamala, V. and Reddy, P.R., 2009, Genetic and geographical divergence in horse gram germplasm from Andhra Pradesh, India. *Pl. Genet. Resou. Char. Utiliz.*, **7**(1): 84-87.
- Sunil, Neelam, Vinod Kumar, Sivraj Natarajan, Kamala Venkateshwaran and Someswara Rao Pandravada, 2014, Evaluation and diversity observed in horse gram (*Macrotyloma uniflorum* (Lam) Verdc.) germplasm from Andhra Pradesh, India. *International J. Plt. Res.*, **4**(1):17-22.
- Suraiya, D., 1980, Selection index in horse gram (*Dolichus biflorus*). M. Sc. Agri Thesis. Kerala Agri. Uni. Vellanikkara, Trichur.
- Suraiya, D., Mercy, S. T., Chandramony, D. and Nayar., 1988, Genetic variability of yield and its components in horse gram [*Macrotyloma uniflorum*]. *Indian J. Agric. Sci.*, **58**(10):798-799.
- Venkateswarlu, O., 2000, Genetic variability in horse gram (*Macrotyloma uniflorum* Lam.). *Agricultural Science Digest*, **20**(1): 64-65.
- Verdcourt, B. 1982, A revision of *Dolichus biflorus* (Leguminosae). Hooker's *Icones Plantarum*. **46**:3609-3613.
- Weber and Morthy, B. R., 1952, Heritable and non-heritable relationship and variability of oil content and agronomic characteristics in the F₂ generation of soybean crosses. *Agron. J.*, **44**: 202-209.
- Wright, S., 1921, Correlation and causation. *J. Agril. Res.*, **20**: 557-585.
- Yarguntappa, R., 1987, Studies on genetic variability, correlation and path coefficient analysis in horse gram [*Macrotyloma uniflorum* L. Verdec]. *M.Sc., (Agri) Thesis*, U.A.S., Bangalore.
- Zeven, A. C. and de Wet, J. M. J., 1982, Dictionary of cultivated plants and their regions of diversity. Center for Agricultural Publication and Documentation, Wageningen.

Appendix I. Meteorological data for the year 2014-15 and average data of 32 years (1981-2013)

Months	Rainfall (mm)		No. of rainy days	Maximum Temperature (°C)		Minimum Temperature (°C)		Relative humidity (%)	
	2014	Mean (1981-2013)	2014	2014	Mean (1981-2013)	2014	Mean (1981-2013)	2014	Mean (1981-2013)
January	0.0	4.01	0	29.70	29.95	15.20	15.60	58.00	56.46
February	6.4	2.79	1	31.70	32.90	16.10	17.95	49.50	47.95
March	27.4	5.28	2	34.50	36.40	20.10	21.00	45.00	44.46
April	27.0	22.69	2	38.00	38.60	22.70	23.65	40.00	42.79
May	68.6	38.97	4	37.60	39.11	22.90	24.05	53.00	48.00
June	54.4	83.69	4	35.00	33.73	22.70	22.45	62.00	63.43
July	151.6	76.69	7	30.10	30.83	21.60	22.05	76.00	69.73
August	245.7	77.23	8	30.20	30.50	21.30	21.20	76.00	72.00
September	59.4	150.92	4	30.70	31.38	21.10	21.40	72.00	69.40
October	65.3	100.39	4	31.90	31.18	19.60	20.85	66.00	63.57
November	15.0	28.38	3	30.40	29.78	15.60	16.70	63.50	59.37
December	16.0	6.78	2	29	29.10	13.00	13.95	62.00	55.18
Total	736.8	597.81	41	-	-	-	-	-	-

Appendix II: Mean values of the 13 characters for the 111 entries of horse gram germplasm lines

Genotypes	Days to 50% Flowering	Days to Maturity	Plant Height (cm)	No. Primary Branches	No. pods/plant	Pod weight t/plant (g)	Pod length (cm)	No. seeds/pod	Seed weight/plant (g)	Fodder Weight /Plant (g)	100 seed weight (g)	Harvest index (%)	Plot yield (Kg/ha)
GPM-6	42.5	111.0	61.5	2.5	27.1	4.79	4.55	5.1	4.35	5.60	3.95	41.4	1374.0
BJPL-1	49.0	113.0	77.0	3.5	31.1	4.70	4.74	5.3	4.15	4.40	4.05	46.0	1166.6
GPM-23	47.0	101.5	64.3	2.4	16.2	2.80	4.71	5.2	2.15	2.95	4.50	38.5	1268.5
CRHG-9	44.0	98.5	63.6	3.0	31.5	4.45	4.66	4.9	2.80	5.55	4.10	27.8	1507.4
DS22	41.5	92.0	53.2	2.7	32.7	5.35	4.60	5.1	3.40	3.25	3.80	39.6	1138.8
IC100938	49.0	100.5	63.4	2.9	24.4	4.50	4.91	4.5	3.40	5.85	3.65	33.6	987.9
DEH-1	45.5	93.0	57.2	1.8	50.0	8.65	5.05	5.3	5.60	5.75	4.20	38.6	1042.5
PHG-9	45.5	102.0	50.6	2.7	31.6	5.40	4.95	4.7	3.95	2.95	4.15	46.9	1256.4
VJPL-2	43.5	92.5	52.3	3.2	50.3	6.10	4.87	4.0	3.50	3.15	3.90	38.3	1673.1
IC100935	49.5	103.0	56.6	2.6	24.0	3.95	5.00	5.1	2.60	4.65	4.15	30.3	1175.0
KBHG-1	50.5	115.5	58.5	1.8	15.1	3.20	4.78	4.7	2.00	4.00	4.10	28.8	1037.0
AK-42	54.5	118.0	48.0	3.1	22.4	3.95	4.86	5.2	2.85	2.55	4.30	43.7	807.4
GPM-30	45.5	106.5	49.4	3.4	17.3	2.50	4.77	4.4	1.85	2.40	4.20	37.2	1229.6
BLHG-1	53.5	94.0	64.3	2.3	19.3	3.65	4.63	4.7	2.65	3.50	4.10	37.1	972.2
BGM1183	40.5	94.5	60.3	2.8	42.6	5.15	4.86	4.6	2.75	3.05	3.90	33.7	1041.6
AK-21	49.5	92.0	50.5	1.9	25.1	3.50	4.98	4.6	2.50	2.50	3.80	41.9	696.2
CRHG-4	45.0	109.0	49.9	4.4	53.8	9.70	4.82	5.4	5.55	4.00	3.75	40.5	855.5
CRHG-6	42.0	111.0	39.2	3.3	26.6	3.05	4.79	3.9	2.35	1.25	3.60	55.2	437.0
CRHG-8	43.5	106.0	41.5	3.4	23.2	4.55	4.57	4.5	3.15	2.30	3.50	46.0	901.8
CRHG 19R	45.5	114.5	44.0	2.5	34.0	4.60	4.94	4.4	4.10	1.95	4.25	63.3	700.0
CRIDA 18R	50.5	96.5	42.3	4.1	33.0	4.15	4.59	4.6	3.10	2.45	3.65	47.7	637.0

GPM-11	66.0	119.5	63.9	4.6	35.6	6.35	4.57	6.0	4.40	4.40	3.90	40.8	1119.4
GPM-23	59.0	116.0	61.6	3.1	31.6	4.95	4.48	4.2	2.60	3.55	3.90	30.6	1086.1
RS28-607	53.5	117.5	53.7	2.8	25.6	3.90	4.69	5.1	2.70	3.85	3.95	34.7	1213.8
GPM-422	51.5	116.0	56.6	3.5	42.6	4.95	4.69	5.0	3.85	3.20	3.85	47.3	1033.3
GPM-62	63.0	117.5	54.5	2.8	32.4	5.10	4.97	4.8	3.20	2.35	4.05	43.3	920.3
GPM-13	66.0	122.5	64.9	3.2	21.9	4.90	4.52	5.1	2.80	4.75	4.05	29.0	791.6
GPM-51	65.5	113.5	59.7	3.5	20.3	4.95	4.69	5.4	3.15	5.15	3.95	31.8	1221.2
AK-44	53.5	102.0	64.5	4.0	33.2	5.45	4.45	5.4	3.45	7.50	3.90	26.5	846.2
AK-22	45.0	116.5	66.2	2.1	29.6	7.2	4.61	4.9	4.40	4.05	3.75	40.3	1177.7
GPM-18	53.0	119.5	68.9	3.1	19.3	2.90	4.39	5.4	2.40	4.75	3.90	31.7	940.7
GPM-25	64.0	114.5	69.6	3.2	19.5	4.10	4.37	4.9	2.95	6.20	3.90	28.6	925.0
GPM-44	46.5	115.0	70.2	3.1	31.6	4.60	4.56	5.0	3.95	6.45	3.95	35.5	926.8
BHG-1	48.5	114.5	53.4	2.5	23.7	3.65	4.76	5.7	3.05	2.65	3.80	53.5	1227.7
GPM-63	46.5	112.0	82.6	3.8	25.5	5.10	4.48	5.6	3.90	9.00	4.10	27.8	1092.5
GPM-03	57.0	119.5	74.9	2.9	39.2	4.35	5.22	6.0	3.30	9.85	4.05	23.4	1338.8
GPM-4.4-113	49.0	114.5	66.1	3.2	35.2	4.05	4.73	5.4	2.55	4.40	3.90	30.4	1204.9
GPM-37	51.5	114.5	70.5	3.3	27.8	4.15	4.54	5.1	2.75	6.35	3.90	26.5	796.2
GPM-49	62.5	114.0	49.8	2.7	28.1	3.65	4.70	4.2	2.55	3.05	4.40	37.3	851.8
VLG-19	60.0	119.5	66.8	2.6	22.2	3.90	4.81	5.7	2.70	5.50	3.85	28.9	753.7
GPM-4-61-4-1	55.5	115.0	72.7	3.3	31.4	5.20	4.39	6.0	3.60	7.35	3.80	28.7	791.6
GPM-36	63.0	115.5	59.2	2.2	28.3	5.80	4.99	5.0	3.10	6.25	3.90	25.6	683.3
DHG-04	53.5	114.5	89.8	3.6	27.3	4.05	4.40	5.2	3.00	4.25	3.25	36.9	575.9
PHG-12	56.5	115.5	54.9	2.1	30.2	4.35	4.97	5.8	2.90	4.35	3.80	33.3	556.4
GPM-28	43.0	113.5	64.1	1.8	23.2	3.30	4.81	4.4	2.20	5.00	3.65	26.0	882.4
LONE-1	54.5	100.5	57.2	3.2	42.4	7.55	4.85	4.8	4.45	4.70	4.15	36.1	938.8

GHI-641	59.5	117.5	67.8	2.6	37.9	6.75	4.41	5.9	4.30	7.90	3.70	29.3	761.1
GPM-171	53.0	101.0	57.6	2.4	31.3	6.25	4.61	4.8	3.60	3.60	3.95	37.2	1171.3
GPM-46	56.5	113.5	56.4	3.0	49.7	6.55	5.04	5.1	3.90	3.95	4.10	38.1	936.1
PHG-02	66.0	121.5	61.2	4.4	36.7	6.00	4.48	5.5	3.95	5.30	3.80	35.2	750.0
PHG-21	65.0	114.5	50.4	3.2	22.9	3.60	5.00	5.4	2.75	3.10	4.00	40.5	987.9
CRHG-07	66.0	116.0	61.9	3.9	38.6	6.05	4.83	4.6	3.95	7.00	4.00	30.3	755.5
PS-2-4	63.5	114.0	66.1	3.1	32.4	4.75	4.36	5.3	3.25	4.75	3.80	34.2	664.8
GPM-58	66.0	123.5	72.9	2.5	30.8	5.50	4.32	5.3	3.35	8.75	4.20	23.6	521.3
GPM-48	62.5	93.5	54.9	5.2	46.1	7.75	4.82	5.1	4.35	3.40	4.00	39.0	1049.1
GPM-44-2	59.0	120.5	65.1	2.5	26.2	4.35	4.17	5.2	2.75	5.90	3.60	26.8	894.4
GPM-12-B	51.0	112.0	69.8	2.4	46.3	7.60	4.62	5.1	4.35	9.40	4.25	25.5	894.4
SHG-317	69.0	113.5	66.4	2.9	36.1	6.35	4.70	5.3	4.00	6.25	3.80	31.8	831.5
VLG-08	52.5	115.5	71.3	3.5	34.8	6.05	4.86	5.2	3.90	6.15	4.00	30.6	735.2
GPM-65	67.0	99.5	61.7	3.8	44.9	8.30	4.83	4.8	5.20	7.30	3.85	33.7	1411.1
GPM-66	48.5	97.5	50.2	3.2	20.7	3.45	4.97	4.2	2.60	3.60	3.70	36.6	1176.8
8B	65.0	114.5	67.0	2.7	43.5	8.50	4.78	5.9	5.60	7.05	3.95	35.8	1147.2
GPM-92	57.5	120.5	68.6	2.5	32.6	5.20	5.13	5.7	3.40	5.05	3.90	33.0	1092.6
14GH 5R	64.5	119.5	58.8	3.2	33.5	6.30	4.52	5.1	4.40	4.30	4.00	41.8	965.7
12B	66.5	123.5	75.1	2.9	40.8	7.70	4.32	5.4	5.00	6.30	4.00	35.6	1372.2
GPM-59	67.5	120.5	68.4	2.2	39.7	7.15	4.71	6.0	4.35	8.85	4.00	27.1	846.3
GPM-79	60.5	116.0	65.0	2.8	29.1	5.85	5.01	5.6	4.20	6.25	4.00	34.6	875.0
GPM-32	62.0	117.0	72.7	2.3	48.8	7.65	4.96	5.8	4.20	6.75	4.05	28.6	1290.7
CRHG-05	55.0	94.5	50.5	4.2	54.2	10.70	4.74	5.6	4.20	4.85	3.80	42.2	1405.5
GPM-22	65.5	115.0	54.4	2.5	22.9	5.65	4.27	4.8	6.60	5.65	4.25	30.8	1000.0
BHL-78	63.0	114.0	63.6	3.3	33.6	7.20	4.74	5.4	3.50	4.70	4.05	38.8	1154.6

BHL-44	46.5	112.5	68.5	2.8	38.6	8.15	4.74	6.2	4.55	7.00	3.95	35.3	941.6
BHL-15	65.0	97.5	62.0	2.7	28.3	6.15	4.46	5.3	5.35	5.75	3.90	35.0	1105.5
BHL-60	67.0	97.5	75.1	3.4	53.8	9.15	4.49	5.0	4.15	5.05	3.80	37.5	1020.4
BHL-20	62.5	124.5	74.2	2.7	20.6	3.40	4.45	5.2	3.15	3.75	3.90	44.1	906.5
BHL-154	66.5	102.0	69.8	2.7	18.5	3.60	4.24	4.8	2.65	4.35	4.00	33.8	1113.9
BHL-48	62.0	115.5	73.2	2.3	26.1	4.00	4.34	5.6	2.85	6.85	3.85	26.4	870.4
BHL-26	63.5	100.5	67.5	2.7	27.4	4.85	4.47	6.0	3.70	4.77	3.90	38.6	950.9
BHL-66	64.5	109.0	58.7	2.6	32.8	6.00	4.46	5.4	3.95	5.70	3.75	33.4	620.4
BHL-128	56.0	119.5	66.3	3.4	28.7	5.15	4.55	4.5	3.05	4.25	3.65	32.8	1127.7
BHGM-1	69.0	118.0	38.8	2.1	29.5	4.40	4.51	4.9	2.50	3.25	3.75	32.6	424.0
BHGM-2	67.5	119.0	56.3	2.8	32.6	4.05	4.70	4.5	2.30	4.40	4.10	26.5	477.7
BHGM-3	67.0	120.5	60.5	2.4	42.7	6.00	4.53	4.7	3.50	5.10	3.70	31.7	387.0
BHGM-4	68.0	103.5	50.8	3.3	53.7	7.80	4.76	5.1	4.00	3.95	3.70	34.0	612.0
BHGM-5	56.5	106.0	43.3	2.6	31.2	4.50	4.64	5.2	3.15	2.50	3.65	45.0	450.0
BHGM-6	55.5	101.5	47.9	4.0	47.7	3.80	4.75	4.9	2.70	1.60	3.70	53.5	594.4
BHGM-7	58.0	99.0	68.0	3.0	26.8	4.35	4.56	5.2	3.00	5.40	3.65	31.6	1079.6
BHGM-8	67.0	102.5	43.3	3.4	27.1	3.25	4.50	5.0	2.80	1.20	3.70	62.9	615.7
BHGM-9	67.0	95.5	50.4	3.5	35.1	3.00	4.81	5.2	2.15	1.70	3.55	47.5	1307.4
BHGM-10	52.0	103.0	69.4	2.6	33.8	5.85	4.39	5.8	4.10	4.75	4.00	38.6	766.6
BHGM-11	63.5	103.5	41.7	4.1	30.2	4.30	4.53	5.4	3.35	2.45	3.60	50.6	475.9
BHGM-12	59.5	110.5	39.2	3.4	25.0	4.10	4.26	5.2	2.65	1.50	3.50	47.3	512.9
BHGM-13	60.0	115.5	69.6	2.8	26.3	3.75	4.32	4.8	2.40	3.65	3.85	32.5	562.9
BHGM-14	66.0	95.5	44.7	2.7	29.7	4.50	4.07	4.6	2.80	3.35	3.25	36.1	540.7
BHGM-15	49.0	91.5	53.8	3.5	37.3	4.30	4.77	5.5	2.80	1.50	3.55	48.8	1127.8
BHGM-16	49.5	93.0	50.0	4.0	44.9	6.25	4.52	5.2	4.50	2.50	3.30	51.7	1109.2

BHGM-17	44.0	96.5	50.6	3.7	26.7	4.50	4.37	4.9	2.75	2.10	3.65	41.7	879.6
BHGM-18	43.0	92.5	45.2	3.0	21.8	4.45	4.32	5.0	3.15	4.00	3.55	36.6	1023.1
BHGM-19	55.5	99.5	55.0	3.9	36.4	5.90	4.56	4.7	2.95	3.60	4.00	31.9	746.3
BHGM-20	64.5	101.5	54.7	3.0	21.1	3.10	4.56	5.2	2.25	3.20	3.85	39.9	662.9
BHGM-21	65.5	102.5	61.9	3.3	23.9	3.45	4.37	5.3	2.55	2.40	3.35	43.6	777.7
BHGM-22	63.0	101.5	50.0	2.2	17.6	2.60	4.47	5.1	2.00	2.35	3.50	43.2	562.9
BHGM-23	66.5	104.5	63.7	2.3	27.5	4.30	4.44	5.5	2.8	4.15	3.60	33.2	831.4
BHGM-24	61.5	119.5	53.6	2.1	20.9	3.10	4.62	5.9	2.65	3.65	3.95	41.1	738.9
BHGM-26	45.0	99.5	56.4	3.9	68.0	8.10	4.45	4.8	2.65	3.20	3.50	45.1	1410.2
BHGM-27	59.0	99.5	52.4	3.6	44.4	6.20	4.65	5.6	4.40	4.15	3.45	42.4	670.3
BHGM-28	67.0	98.5	30.9	2.5	23.3	3.50	4.61	5.5	2.45	1.80	3.20	47.3	351.8
BHGM-29	46.5	92.5	53.4	3.8	36.5	4.50	4.40	4.8	2.85	1.85	3.15	44.6	1422.2
BHGM-30	61.5	116.0	55.3	2.7	29.8	4.90	4.51	5.0	3.10	2.30	4.05	42.9	603.7
Kavalgi local	52.0	112.0	65.1	2.5	29.4	4.70	4.88	5.3	3.15	4.25	4.20	36.7	429.6
Bailhongal local	62.0	119.0	59.3	2.5	33.4	5.60	4.78	5.3	3.4	8.15	4.10	24.8	1292.6
Mean	56.59	108.80	59.38	3.01	32.09	5.15	4.64	5.13	3.38	4.47	3.85	37.08	924.32
C.V.	4.44	0.83	19.22	23.65	22.28	24.67	7.09	11.74	23.67	23.72	6.41	18.68	24.06
F ratio	21.84	216.79	1.62	1.64	3.75	3.34	0.95	1.20	2.49	2.49	2.10	2.67	3.19
F Prob.	0.00	0.00	0.0059	0.0049	0.00	0.00	0.60	0.16	0.00	0.00	0.00	0.00	0.00
S.E.	1.77	0.64	8.07	0.503	5.05	0.89	0.23	0.42	0.56	0.56	0.17	4.89	157.28
C.D. 5%	4.98	1.79	22.62	1.41	14.17	2.51	-	-	1.58	1.58	0.49	13.72	440.82
C.D. 1%	6.59	2.38	29.2	1.86	18.74	3.33	-	-	2.09	2.09	0.64	18.15	583.06

Appendix III. Qualitative characters observed in horse gram germplasm lines

Entry name	Stem colour	Seed colour	Seed lustre	Seed size
GPM-6	1	2	1	1
BJPL-1	2	2	1	2
GPM-23	2	1	1	2
CRHG-9	1	2	1	2
DS22	1	2	1	2
IC100938	1	2	1	2
DEH-1	2	2	1	2
PHG-9	2	2	1	2
VJPL-2	1	2	1	2
IC100935	1	2	1	1
KBHG-1	1	2	1	2
AK-42	1	2	1	2
GPM-30	2	2	1	2
BLHG-1	2	2	1	2
BGM1183	2	3	1	2
AK-21	1	2	1	2
CRHG-4	1	5	1	2
CRHG-6	1	1	1	2
CRHG-8	1	1	1	2
CRHG 19R	1	3	1	2
CRIDA 18R	1	1	1	2
GPM-11	2	1	1	2
GPM-23	1	2	1	2
RS28-607	1	2	1	2
GPM-422	1	3	1	2
GPM-62	1	4	1	2
GPM-13	2	1	1	2
GPM-51	1	2	1	1
AK-44	1	2	1	1
AK-22	1	2	1	1
GPM-18	2	2	1	2
GPM-25	1	2	1	1
GPM-44	1	2	1	2
BHG-1	1	2	1	2
GPM-63	1	2	1	2
GPM-03	2	2	1	2
GPM-4.4-113	1	2	1	2
GPM-37	2	2	1	2

GPM-49	2	3	1	1
VLG-19	2	2	1	2
GPM-4-61-4-1	1	2	1	2
GPM-36	1	2	1	2
DHG-04	1	1	1	2
PHG-12	1	2	1	2
GPM-28	1	3	1	3
LONE-1	1	1	1	2
GHI-641	1	2	1	2
GPM-171	1	2	1	2
GPM-46	1	3	1	2
PHG-02	1	2	1	2
PHG-21	1	2	1	2
CRHG-07	1	2	1	1
PS-2-4	1	2	1	3
GPM-58	2	2	1	2
GPM-48	1	2	1	2
GPM-44-2	2	2	1	2
GPM-12-B	2	2	1	2
SHG-317	1	2	1	1
VLG-08	1	2	1	2
GPM-65	1	2	1	2
GPM-66	1	2	1	2
8B	1	2	1	1
GPM-92	2	2	1	2
14GH 5R	2	2	1	2
12B	1	2	1	2
GPM-59	2	1	1	2
GPM-79	2	2	1	2
GPM-32	1	2	1	2
CRHG-05	1	2	1	2
GPM-22	1	1	1	2
BHL-78	2	2	1	2
BHL-44	2	2	1	2
BHL-15	2	2	1	2
BHL-60	2	2	1	2
BHL-20	2	1	1	1
BHL-154	2	1	1	1
BHL-48	2	2	1	2
BHL-26	2	2	1	1
BHL-66	2	2	1	1
BHL-128	2	1	1	2

BHGM-1	1	1	1	3
BHGM-2	1	1	1	2
BHGM-3	1	1	1	2
BHGM-4	1	1	1	2
BHGM-5	1	1	1	2
BHGM-6	1	1	1	3
BHGM-7	2	1	1	2
BHGM-8	2	1	1	3
BHGM-9	2	2	1	3
BHGM-10	2	2	1	2
BHGM-11	2	1	1	3
BHGM-12	2	2	1	2
BHGM-13	1	2	1	2
BHGM-14	1	1	1	2
BHGM-15	1	1	1	2
BHGM-16	1	1	1	2
BHGM-17	1	1	1	2
BHGM-18	1	1	1	2
BHGM-19	1	2	1	2
BHGM-20	1	1	1	2
BHGM-21	1	1	1	2
BHGM-22	1	1	1	2
BHGM-23	1	2	1	2
BHGM-24	1	1	1	1
BHGM-26	1	1	1	3
BHGM-27	1	1	1	2
BHGM-28	1	1	1	3
BHGM-29	1	1	1	2
BHGM-30	1	1	1	1
Kavalgi local	2	1	1	2
Bailhongal local	2	2	1	2

Stem colour: Red-1, Green-2, Seed colour: Cream-1, Brown-2, Dark brown-3, Light Black-4, Black-5, Seed size: Bold-1, Medium-2, small-3., Seed Luster: Luster-1, Nonluster-2

ASSESSMENT OF GENETIC DIVERSITY AND VARIABILITY FOR PRODUCTIVITY AND QUALITY TRAITS IN HORSE GRAM [*Macrotyloma uniflorum* (Lam.) Verdc].

POORNIMA B. S.

2015

Dr. G. M. SAJJANAR

Major advisor

ABSTRACT

Horse gram being highly drought tolerant crop and having nutritionally rich grains, plays major role in climate change resilient agriculture and forms potential food source for future. However, work on genetic improvement is meagre and it needs to be strengthened. Therefore, present investigation was carried out to assess the genetic variability, genetic diversity and associations among 111 horse gram germplasm lines for various qualitative and quantitative traits, and to study varietal differences for plant nitrogen content, and grain nutrients content (protein, calcium, iron and zinc) among 21 genotypes.

Based on D^2 values, the genotypes were grouped into 16 clusters. Cluster II was the largest comprising of 51 genotypes, followed by cluster I (21 genotypes), Cluster III (19 genotypes) and cluster XII (8 genotypes). The remaining 12 clusters were solitary. Inter cluster distances ranged from 3.77 to 24.89. Highest inter cluster distance was obtained between cluster III and IX. Among the traits, days to maturity contributed highest (71.20 %) towards the genetic divergence. The genotypes of solitary clusters which secured overall high ranking across thirteen characters were GPM 65, GPM-03, 12B, BHGM-26 and BHL-15.

Genetic variability studies revealed high GCV and PCV estimates observed for number of pods per plant, high heritability and genetic advance for days to 50% flowering and days to maturity. Correlation analysis revealed positive and highly significant association of seed yield with pod weight per plant, 100 seed weight and pod length, and highly significant negative association with days to 50% flowering.

Nutritional quality analysis revealed the range of values for grain micronutrients viz., calcium (38.43-104.812 mg/100g), iron (0.39-7.083mg/100g), zinc (0.966-5.467 mg/100g), and grain protein (17.21 to 25.63%) and plant nitrogen (0.69 to 1.33%) contents.