# VARIABILITY IN HORSEGRAM
## (*Macrotyloma uniflorum (Lam.) Verdc.*)
## UNDER OPEN AND PARTIALLY SHADED CONDITIONS

*by*

**SWATHY SIVAN**
**(2017 -11- 033)**

**THESIS**

**Submitted in partial fulfilment of the**

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**COLLEGE OF AGRICULTURE**
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## DECLARATION

I, hereby declare that this thesis entitled **"VARIABILITY IN HORSEGRAM (*Macrotyloma uniflorum (Lam.) Verdc.*) UNDER OPEN AND PARTIALLY SHADED CONDITIONS"** is a bonafide record of research work done by me during the course of research and the thesis has not previously formed the basis for the award to me of any degree, diploma, associateship, fellowship or other similar title, of any other University or Society.

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## CERTIFICATE

Certified that this thesis entitled **"VARIABILITY IN HORSEGRAM (*Macrotyloma uniflorum (Lam.) Verdc.*) UNDER OPEN AND PARTIALLY SHADED CONDITIONS"** is a record of research work done independently by Ms. Swathy Sivan (2017-11-033) under my guidance and supervision and that it has not previously formed the basis for the award of any degree, diploma, fellowship or associateship to him.

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***Swathy Sivan***

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## LIST OF ABBREVIATIONS AND SYMBOLS USED

| | |
|---|---|
| % | Per cent |
| CD | Critical Difference |
| C.V | Coefficient of variation |
| cm | Centimetre |
| mg | Milligram |
| RBD | Randomised Block Design |
| Cluster$^{-1}$ | Per cluster |
| DAS | Days After Sowing |
| *et al.* | And others |
| Fig. | Figure |
| g | Gram |
| g$^{-1}$ | Per gram |
| Kg | Kilo gram |
| KAU | Kerala Agricultural University |
| kg ha$^{-1}$ | Kilogram per hectare |
| kg plot$^{-1}$ | Kilogram per plot |
| Plant$^{-1}$ | Per plant |
| Plot$^{-1}$ | Per plot |
| Pod$^{-1}$ | Per pod |
| *Via* | Through |
| Mm | Millimetre |

| | |
|---|---|
| No. | Number |
| CGR | Crop Growth Rate |
| cv | Cultivar |
| Sl. | Serial |
| sp. or spp. | Species (Singular and Plural) |
| LAI | Leaf Area Index |
| *viz.* | Namely |
| *i.e* | that is |
| d.f | Degrees of freedom |
| S. E | Standard Error |
| mg $g^{-1}$ | Milligram per gram |

# *Introduction*

# 1. INTRODUCTION

Pulses have been used as an ideal source of dietary protein since the beginning of civilization. They constitute the second most important food group in the world after cereals and are vital ingredients for a balanced human diet. Over the last few decades, our pulse production has been largely limited and restricted to a handful of conventional grain legumes. This has forced many species of protein rich pulse crops, which are treasure- troves of vital nutrients along with proteins to be neglected. These under-utilized pulses with their unparalleled potentials, are now being recognized as crucial in eradicating malnutrition, maintaining food and nutritional security and generating income for the rural poor.

Horsegram [*Macrotyloma uniflorum* (Lam.) Verdc.], belonging to the family Fabaceae, is an under-exploited hardy pulse crop of the semi-arid tropics and is one of the most protein-rich lentils cultivated. It is considered as an important pulse crop since the beginning of agriculture in many parts of South Asia, particularly the peninsular India, from where it is said to have originated. The crop is often referred to as poor mans' pulse and recently, the US National Academy of Sciences has identified this pulse crop as a potential source of food for the future generations owing to its exceptional nutritional profile, drought-resistance and general hardiness.

As an edible crop, horsegram is an excellent source of protein, carbohydrates, dietary fibre and micronutrients, especially iron, calcium, potassium and molybdenum. In fact, it is said to have the highest calcium content among pulses. Horsegram has a very high calorific value, almost no fat and a very low sodium and lipid content. As it can provide energy for longer periods, it is usually fed to race horses. Apart from being a nutrient dense pulse, horsegram is also endowed with miraculous therapeutic properties. According to Ayurveda, horsegram is regarded as one of the *Swedopaga* drugs and its therapeutical utility has been described extensively in Charaka Samhita. It is traditionally used to cure kidney stones, bronchitis, asthma, urinary discharges, leucoderma, piles and heart

diseases. Studies have also proved that raw horsegram seeds have the ability to reduce blood sugar level by slowing down carbohydrate metabolism and reducing insulin resistance.

Horsegram is also grown as a green manure because of its high potential for immobilization of atmospheric nitrogen. Being a drought hardy crop, horsegram not only improves the soil quality but also prevents soil erosion to a great extent.

In Kerala, horsegram is quite popular as a miracle pulse crop among the poor and marginal farmers since earlier days. It is traditionally grown in paddy fields and terraced uplands during rabi season and the cultivation is mostly restricted to the northern districts. Largely mistaken as a minor pulse due to the entrenched biases surrounding it, horsegram has received far less research compared to many other conventional pulse crops. Although its cultivation practices are relatively easy, not much work has been done in improving its genetic potential. Limited crop improvement programmes and lack of systematic breeding has also prevented horsegram from being established as a major pulse crop in our state.

Germplasm serves as an indicator for the genetic wealth of a country as it holds the major share of favorable genes in it. The knowledge regarding the existing variability in the genetic stock is an essential pre-requisite for initiating any crop improvement programme. Estimates of various genetic parameters would help in the better understanding of the nature and extent of variability in a population and would thus be useful in deciding appropriate selection techniques. Yield, being a complex trait, is generally governed by a number of polygenes which exhibits low heritability and hence direct selection offers very limited scope. As a result, the efficiency of selection can be improved only by determining the association existing between yield and other plant characters, which would serve as simple guides for spotting out high yielders.

Rapid urbanization and limited land resources pose a significant threat for the popularization of horsegram as a pure crop in our state. Since our farming

system is primarily homestead based, evolving varieties which are suitable as intercrops will be a great boon to the farming community. Hence, in the present scenario, it is worthwhile to study the performance of horsegram both under open and partially shaded conditions in coconut gardens.

Based on these facts, the present study has been undertaken with the following objectives:

- To assess the variability present in different accessions of horsegram collected from diverse regions.
- To evaluate the performance of the accessions under open and partially shaded conditions
- To identify the best accession in terms of yield and protein content.

# *Review of Literature*

# 1. REVIEW OF LITERATURE

## 2.1. ORIGIN AND DISTRIBUTION

The horsegram is believed to be a native of old world tropics and the genus *Macrotyloma* contains around 25 species which is indigenous to Asia and Africa. It is one among the most ubiquitous archeological pulse finds, which implies its widespread importance since the Neolithic age. Although Vavilov (1951) has identified India as the primary centre of origin of horsegram, there is considerable evidence to suggest that Africa could also be its primary centre of origin, owing to the vast diversity of species reported from there. However, knowledge regarding the regional origin of this crop is still obscure as very limited studies has been conducted in their wild progenitors from South Asia (Fuller, 2002). Now-a-days, horsegram is widely cultivated as a low grade pulse in many South-East Asian countries like India, Bangladesh, Myanmar, Bhutan and Sri Lanka. In tropical countries like Australia and Africa, it is grown as a forage and green manure crop (Chahota, 2009). This crop is particularly popular in the Indian peninsula, mostly in the states of Karnataka, Tamil Nadu and Andhra Pradesh, which accounts for nearly 90% of the total Indian acreage under this crop (Sundararaj and Thulasidas,1993). Some wild relatives of horsegram also have been reported from countries like Australia, Papua New Guinea, Africa and India.

## 2.2. TAXONOMY

Horsegram belongs to the subfamily Faboideae under the family Fabaceae. According to Linnaeus classification (1753), initially horsegram was scientifically known as *Dolichos biflorus* in archaeo-botanical literature and Indian floristics (Saraswat,1992). However, detailed studies on the species by Verdcourt (1971) showed that it does not belong to the genus *Dolichos* and it was reassigned under a distinct genus – *Macrotyloma* and named it *Macrotyloma uniflorum.* The genus *Macrotyloma* could be easily distinguished from the genus *Dolichos* through their unique style,

standard and their peculiar pollen characteristics. Thus horsegram is now included in a genus which contain three economic plants: *M. uniflorum, M. axillare* (E.Mey.) Verdc. (a fodder crop), and *M. geocarpum* (Harms) Maréchal & Baudet, the African ground bean. Macrotyloma comprises of 25 species out of which four varieties have been distinguished so far -

*Macrotyloma uniflorum* (Lam.) Verdc.var. benadirianum (Chiov.) Verdc.

*Macrotyloma uniflorum* (Lam.) Verdc.var. stenocarpum (Brenan) Verdc.

*Macrotyloma uniflorum* (Lam.) Verdc.var. uniflorum

*Macrotyloma uniflorum* (Lam.) Verdc.var.verrucosum Verdc.

## 2.3. BOTANY

Botanically, horsegram is a slender, twining annual herb, growing to a height of about 30–60 cm (Sundararaj and Thulasidas,1993). The plant is profusely branched at the base and the branches intervene among themselves or with the companion crop plants. Leaves are ovate, rounded at the base, 3.5-7.5cm long, trifoliate, with membranous leaflets and the stipules are usually minute and oblong. Flowers are generally yellow or greenish yellow in color with a violet blot on the standard and are borne singly in leaf axils (Sharma, 1995). The flower bracts are lanceolate-linear with one placed at the base of each pedicel and two laterally at the base of each flower (Venkidasamy *et al.* 2019). The flower is papilionaceous, complete, bisexual, zygomorphic, pentamerous, pedicellate and hypogynous. The calyx is companulate and gamosepalous, while the corolla is polypetalous with descendingly imbricate aestivation. Stamens are usually diadelphous (9+1), with alternate short and long filaments. Carpels are unilocular, having four to six ovules on marginal placentation, with curved terminal style and hairy. The fruits are linear, oblong pods with a length of 3-8 cm and are often pubescent, tipped with a persistent style. Pods are dehiscent with 5-10 small flattened seeds which may appear light red, brown, grey or black in

colour (Venkidasamy *et al.* 2019). The envelope of the seed is usually hard with a small discreet hilum (Kirtikar and Basu, 2003).

Horsegram is a short day plant; however, some lines show day neutral properties as well and matures in 120 - 180 days after planting (Prasad and Singh, 2015). The plant is self-fertile with cleistogamous flowers and exhibits diploid chromosome numbers of 2n = 20, 22, 24 (Neelam *et al.* 2014). The chromosomal evolution in horsegram is believed to have progressed in two different directions, with one group having twenty small chromosomes (*M. uniflorum, M. baumani* and *M. axillare*) and the other group having twenty-two large chromosomes (*M. glabrescence, M. lignosus* and *M. argentinus*). The intermediate types usually have perennial tuberous roots and annual stems. However, knowledge regarding the species relationships are not thoroughly understood. The crop flourishes well in wide range of soils and is considered as native to the drier climatic regions of India (Fuller and Murphy, 2018). The seeds germinate reasonably well under drought conditions with very poor soils due to the presence of dehydrins, which appears to be the main stress-sensitive gene in various abiotic stresses.

## 2.4. VARIABILITY

Plant breeding in the true sense relates to the efficient management and utilization of the variability present in an existing population. The most important genetic parameter which provides an efficient estimation of variability is the coefficient of variation. Many studies have been conducted to analyze the extend of variability in pulse crops by working out the phenotypic and genotypic coefficient of variation. However, the extent of genetic variability is always more important than the total variation since, greater the genetic diversity, wider would be the scope for selection. Some of the studies are briefly reviewed below:

In horsegram, Aggarwal and Kang (1976) reported that the coefficient of genetic variation was the lowest (0.68) for days to maturity and the highest (33.82) for yield plant$^{-1}$.

Variability studies were conducted in forty-eight varieties of horsegram by Sreekantaradya *et al.* (1975) and it was reported that the highest phenotypic and genotypic variance was observed for plant height, pods plant$^{-1}$ and seeds pod$^{-1}$. These characters were also reported to exhibit high genotypic and phenotypic coefficient of variation. However, only moderate variance was shown by seed yield plant$^{-1}$.

According to Shivshankar *et al.* (1977), there exists significant difference among different horsegram accessions in terms of morphological and growth characters such as height of the plant, number of primary and secondary branches, days to 50% flowering, pods plant$^{-1}$, seed yield etc. Among the different characters assessed, higher genotypic coefficient of variation was exhibited by number of secondary branches (79.7), whereas it was moderate for number of pods plant$^{-1}$, primary branches, length of primary branches, 100-seed weight, days to 50% flowering, pods plant$^{-1}$ and seed yield. The lowest genotypic coefficient of variation was shown by plant height (8.66) and seeds pod$^{-1}$ (4.71).

A study on variability in horsegram by Ramakrishna *et al.* (1978) revealed that, out of the different characters studied, coefficient of genotypic variations was the lowest (6.14) for pod length and the highest (102.1) for plant height.

Generally, variability is mostly exhibited by those characters which are closely associated with post flowering period in horsegram (Ganeshaiah, 1980). Studies in hundred horsegram genotypes revealed significant variation among all the eighteen characters analyzed. The highest genotypic and phenotypic variability was shown by the number of secondary branches and high heritability estimates were found for number of days to maturity and to flowering.

In a study conducted by Suraiya *et al.* (1988) with 15 genotypes of horsegram, characters like plant height, number of pods plant$^{-1}$, days to 50% flowering and days to

maturity showed the highest genotypic and phenotypic variance, while the lowest values were given by 100-seed weight.

Studies by Balan *et al.* (1991) revealed high genotypic and phenotypic variances for number of pods followed by plant height and number of nodes. These characters were also reported to show high estimates of genotypic coefficient of variation.

Nine horsegram genotypes were assessed for eight agro-morphological characters by Rao and Chandrakar (1994) and reported that characters like plant height, number of pod bearing nodes plant$^{-1}$, number of seeds plant$^{-1}$ and seed yield plant$^{-1}$ exhibited highest genotypic and phenotypic variation.

Rao and Nanda (1994) reported that studies on eighteen different horsegram genotypes exhibited considerable variability for traits like plant height, number of days to maturity, number of pod bearing nodes plant$^{-1}$, number of pods plant$^{-1}$, seed yield and harvest index, with GCV values ranging from 1.37 to 16.29 and PCV values ranging from 5.79 to 32.81.

Evaluation of hundred and three genotypes of horsegram during kharif, rabi and summer seasons by Savithramma (1994) showed that in all the three seasons, the differences between GCV and PCV were narrow for characters such as days to flowering, pod yield, seeds pod$^{-1}$, 100-seed weight, threshing and protein percentage. This indicates the minimum influence of environment on the expression of these characters and hence their phenotypic values will be reliable for selection. However, moderate to high estimates of PCV and GCV were observed for days to maturity, plant height, number of primary branches, biomass plant$^{-1}$, seed yield, number of pods plant$^{-1}$, number of secondary branches, pod length and harvest index.

According to Sood *et al.* (1994), in horsegram, the magnitude of genotypic and phenotypic coefficients of variation were similar for some characters like days to flowering, days to maturity and 100-seed weight, which indicates little influence of the environment in the expression of these characters, while seed yield showed higher coefficients at both the levels.

Samal and Senapathi (1997) reported that, in horsegram, wide variation exists among various characters such as plant height, number of branches plant$^{-1}$, pods plant$^{-1}$, days to 50% flowering and yield plant$^{-1}$ whereas 100-seed weight showed minimum variance. Both genotypic and phenotypic coefficient of variation was found to be low for days to flowering, indicating less scope for its improvement through selection. Except for number of branches plant$^{-1}$, influence of the environment as indicated by the difference between PCV and GCV was very low for most of the traits studied.

Genetic variability studies in diverse horsegram genotypes by Nagaraja (1997) showed that number of days to flowering and number of days to maturity exhibited low estimates of PCV and GCV, while high values were recorded for number of primary branches.

Lad *et al.* (1999) reported that a wide range of variability exists for yield and yield related characters in horsegram. In almost all the characters studied, the phenotypic variance was found to be higher than the genotypic variance. All characters except number of branches plant$^{-1}$, pod length, grains pod$^{-1}$ and 100-seed weight showed a greater magnitude of genotypic variance.

According to Tripathi (1999), in horsegram, high genotypic and phenotypic coefficient of variation was observed for number of branches plant$^{-1}$, seeds pod$^{-1}$ and seed yield plant$^{-1}$ which indicates a high magnitude of variability for these traits.

Twenty-one horsegram genotypes were evaluated during the late kharif season by Nehru *et al.*, (2000), to determine the variability parameters for yield. It was observed that, grain yield and biomass yield plant$^{-1}$ showed high variability, whereas nodes on main stem, plant height, and nodes and pods on primary branches exhibited moderate variability. The least variability was observed for traits like number of primary branches, pod length and number of seeds pod$^{-1}$. Genotypic coefficient of variation (GCV) was highest for nodes on primary branches, followed by pods on primary branches and biomass yield plant$^{-1}$, while number of nodes on the main stem, pod length and number of primary branches showed lower GCV.

A total of thirty horsegram genotypes were evaluated for six different characters by Prakash and Khanure (2000). It was reported that seed yield plant$^{-1}$ exhibited highest (42.04) genotypic coefficient of variation while, the lowest value (1.73) was given by days to 50% flowering. Pods plant$^{-1}$ showed the least (0.24) differences between PCV and GCV, indicating very low environmental influence. On the other hand, yield plant$^{-1}$ exhibited high gap (3.20) between GCV and PCV, suggesting that this trait is highly influenced by the environment.

Genetic variability in twenty diverse genotypes of horse gram was studied by Venkateswarlu (2000). It was observed that the genotypes differed significantly for all the seven traits studied. The genotypic coefficient of variation was the highest for pods plant$^{-1}$ (39.2), whereas very low GCV estimates was observed for days to maturity.

Thirty-five horsegram genotypes were evaluated for their variability by Dogra (2004) and reported that crop growth rate and seed yield plant$^{-1}$ exhibited higher genotypic and phenotypic coefficients of variation, thereby proving that direct selection of these characters would be effective. It was observed that phenotypic coefficient of variation for harvest index and pods plant$^{-1}$ was high, whereas their genotypic coefficient of variation was moderate. As for the rest of characters, both phenotypic and genotypic coefficients were low.

Ram *et al.* (2005), conducted genetic studies on the variability parameters in horsegram under two environmental conditions using eighteen genotypes and concluded that the analysis of variance showed significant genotypic differences among the genotypes for all the nine traits studied. The GCV and PCV were higher for grain yield, branches plant$^{-1}$ and seeds pod$^{-1}$, moderate for 100-seedweight, pods plant$^{-1}$ and stand at maturity, while low for plant height, days to flowering and days to maturity under both the environments.

Variability studies in thirty-five diverse genotypes of horsegram by Kalia and Dogra (2007) revealed high genotypic and phenotypic coefficient of variation for crop growth rate and seed yield plant$^{-1}$. Pods plant$^{-1}$ and harvest index exhibited high

phenotypic coefficient of variation, whereas the genotypic coefficient of variation of these crops were found to be moderate.

In a study of eighty-eight horsegram genotypes conducted by Singhal *et al.* (2010), the phenotypic coefficient of variation was found to be higher than the genotypic coefficient of variation for all the traits except for days to 50% flowering.

Sahoo *et al.* (2010) evaluated a set of forty-eight horsegram genotypes for their variability and reported that high coefficient of variation both at genotypic and phenotypic levels were exhibited by number of pods cluster$^{-1}$, number of clusters plant$^{-1}$, number of pods plant$^{-1}$, pod yield plant$^{-1}$, biological yield plant$^{-1}$, number of branches plant$^{-1}$, seed yield plant$^{-1}$, biological yield per day and plant height.

Variation in quantitative and qualitative characters were evaluated in twenty-two genotypes of horsegram by Kulkarni and Mogle (2011) and concluded that out of the different characters studied, five economic characters viz. days to 50% flowering, plant height (cm), no. of pods plants$^{-1}$, 1000 seed wt. and biomass (g) exhibited high variance. Thousand seed weight showed a considerable variation ranging from 24.94g (C-II) to 34.10g (IC-341291), whereas characters like number of seeds pod$^{-1}$ and pod length showed less variation among the genotypes, ranging from 3.61 to 6.84 seeds pod$^{-1}$ and 3.86 to 5.36 cm pod length respectively.

Durga (2012) revealed that, in a study constituting twenty-three cultivars of horsegram, PCV was found to be marginally higher than their corresponding GCV for all the characters studied, reflecting the influence of the environment on all the traits and indicating that phenotype based selection will hold good for a genetic basis. Here, the highest GCV was observed for characters viz., pod hulm plant$^{-1}$ (42.26 g), followed by pods plant$^{-1}$ (34.44 g) and seed yield plant$^{-1}$ (34.10 g). on the other hand, GCV estimates were found to be lower for germination rate (1.21%), seedling vigour index I (4.41) and seedling length (4.03 cm), suggesting a narrow range of variability for these characters.

Experimental studies in twenty-six horsegram accessions for variation by Khulbe *et al.* (2013) revealed moderate to high range of variability in all characters

studied. High estimates for genotypic coefficient of variation was recorded for number of pods plant$^{-1}$ and yield plant$^{-1}$ while low values were given by days to maturity and seeds pod$^{-1}$.

According to Latha *et al.* (2013), except for hundred seed weight, all other characters showed marginally high levels of phenotypic coefficient of variation than their corresponding genotypic coefficient of variation, suggesting the limited influence of the environment over these characters. High estimates of GCV and PCV were recorded for plumule length, radicle length and vigour index. Both seed length and thickness exhibited low values for both GCV and PCV which indicates narrow range of variability.

A study by Varma *et al.* (2013) in twenty-three horsegram genotypes revealed that maximum difference between phenotypic and genotypic coefficient of variation was noticed for number of primary branches per plant while the minimum was noticed for test weight. Pods plant$^{-1}$ exhibited the highest GCV (20.96) followed by seed yield plant$^{-1}$ (17.22), whereas low GCV estimates were recorded for primary branches plant$^{-1}$ (3.91) and pod length (3.79).

Thirty-eight accessions of horsegram were evaluated by Sunil *et al.* (2014) and reported that all the accessions had high trailing habit and determinate growth but exhibited broad variation in vigour, pod stem colour, seed colour and flower colour. Plant height, number of clusters plant$^{-1}$, number of primary branches and number of seeds pod$^{-1}$ were also found to exhibit significant variation.

Poornima (2015) reported that number of pods plant$^{-1}$ exhibited the highest values for phenotypic and genotypic coefficient of variation, while moderate estimates were given by plant height, number of primary branches plant$^{-1}$ and number of seeds pod$^{-1}$. Days to maturity and pod length recorded the least estimates for genotypic and phenotypic coefficients of variation.

Studies regarding variances for seven characters in thirty-four diverse horsegram genotypes were done by Vijayakumar *et al.* (2016), revealed significant differences among all the genotypes for all the characters under the study, while

differences between replications were insignificant. Among the characters studied, seed yield (31.18 and 25.19) recorded higher PCV and GCV values, while moderate values were noted for plant height (16.85 and 11.35). Low PCV and GCV values were obtained for days to 50% flowering (5.14 and 5.13).

The extent of genetic variability between twelve quantitative traits in two hundred and fifty-two horsegram genotypes was assessed by Priyanka *et al.* (2019). The highest genotypic and phenotypic coefficient of variation was recorded for characters like single plant yield (48.881% and 49.371%), followed by number of pods plant$^{-1}$ (45.370% and 45.657%). GCV and PCV were found to be lowest for days to maturity (2.913% and 2.996%) followed by days to 50% flowering (5.299% and 5.374%). Moderate values for GCV and PCV were scored by pod length, pod width, number of seeds pod$^{-1}$ and hundred seed weight. In most of the traits studied, PCV was found to be slightly higher than GCV indicating the importance of greater genetic variability with less environmental influence.

## 2.5. HERITABILITY AND GENETIC ADVANCE

In any breeding programme, heritability ($h^2$) acts as a predictive measure for designing the selection procedure. It provides information regarding the heritable portion of the observed effects. Johnson *et al.*, (1955) classified heritability into low (below 30%), medium (30% - 60%) and high (above 60%). Those characters exhibiting high heritability along with high genetic advance are most likely controlled by additive gene action (Panse, 1957). Hence heritability estimates coupled with genetic gains are more important in crop improvement than heritability alone.

High heritability coupled with high genetic advance was reported for number of seeds pod$^{-1}$ and pods plant$^{-1}$ by Sreekantaradya *et al.* (1975). However, seed yield exhibited moderate heritability and genetic advance.

According to Aggarwal and Kang (1976), low values of heritability associated with genetic advance was observed for plant height and high estimates for heritability

and genetic advance for number of branches plant$^{-1}$, pods plan$^{-1}$t and seed yield. High heritability and moderate genetic advance was reported for days to maturity.

Low values for heritability associated with low genetic advance were reported for plant height, pods plant$^{-1}$, seeds pod$^{-1}$, days to maturity and seed yield by Shivashankar *et al.* (1977). While moderate heritability was observed for 100-seed weight, number of branches per plant exhibited high heritability and genetic advances.

According to Ganeshaiah (1980), plant height and number of branches plant$^{-1}$ showed high heritability coupled with high genetic advance, whereas pods nod$^{-1}$ gave the lowest values.

Moderate values for heritability and genetic advance were reported for pod bearing nodes by Kallesh (1981) in horsegram. The study concluded that pods plant$^{-1}$ and seeds pod$^{-1}$ exhibited high levels of heritability and genetic advance, while high heritability with moderate genetic advance was observed for days to maturity.

Studies in twenty-one varieties of horsegram by Birari *et al.* (1987) revealed that characters like yield hectare$^{-1}$, pod maturity, number of days to first flowering and 100-seed weight exhibited higher heritability values compared to number of pods plant$^{-1}$ and number of seeds pod$^{-1}$. Highest genetic advance was observed for yield hectare$^{-1}$ followed by number of seeds pod$^{-1}$.

Singh (1990) reported high estimates of heritability for days to 50% flowering and 100-seed weight and lower heritability for plant height, number of branches plant$^{-1}$ and number of pods plant$^{-1}$.

High heritability coupled with high genetic advance was reported for number of pods, number of nodes, weight of pods, seed yield and plant height by Balan *et al.* (1991).

According to Mathew (1991), high values for heritability were recorded for 100-seed weight, days to flowering and days to maturity. Moderate heritability was observed for pod length, plant height, number of branches, number of pods plant$^{-1}$ and number of seeds pod$^{-1}$. Seed yield plant$^{-1}$ and harvest index showed low levels of heritability.

Dobhal and Rana (1994) reported that high heritability was observed for characters like number of clusters plant$^{-1}$, number of pods plant$^{-1}$ and seed yield per plot.

Results of studies conducted by Rao and Chandrakar (1994) in nine horsegram genotypes revealed that the character days to maturity exhibited high heritability and high genetic advance, while seed yield showed low heritability with high genetic advance.

According to Rao and Nanda (1994), heritability estimates were low for all the seven yield related components studied in eighteen horsegram genotypes and the genetic advance ranged from 0.56 to 16.66 and it was found to be the highest for seed yield followed by number of pods plant$^{-1}$.

One hundred and three genotypes of horsegram were studied for seventeen quantitative characters by Savithramma (1994) and it was revealed that broad sense heritability and genetic gain were found to be high for days to 50% flowering in kharif season, but low in other environments. Moderate estimates of heritability and genetic advance were observed for number of primary branches plant$^{-1}$ and number of seeds pod$^{-1}$. Low heritability coupled with medium to high genetic advance were noticed for traits like number of secondary branches plant$^{-1}$, plant biomass, harvest index and pod yield plant$^{-1}$. Characters such as pods plant$^{-1}$, seed yield plant$^{-1}$ and per day productivity exhibited low to medium heritability with low to high genetic advance, while low heritability combined with low genetic advance was exhibited by threshing percentage.

Heritability studies conducted by Sood *et al.* (1994) in diverse horsegram genotypes revealed that the highest heritability percentage was shown by days to 75 percent flowering (94%), followed by days to 75 percent maturity (76%), 100-seed weight (73.8%) and seed yield (73.6%). The genetic advance was found to be high for seed yield (233.67), moderate for days to 75% flowering and days to 75% maturity and very low for 100-seed weight (0.43).

In horsegram, it was reported by Senapati *et al.* (1998) that seed yield plant$^{-1}$ exhibited the highest level of heritability, followed by leaf width, leaf length, pods per

plant, 100-seed weight, number of seeds pod$^{-1}$ and number of pods plant$^{-1}$. On the other hand, plant height, number of primary branches plant$^{-1}$ and seedling length showed the lowest heritability estimates.

In another study by Tripathi (1999), high heritability estimates were recorded for days to 50 per cent flowering, days to maturity, pods plant$^{-1}$, seed yield plant$^{-1}$, harvest index and 100-seed weight, while characters like plant height, number of branches plant$^{-1}$ and seeds pod$^{-1}$ showed moderate heritability.

Variability parameters for yield were determined by Nehru *et al.*, (2000) using twenty-one genotypes of horsegram during the late kharif season. The study showed that high genetic advance was exhibited by characters like nodes on primary branches, pods on primary branches and biomass yield plant$^{-1}$; moderate genetic advance by grain yield plant$^{-1}$; and low genetic advance by pod length, number of primary branches, seeds pod$^{-1}$, nodes on main stem and pods on main stem.

An association of high heritability with high genetic gain was observed for number of pods plant$^{-1}$, suggesting additive gene effects and consequently a high genetic gain for phenotypic selection by Prakash and Khanure (2000). However, characters like 100-seed weight and yield plant$^{-1}$ shows high heritability coupled with low genetic gain, indicating the presence of non-additive gene action.

Venkateswarlu (2000) studied the genetic variability in twenty different genotypes of horse gram and reported that the highest heritability estimate of 97.8 was exhibited by days to 50% flowering, followed by clusters plant$^{-1}$, pods plant$^{-1}$ and seed yield plot$^{-1}$. Hence selection for these characters is most likely to be effective while selection for branches plant$^{-1}$ is bound to be ineffective as it is the least heritable trait. Two characters namely, pods plant$^{-1}$ and clusters plant$^{-1}$ showed high heritability coupled with high genetic advance, which indicates the preponderance of additive gene effects for these traits.

High heritability combined with high genetic gain was reported for leaf area index and crop growth rate by Dogra (2004). The study concluded that high heritability values observed for leaf area index, leaf area, days to maturity and crop growth

indicates that selection for these characters on the basis of phenotype could be relied upon.

According to Ram *et al.* (2005), characters such as grain yield, branches plant$^{-1}$, seeds pod$^{-1}$, 100-seed weight and pods plant$^{-1}$ exhibited high heritability, coupled with high genetic advance which suggests that these characters are controlled by additive gene action and hence their improvement through simple selection is possible. Plant height showed high heritability and moderate genetic advance, while days to flowering and stand at maturity had moderate heritability and moderate genetic advance under both environmental conditions, suggesting that these traits are controlled by non-additive gene action and hence their selection is possible through indirect selection methods.

High heritability coupled with high genetic advance was reported for leaf area index and crop growth rate by Kalia and Dogra (2007) based on their studies of thirty-five horsegram genotypes.

Raina *et al.* (2007) evaluated thirty-two diverse genotypes of horsegram and revealed that high heritability coupled with high genetic advance was noticed in plant height, leaf area, internode length, pods plant$^{-1}$ and 100-seed weight. On the other hand, economic traits such as seed yield plant$^{-1}$ and biological yield plant$^{-1}$ exhibited moderate heritability and genetic advance.

Sahoo *et al.* (2010) conducted heritability studies in a set of forty-eight horsegram genotypes and concluded that except for seed pod$^{-1}$, 100-seed weight, harvest index, shelling percent and pod length, all other characters showed high heritability in broad sense. However, high heritability with high genetic advance was observed for number of pods cluster$^{-1}$, number of cluster plant$^{-1}$, number of branches plant $^{-1}$, pod yield, seed yield and biological yield.

According to Durga (2012), high heritability was exhibited by seed yield plant $^{-1}$ (98.2%) followed by the pod hulm plant $^{-1}$ (97.7%) and leaf width (91.3%). Some other characters which were noticed for high heritability includes leaf length (88.1%), test weight (85.4%), the number of seeds pod$^{-1}$ (79.2%) and the number of

pods plant$^{-1}$ (71.3%), respectively. However, characters like the number of primary branches plant$^{-1}$ (12.5%), plant height (19.1%) and seedling length (20.4%) showed lowest heritability, which proves that selection would be ineffective for these characters. High heritability coupled with high genetic advance were reported for seed yield plant$^{-1}$ and pod hulm plant$^{-1}$ while, leaf width and length recorded high heritability coupled with moderate genetic advance.

Heritability studies by Khulbe *et al.* (2013) revealed that high level of broad sense heritability was exhibited by days to 50% flowering (73%) followed by plant height (64%) and yield plant$^{-1}$ (60%) and low level of heritability was given by number of seeds plant$^{-1}$ (14%). High genetic advance was reported for pods plant$^{-1}$ (19.32) and low for seeds pod$^{-1}$ (0.14).

Latha *et al.* (2013) reported high heritability coupled with high genetic advance for characters like seed volume, 100-seed weight, germination percentage, plumule length, radicle length, vigour index, yield plant$^{-1}$, number of pods plant$^{-1}$ and number of seeds pod$^{-1}$. Low genetic gain and moderate heritability was reported for seed length and seed thickness.

According to Varma *et al.* (2013), high heritability (64.2) coupled with high GCV (17.22) and high genetic advance as percent mean (28.54) was observed for seed yield plant$^{-1}$. However, the highest heritability estimates were recorded for test weight (80) followed by seedling vigour index I (78.6), leaf width (77.8) and seedling length (75.3).

In a study by Vijayakumar *et al.* (2016), days to 50% flowering showed high heritability along with moderate genetic advance in horsegram, while, seed yield ha$^{-1}$ exhibited high heritability coupled with high genetic advance.

Priyanka *et al.* (2019) studied the extend of heritability and genetic advance in two hundred and fifty-two germplasm assessions of horsegram and concluded that out of the twelve quantitative characters studied, high genetic advance as percent of mean (GAM) coupled with high heritability was observed for all the traits except days to

maturity and days to 50% flowering indicating the preponderance of additive gene action in the expression of these traits. Low GAM with high heritability was exhibited by days to maturity which underlines the importance of non-additive effects of the genes and the high heritability results due to favorable environmental conditions.

## 2.6. CORRELATION STUDIES

The correlation coefficient measures the strength of association between two characters and the direction of their relationship. In plant breeding, correlation analysis is highly significant, as it reveals the relative importance of different plant traits, which can be of great value in any crop improvement programme and later form the basis for selection. Moreover, during the selection of several characters at the same time, the knowledge regarding association of characters is highly useful to avoid undesirable correlated changes in other characters.

In a study comprising of forty-five genotypes of horse gram by Aggarwal and Kang (1976), it was observed that grain yield was positively correlated to characters like number of pods plant$^{-1}$, seed size, 100-grain weight, pod length, number of branches and plant height, whereas it is negatively correlated to days to flowering and days to maturity.

Shivashankar *et al.* (1977) reported a strong positive correlation of seed yield with seeds pod$^{-1}$ and nodes plant$^{-1}$, while number of days to flowering and days to maturity exhibited negative correlation with grain yield.

According to Kallesh (1981), there exists a highly positive correlation of yield with plant height, pods plant$^{-1}$ and seeds pod$^{-1}$. It was also reported that the number of fruiting nodes with pods plant$^{-1}$ and seeds plant$^{-1}$ showed significant and positive correlation.

A strong positive correlation of yield with number of days to first pod maturity, number of pods plant$^{-1}$ and number of seeds pod$^{-1}$ was reported by Birari *et al.* (1987).

It was also observed that 100-seed weight was negatively correlated with all other characters under study.

It was reported by Yarguntappa (1987) that seed yield plant$^{-1}$ exhibited a strong positive correlation with number of pods plant$^{-1}$, days to 50% flowering, days to maturity, seeds pod$^{-1}$, plant height and 100-seed weight both at genotypic and phenotypic levels. It was reported that days to 50% flowering was positively correlated to days to maturity, plant height, number of pods plant$^{-1}$ and seed yield plant$^{-1}$ at both levels and with seeds pod$^{-1}$ only at genotypic levels. He also noticed that plant height possessed positive and significant association with number of pods plant$^{-1}$, days to maturity, days to 50% flowering, seeds pod$^{-1}$ and seed yield at both levels. Number of seeds pod$^{-1}$ was correlated to pods plant$^{-1}$, seed yield, days to maturity and plant height whereas, 100-seed weight was positively correlated with days to maturity and seed yield.

A strong positive correlation of pod yield both at phenotypic and genotypic levels with pod number, pod width, pod length and seeds pod$^{-1}$ in horsegram was reported by Kabir and Sen (1989). As per the results, days to flowering and 100-seed weight exhibited positive significant correlation with pod yield plant$^{-1}$ at genotypic level. Phenotypic correlation coefficient of pod width with pod yield was higher than genotypic correlation, indicating the influence of the environment on the association of two characters at genetic level. It was also reported the existence of a positive correlation of yield with plant height, pods plant$^{-1}$ and seeds pod$^{-1}$ and also number of fruiting nodes with pods plant$^{-1}$ and seeds pod$^{-1}$.

Factor analysis on sixty-one diverse horsegram genotypes by Dabhos *et al.* (1990) revealed a positive correlation of seed yield and pod yield with each other and also with the pods on branches and plant$^{-1}$, the cluster on the main stem and seeds pod$^{-1}$.

According to Singh (1990) pod number plant$^{-1}$ was positively correlated to seed yield plant$^{-1}$, while there is a significant negative correlation between seed yield and number of days to flowering and maturity.

Mathew (1991) reported that seed yield plant$^{-1}$ exhibits significant positive correlation with number of branches, number of pods plant$^{-1}$, number of seeds pod$^{-1}$, pod length and harvest index. Low positive genotypic correlation was observed with 100-seed weight and days to flowering. Height of plant and days to maturity exhibited negative genotypic correlation with seed yield plant$^{-1}$.

On the basis of correlation studies in horsegram, Rao and Chandrakar (1994) reported that there exists a significant positive correlation of seed yield plant$^{-1}$ with plant height, days to flowering, days to maturity, number of primary branches plant$^{-1}$, number of pods plant$^{-1}$ and number of seeds pod$^{-1}$. They also reported that plant height, days to maturity, number of primary branches plant$^{-1}$ and number of pods plant$^{-1}$ were positively and significantly correlated to each other. Harvest index was found to be significantly but negatively correlated to days to maturity and plant height.

Rao and Nanda (1994) reported a negative correlation of seed yield with number of days to flowering. Among the eight traits under study, only harvest index exhibited positive correlation with seed yield.

Ten genotypes of horsegram were studied for their seed yield by Sood *et al.* (1994) and came to the conclusion that there exists a negative correlation between seed yield and days to 75% flowering and days to 75% maturity. It was also reported that the simultaneous selection for two characters *viz.* high seed yield and early maturity is possible.

According to Sahane *et al.* (1995), there was a linear increase in total number of leaves, leaf area and leaf area index from sowing to 75 days after sowing. It was reported that the number of leaves plant$^{-1}$ at 60 days after sowing was significantly correlated with the seed yield plant$^{-1}$.

Significant and positive association of seed yield with biomass, pods plant$^{-1}$ and pod yield was reported by Savithramma (1994) both at phenotypic and genotypic levels. A significant positive correlation of harvest index with seed yield and pods plant$^{-1}$ and per day productivity with pod yield and seed yield was observed.

According to Samal and Senapati (1997), yield plant$^{-1}$ is positively correlated to number of pods plant$^{-1}$, seeds pod$^{-1}$ and branches plant$^{-1}$, while Lad *et al.* (1999) reported a strong positive correlation of yield with pods plant$^{-1}$, pod length, grains pod$^{-1}$ and dry weight of pods plant$^{-1}$.

Nehru *et al.* (2000) conducted a study to determine the variability parameters for yield and correlation between yield and yield components using twenty-one *Macrotyloma uniflorum* genotypes during the late kharif season. The correlation studies of this experiment revealed that number of pods on main stem and 100-seed weight are the traits which can be considered while selecting for yield.

In a study by Prakash and Khanure (2000) using thirty horsegram genotypes, seed yield was found to be positively correlated with plant height (0.536), number of branches plant $^{-1}$ (0.508) and number of pods plant$^{-1}$ (0.903) at the genotypic level. However, at phenotypic level, number of branches plant$^{-1}$ showed positive but non-significant association with seed yield plant$^{-1}$.

Correlation analysis by Roopadevi *et al.* (2002) revealed that seed yield was significantly and positively correlated with growth characters like plant height, number of branches, number of leaves leaf area index and nodule number. The yield components such as number of pods plant$^{-1}$, seeds pod$^{-1}$, pod length and 100-seed weight were also found to have a positive and significant correlation with seed yield.

Correlation studies in thirty-five horsegram genotypes by Dogra (2004) revealed that generally, genotypic correlation coefficients were higher in magnitude compared to the corresponding phenotypic correlation coefficients, which indicates the inherent association existing among the various traits. Seed yield plant$^{-1}$ was found to be significantly and positively associated with leaf area index, leaf area, pods plant$^{-1}$, seeds pod$^{-1}$ and biological yiled plant$^{-1}$. However, it was negatively correlated with days to 75 per cent flowering and days to 50 per cent flowering.

Sarkar *et al.* (2005) reported that the phenotypic correlation coefficients were lower than the corresponding genotypic correlation coefficients for the various

quantitative characters studied in horsegram. Days to 50% flowering and 100-seed weight were significantly and positively correlated to seed yield plant$^{-1}$.

According to Raina *et al.* (2007), economic yield in horsegram recorded a strong positive correlation with biological yield plant$^{-1}$, fruiting nodes plant$^{-1}$, height of the plant, leaf area, 100-seed weight and internodal length.

Correlation studies in thirty-five horsegram genotypes by Rama *et al.* (2007) showed that leaf area index at thirty-five days after sowing, leaf area at seventy days after sowing, leaf area index at seventy days after sowing, number of pods plant$^{-1}$, number of seeds pod$^{-1}$ and biological yield plant$^{-1}$ were significantly and positively correlated to seed yield plant$^{-1}$, both at phenotypic and genotypic levels.

Association of seed yield with other characters was studied by Prabha *et al.* (2010) and she concluded that plant height, pod length and number of seeds pod$^{-1}$ were positively correlated to seed yield and that they were very important for the genetic improvement in horsegram.

Latha *et al.* (2013) analyzed the relationship between the seed physical and physiological characters in horsegram genotypes. Significant positive correlation was observed between different characters such as length and breadth, breadth and volume, length and volume, thickness and volume, 100-seed weight and volume, 100-seed weight and germination percentage, germination percentage and vigour index, germination percentage and seedling vigour, plumule length and radicle length, and between radicle length and vigour index.

Significant positive correlation between seed yield plant$^{-1}$ and number of pods plant$^{-1}$ was reported by Sunil *et al.* (2014), on the basis of the studies in thirty-eight horsegram accessions during two post rainy seasons.

According to Poornima (2015) seed yield is positively and significantly associated with 100 seed weight, pod weight plant$^{-1}$ and pod length, while there is a significant negative association with days to 50% flowering.

Vijayakumar *et al.* (2016) reported that the correlation coefficients at genotypic level were generally higher than that at the corresponding phenotypic level. They

observed that the seed yield hectare$^{-1}$ was positively and significantly correlated with 100-seed weight at genotypic level. A strong positive significant association of plant height with days to 50% flowering was observed both at genotypic and phenotypic levels. Similarly, plant height also showed a positive significant correlation with number of seeds pod$^{-1}$ at both levels. A significant negative correlation was reported between 100-seed weight with days to 50% flowering and number of seeds pod$^{-1}$.

According to Priyanka *et al.* (2019), single plant yield exhibited significant positive correlation with plant height (rg = 0.3266, rP = 0.3154), number of clusters plant$^{-1}$ (rg = 0.6876, rP = 0.6793), number of pods cluster$^{-1}$ (rg = 0.7170, rP = 0.7060), number of pods plant$^{-1}$ (rg = 0.9412, rP = 0.9365), pod length (rg = 0.5659, rP = 0.5332) and number of seeds pod$^{-1}$ (rg = 0.4877, rP = 0.4755) at both genotypic and phenotypic level. However, pod width and hundred seed weight showed negative correlation with yield.

## 2.7. PATH COEFFICIENT ANALYSIS

On the basis of path coefficient analysis in forty-five genotypes of horsegram, Aggarwal and Kang (1976) suggested that the character pods plant$^{-1}$ could be used to select for higher yield, while it was reported by Ganeshaiah (1980) that pod weight and 100-seed weight can contribute more to yield than number of seeds pod$^{-1}$.

According to Kallesh (1981) number of fruiting nodes plant$^{-1}$ and pods plant$^{-1}$ were the major yield contributing characters and the indirect effect of all the other variables through these characters was found to be high and positive.

It was reported by Yarguntappa (1987) that the number of pods plant$^{-1}$ exerted the maximum direct and positive effect on seed yield and its indirect effect through days to 50% flowering, pods bearing nodes plant$^{-1}$ and number of pods node$^{-1}$ were moderate. It was observed that days to 50% flowering showed comparatively high direct effect on seed yield, but its indirect effect on seed yield through number of pods plant$^{-1}$ was higher than its direct effect, while its indirect influence through plant height

and days to maturity was very low and negative. The direct contribution of 100-seed weight on yield was found to be closer to its phenotypic correlation coefficient. It was reported that number of seeds pod$^{-1}$ had a low positive direct influence on seed yield and its indirect effect through pods plant$^{-1}$ on yield was more than its direct effect.

Path analysis by Kabir and Sen (1989) revealed a high positive direct effect of pod length on pod yield followed by number of pods, pod width and number of seeds pod$^{-1}$ while, negative direct effect was exhibited by days to flowering and 100-seed weight.

According to Singh (1990), number of pods plant$^{-1}$ was an important yield component in horsegram. Pod length exhibited maximum direct effect on pod yield followed by pod number, pod width and number of seeds pod$^{-1}$, whereas 100-seed weight and days to flowering showed direct but negative effect.

It was reported by Dobhal and Rana (1994) that maximum direct effect on seed yield was exhibited by clusters plant$^{-1}$ followed by days to flowering and pods plant$^{-1}$ in twenty-one diverse genotypes of horsegram.

Path analysis of direct and indirect effects of several characters in horsegram by Balan and Das (1994) revealed that pod weight plant$^{-1}$ has the greatest positive direct effect on seed yield plant$^{-1}$.

Maximum direct contribution of biomass and pod yield plant$^{-1}$ on seed yield was reported by Savithramma (1994) based on the work in hundred and three horsegram genotypes under kharif, rabi and summer seasons. High direct effects on seed yield by harvest index and biomass plant$^{-1}$ was observed during rabi season, while high indirect effect on seed yield through pod yield plant$^{-1}$ was reported during kharif season. During summer season, high direct effects on seed yield was contributed by harvest index and pod yield plant$^{-1}$ while, number of pods plant$^{-1}$ exhibited high indirect effect on seed yield through pod yield plant$^{-1}$.

Sood *et al.* (1994) reported that days to 75% flowering and days to 75% maturity has direct negative effect on seed yield. 100-seed weight exhibited indirect positive effect on seed yield *via* days to 75% flowering and days to 75% maturity.

Path coefficient of twenty horsegram genotypes were studied by Nagaraja *et al.* (1999) and reported that maximum direct effect on seed yield was contributed by number of primary branches, pod bearing nodes plant$^{-1}$ and pod yield plant$^{-1}$.

Prakash and Khanure (2000) reported that pods plant$^{-1}$ (0.870) have the highest positive direct effect, followed by 100-seed weight (0.152). This direct effect of pods plant$^{-1}$ by itself was found to be substantial as the indirect effects of other characters which show strong positive correlation with yield plant$^{-1}$ was less. Similarly, other characters like plant height and number fo branches plant$^{-1}$ which show positive direct effects are highly sustained by the indirect effects of pods plant$^{-1}$, ultimately resulting in the significant positive correlation of these characters with yield of the plant.

According to Dogra (2004), path analysis in horsegram genotypes revealed strong positive direct association of seed yield plant$^{-1}$ with leaf area (70 DAS) and harvest index while, pods plant$^{-1}$ and leaf area index exhibited a direct negative effect with yield. Leaf area, leaf area index, plant height, number of pods plant$^{-1}$, number of seeds pod$^{-1}$ and biological yield plant$^{-1}$ were also reported to exhibit a high indirect effect on yield improvement *via* harvest index.

Paliwal *et al.* (2005) studied the path coefficients of ten horsegram genotypes and concluded that pods plant$^{-1}$, branches plant$^{-1}$ and 100-seed weight have direct positive effects on seed yield and that selection for these characters would be beneficial in improving the yield of horsegram.

According to Rama *et al.* (2007), biological yield plant$^{-1}$, harvest index and leaf area (at 70 DAS) exhibited high positive and direct effect on seed yield plant$^{-1}$, while leaf area index had a direct negative effect on yield. High indirect effects were exhibited by leaf area, plant height, leaf area index, pods plant$^{-1}$, seeds pod$^{-1}$ and biological yiled plant$^{-1}$ on seed yield through harvest index.

Path analysis studies by Khulbe *et al.* (2013) revealed that pods plant$^{-1}$ and 100-seed weight had direct positive effects on seed yield while, direct negative effect on seed yield was exhibited by plant height. This study suggested that for the selection of

superior genotypes, emphasis must be given for characters like pods plant$^{-1}$ and 100-seed weight.

Path coefficient studies of the direct and indirect effect of seven quantitative characters by Vijayakumar *et al.* (2016) indicated that pod length has the maximum direct positive effect on seed yield hectare$^{-1}$, while it exhibited an indirect effect on seed yield *via* pod width and number of seeds pod$^{-1}$.

Priyanka *et al.* (2019) reported that traits like number of days to maturity (0.3314), number of pods plant$^{-1}$ (1.0057), number of seeds pod$^{-1}$ (0.2372) and 100-seed weight (0.1783) showed highly positive and direct effects on seed yield plant$^{-1}$, while some other yield related characters like plant height, number of cluster plant$^{-1}$, number of pods cluster$^{-1}$, number of seeds pod$^{-1}$ and pod length exhibited positive and indirect effects on yield through number of pods plant$^{-1}$. Positive direct effect was also recorded in 100-seed weight, but it was negatively correlated to yield. Also, the residual effect (0.2017) was found to be low indicating the contribution of traits towards variability.

## 2.8. GENETIC DIVERGENCE

In any crop improvement programme, the selection of various suitable parents for hybridization is an important feature to obtain the desired recombinants. Hence genetic divergence is important in plant breeding as hybrids between lines of diverse origin, generally display a greater heterosis than those between closely related parents.

Balan *et al.* (1992) studied the yield and eight component characters in horsegram, which were then analyzed using $D^2$ statistics for identifying the relative contribution of different characters towards genetic divergence studies. Depending on the results, the genotypes were classified into nine clusters. It was observed that pod weight was the only character which contributed the highest towards $D^2$ value.

Genetic divergence studies by Dogra (2004) helped in grouping thirty-five diverse horsegram genotypes into nine clusters. It was observed that seed yield plant$^{-1}$

contributed the maximum towards genetic divergence at genotypic level, followed by harvest index and pods plant$^{-1}$. Cluster-VII exhibited the highest intra-cluster distance, indicating a greater genetic divergence among the genotypes belonging to this cluster. Maximum inter-cluster distance was observed between cluster VIII and IX and the least between cluster-l and VI followed by cluster-VI and VIII.

Genetic diversity studies of fifty horsegram germplasm accessions collected from different parts of Eastern India was done by Dasgupta *et al.* (2005). The genetic divergence among these genotypes was estimated using Mahalanobis '$D^2$ technique and canonical analysis. As per the results obtained, the genotypes were grouped into ten clusters. The $D^2$ technique and canonical analysis showed close correspondence in the composition of these clusters. However, no relationship was found between geographical origin and genetic divergence in the formation of the clusters, and all the genotypes exhibited wide variability. The major contributors to divergence include characters such as days to flowering, seed yield plant$^{-1}$, 100 seed weight and soluble protein percentage.

Kalia and Dogra (2007) conducted cluster analysis among thirty-five horsegram genotypes and grouped them into nine clusters. Maximum contribution towards genetic divergence was given by crop growth rate followed by seed yield and harvest index at inter cluster level, while at genotypic level, seed yield plant$^{-1}$ contributed maximum towards divergence followed by harvest index and number of pods plant$^{-1}$.

Genetic divergence analysis in nine characters contributing to yield in twenty horsegram accessions was conducted by Sunil *et al.* (2009) and grouped these genotypes into five clusters. The maximum inter cluster distance was given by cluster II and V, followed by cluster IV and V and cluster III and IV.

Arun *et al.* (2010) evaluated a total of fifty-four horsegram genotypes collected from different altitudinal zones of Himalayan region for nine quantitative characters. Accessions collected from higher and lower altitude showed more divergence and differed significantly from those at mid altitude for different traits like days to flowering, days to maturity, seed yield plant$^{-1}$ and plant height.

Study of genetic divergence in eighty-eight horsegram genotypes by Singhal *et al* (2010) revealed the existence of wide diversity among all the genotypes studied. These genotypes were grouped into ten clusters based on the results obtained and it was observed that varieties belonging to clusters VIII and IX had great statistical distance. Hence they may be used for hybridization programmes as they are expected to produce good segregants.

An attempt was made by Prakash *et al.* (2010) to assess the genetic diversity present in hundred horsegram germplasm lines from different sources using Mahalanobis $D^2$ statistics and based on the results obtained these lines were grouped into eighteen different clusters. Cluster was the largest with nineteen genotypes grouped under it followed by cluster III (14) and cluster V (13). The maximum mean value for seed yield was given by the Cluster XII. The inter and intra cluster divergence among the genotypes was varying in magnitude, and it was found that maximum intra-cluster distance was shown by cluster III followed by clusters XI and XIII, while, cluster XII and XV exhibited the widest inter cluster distance. The distance between clusters X and V was found to be minimum indicating their close relationship.

An assessment of genetic diversity in horsegram was carried out by Sahoo *et al.* (2010) using forty-eight genotypes of horsegram, which was later grouped into six clusters using multivariate analysis. It was observed that days to maturity contributed the maximum to genetic divergence followed by days to flowering, while the lowest contribution was made by seeds $pod^{-1}$. Genotypes with lower performance for all the characters except for 100-seed weight and number of branches $plant^{-1}$ were present in Cluster II. Cluster I exhibited higher values for cluster mean in all the characters except for 100-seed weight and pods $cluster^{-1}$, whereas the genotypes of cluster VI had higher mean values for all the characters except for number of branches $plant^{-1}$, clusters $plant^{-1}$ and pod length. Among the six clusters, highest intra cluster distance was exhibited by cluster VI, while least was given by cluster III. Cluster I and II exhibited the maximum inter cluster distance followed by cluster II and VI.

Geetha *et al.* (2011) studied genetic divergence among hundred horsegram accessions using Mahalanobis $D^2$ statistics and grouped them into sixteen different clusters. Among them, cluster VI was the largest with forty-three genotypes followed by cluster I (14) and cluster XV (11). The maximum mean value for seed yield was exhibited by cluster XIV followed by cluster VII. The inter and intra cluster divergence also showed significant variation among the different genotypes. Maximum intra cluster distance was observed for cluster I followed by clusters II and XV, and widest inter cluster distance was noted between cluster I and XIII. Clusters X and XII showed minimum distance, revealing the close relationship between those clusters.

Genetic divergence studies were conducted by Durga (2012) in twenty-three diverse horsegram cultivars, which included three released varieties and twenty local accessions. Using Mahalanobis $D^2$ statistics, these cultivars were grouped into six clusters. Cluster I comprised of fourteen cultivars, cluster II had five cultivars and the other four clusters (III, IV, V and VI) included a single genotype each. Cluster IV (HG 50) and cluster V (HG 11) exhibited the maximum (62.39) inter cluster distance, while cluster I showed maximum intra cluster distance. The other high inter cluster distances were observed between clusters III and VI (59.95), clusters IV and VI (61.20), and clusters III and V (57.72), indicating potentiality of crossing between the genotypes of these clusters. The minimum inter cluster distance was noticed between clusters III and IV, which suggests that the genotypes in these clusters are genetically close.

Varma *et al.* (2013) assessed the genetic diversity in twenty-three horsegram genotypes using Mahalanobis $D^2$ statistics. On the basis of the results, the genotypes were grouped into seven clusters indicating wide diversity in the experimental material for different characters. Maximum number of genotypes (11) were included in cluster I, followed by cluster II with 7 genotypes, while remaining clusters got one genotype each. Cluster V and cluster VII (24.89) showed highest inter cluster distance followed by cluster V and VI (19.67). The maximum cluster mean for number of pods was recorded in cluster V (139.05) and cluster VI (131.88) and that for seed yield in clusters VI (18.77) and cluster VII (17.97). For plant height, maximum value was recorded in

Cluster III (67.91) and for germination in cluster V (99.88). Among individual traits, it was observed that seedling dry weight (50.99 %) contributed highest for divergence followed by seedling length (16.60 %), test weight and seedling vigour index I (8.70 %), followed by seed yield components such as test weight (8.70 %) and seed yield plant$^{-1}$ (5.53 %).

Assessment of genetic diversity in one hundred and eleven genotypes of horsegram was done by Poornima (2015) using $D^2$ technique. Based on the $D^2$ values, they were grouped into sixteen clusters. The largest cluster was cluster II comprising of 51 genotypes, followed by cluster I (21 genotypes), Cluster III (19 genotypes) and cluster XII (8 genotypes). The remaining twelve clusters had one genotype each. The inter cluster distances were found to range from 3.77 to 24.89. Among the traits, maximum (71.20 %) contribution towards the genetic divergence was shown by days to maturity.

In a study to assess the genetic diversity using morpho-agronomical traits in horsegram by Gomashe *et al.* (2018), diversity for qualitative traits were evaluated using Shannon diversity index and that for quantitative traits were done using Ward's method. The study revealed that the Shannon diversity index varied from 0.078 to 0.686, which reflects the existence of sufficient variability among the accessions. Moreover, characters like growth pattern, leaf surface, stem colour and pod surface were reported to give high values for Shannon Diversity Index. In the case of quantitative characters, accessions were classified into two different clusters on the basis of Euclidean distances using Ward's method. Cluster I comprised of seventeen accessions whereas, cluster II had forty-nine accessions, and cluster II was further divided in two sub-clusters (IIa and IIb). The study also revealed that the accessions from cluster I could be used for hybridization program while those from cluster II could be used for developing high yielding varieties for overall yield enhancement.

## 2.9. VARIETAL EVALUATION FOR NUTRITIONAL QUALITY

Horsegram seeds are known to possess excellent nutritional composition (protein, fatty acids, amino acids, flavonoids and minerals) and hence serve as a healthy, nutritious and balanced food for the malnourished and deprived people across the globe. Therefore, many studies have been done by several researchers to evaluate and quantify the nutritional composition and quality of horsegram seeds.

Varietal differences for seed protein content among fifty horsegram genotypes were reported by Patil and Deshmukh (1982) and reported that the seed protein content in horsegram ranged from 17.9 to 28.8%, the highest value being recorded in White Shimoga and lowest in EC-7460. Estimates of heritability for protein content was found to be high while genetic advance was low, indicating non additive gene action for the trait.

Sudha *et al.* (1995) conducted studies in sixteen varieties of whole horsegram and their dehulled seeds and reported that the dehulled samples were high in protein, fat and carbohydrate content compared to their corresponding whole seeded horsegram. However, fibre, moisture, ash and calcium content of dehulled seeds were found to be lower than the whole seeds.

Chemical experiments in four horsegram genotypes was done by Gupta *et al.* (2001) to analyze their proximate principles, protein fractions, tryptophan and methionine content. The analysis revealed the protein content to be in the range 16 - 19.71%, methionine 0.76-1.63 g, and 0.96-2.07 g tryptophan per gram seeds.

Sangita *et al.* (2004) analyzed the protein and oil content in wild horsegram genotype (IC 212722) and reported that the seeds contain 38.37% crude proteins.

The seeds of two horsegram varieties 'AK-21' and 'AK-42' were analyzed for their nutritional and physicochemical properties by Shashi *et al.* (2012). It was reported that the protein content of 'AK-21' and 'AK-42' were found to be 15.10 and 15.32 g percent respectively. The fibre content in both the varieties ranged from 4.57to 5.15 g percent and the energy content ranged between 376.12 – 377.21 kcal/100g.

Studies on varietal differences for plant nitrogen content, and grain nutrients content in twenty-one horsegram genotypes were done by Poornima (2015). Chemical analysis revealed a range of values for grain micronutrients viz., calcium (38.43-104.812 mg/100g), zinc (0.966-5.467 mg/100g), iron (0.39-7.083mg/100g) and grain protein (17.21-25.63%) and plant nitrogen (0.69 - 1.33%) contents.

# *Materials and Methods*

# 3. MATERIALS AND METHODS

The present study entitled "Variability in horsegram [*Macrotyloma uniflorum* (Lam.) Verdc.] under open and partially shaded conditions" was conducted at the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani between 2017 and 2019. Two field experiments were conducted simultaneously with an objective to assess the variability and performance of horsegram genotypes under open and partially shaded conditions, for yield and protein content.

## 3.1 MATERIALS

A survey was undertaken in Kerala, Tamil Nadu and Andhra Pradesh to identify local accessions of horse gram and twenty local accessions were collected. Ten accessions were procured from NBPGR, New Delhi. List of genotypes collected and location of collection is given in Table 1.

## 3.2 METHODS

### 3.2.1. Location

The experiments were carried out at College of Agriculture, Vellayani, located at 8°5' N latitude and 76°9'E longitude and at an altitude of 29 m above mean sea level. The predominant soil type of the experimental site was red loam of the Vellayani series, texturally classified as sandy clay loam.

### 3.2.2. Season

The two experiments were conducted simultaneously from September 2018 to February 2019.

Table 1. List of horsegram [*Macrotyloma uniflorum* (Lam.) Verdc.] genotypes used for the study.

| Genotypes | Name of Genotype | Source |
|---|---|---|
| T1 | Vakalavalasa local | Andhra Pradesh |
| T2 | Chintada local | Andhra Pradesh |
| T3 | Amudalavalasa local | Andhra Pradesh |
| T4 | Nenmara local | Kerala |
| T5 | Thathamangalam local | Kerala |
| T6 | Agali local | Kerala |
| T7 | Chittur local | Kerala |
| T8 | Vadakarapalli local | Kerala |
| T9 | Kannanthara local | Kerala |
| T10 | Perumatti local | Kerala |
| T11 | Melarcode local | Kerala |
| T12 | Palakkad local | Kerala |
| T13 | Nallepilly local | Kerala |
| T14 | Dharmapuri local | Tamil Nadu |
| T15 | Vanjangipeta local | Andhra Pradesh |
| T16 | Peruvamba local | Kerala |
| T17 | Attapadi local | Kerala |
| T18 | Panukuvalasa local | Andhra Pradesh |
| T19 | Pudur local | Tamil Nadu |
| T20 | Kozhinjampara local | Kerala |
| T21 | IC22762 | NBPGR |
| T22 | IC19441 | NBPGR |
| T23 | IC15735 | NBPGR |
| T24 | IC19450 | NBPGR |
| T25 | IC22773 | NBPGR |
| T26 | IC19447 | NBPGR |
| T27 | IC22770 | NBPGR |
| T28 | IC19442 | NBPGR |
| T29 | IC19452 | NBPGR |
| T30 | IC22759 | NBPGR |

### 3.2.3. Planting Material

Seeds were used as the planting material and were dibbled at a spacing of 30 x 25 cm into the raised beds. Each genotype was considered as an individual treatment.

### 3.2.4. Layout of the Experiment

Experiment I : Under open condition.

| | | |
|---|---|---|
| Design | : | RBD |
| Treatments | : | 30 |
| Replications | : | 3 |
| Spacing | : | 30cm × 25cm |
| Plot size | : | $1.88m^2$ |

Experiment II : Under partially shaded condition in coconut garden.

| | | |
|---|---|---|
| Design | : | RBD |
| Treatments | : | 30 |
| Replications | : | 3 |
| Spacing | : | 30cm × 25cm |
| Plot size | : | $1.88\ m^2$ |

The study was conducted in coconut garden, planted at a spacing of 7.8 x 7.8 m. Average shade percent of the garden was 24%.

Twenty-five plants were maintained in each plot.

## 3.3. MORPHOLOGICAL CHARACTERIZATION

Five plants were randomly selected from each plot and were tagged for recording the biometric characters. Observations were recorded and mean worked out for further analysis.

### 3.3.1. Biometrical Observations

#### *3.3.1.1. Number of days for sprouting*

The number of days taken from the date of sowing to the date of emergence of the sprouts above the ground level was recorded.

#### *3.3.1.2. Number of primary branches plant$^{-1}$*

The total number of primary branches in the selected five plants were counted at full maturity and their average worked out.

#### *3.3.1.3. Number of secondary branches plant$^{-1}$*

The total number of secondary branches in each observational plant were counted at full maturity and their average was worked out.

#### *3.3.1.4. Days to 50% flowering*

The number of days taken from sowing to flowering in 50 percent of the plants in the plot was observed and recorded.

#### *3.3.1.5. Days to maturity*

The number of days taken from the date of sowing to the date when 80 per cent of the pods in the plot reach maturity (all plants constituting the sample in each plot were harvested on the same day).

#### *3.3.1.6. Number of nodes plant$^{-1}$*

The total number of nodes present in the selected plants were counted and recorded.

#### *3.3.1.7. Number of pods plant$^{-1}$*

The total number of pods harvested from the observational plants were recorded.

#### *3.3.1.8. Number of seeds pod$^{-1}$*

Ten pods per plant were selected at random and shelled. The number of seeds per pod were counted and recorded.

#### *3.3.1.9. Pod length*

A random sample of five pods per plant were collected, the length was measured and expressed in centimeter.

***3.3.1.10. Yield plant$^{-1}$***

Seed yield from each observational plant was recorded in grams and average was worked out.

***3.3.1.11. 100 Seed weight***

Hundred well dried seeds were taken at random from each treatment weighed and expressed in grams.

***3.3.1.12. Plant height***

The height of the randomly selected five plants were measured at maturity from ground level to the tip of the plant in the field using metre scale and expressed in centimeters.

***3.3.1.13. Harvest Index***

Harvest index was estimated using the formula

$$HI = \frac{\text{Economic yield}}{\text{Biological yield}} \times 100$$

Harvest index was recorded as the ratio of seed yield to the total biological yield and expressed in percentage.

***3.3.1.14. Crop duration***

The total duration of the crop from the date of sowing to the date of final harvest of the pods was observed and recorded.

***3.3.1.15. Crude protein***

Per cent crude protein content (N x 6.25) in horsegram was estimated by the conventional Kjeldahl method as reported by Mckenzie and Wallace (1954).

## 3.4 STATISTICAL ANALYSIS

The analysis of variance for each character for two experiments was calculated and the pooled analysis was also worked out to compare the crop performance for each character in open and partially shaded conditions.

### 3.4.1. Analysis of Variance

Analysis of variance was worked out using the replicated data and the variations occurring within and between the genotypes were identified. The

difference between the genotypes was tested using Critical Difference (CD) values. Usually, it is worked out using per replication mean value of each treatment (Panse and Sukhatme, 1967).

| *Sources of variation* | *d.f* | *Sum of squares* | *Mean squares* | *F ratio* |
|---|---|---|---|---|
| Replications | t-1 | SSR | MSR | MSR/MSE |
| Treatment | r-1 | SST | MST | MST/MSE |
| Error | (t-1)(r-1) | SSE | MSE | |
| Total | rt-1 | | | |

Where, r= number of replications

t= number of treatments

SSR= sum of squares for replication

SST= sum of squares for treatments

SSE= sum of squares for error

Critical Difference, CD= $t_{\alpha}\sqrt{\frac{2MSE}{r}}$,

where tα is students't table value distribution at error d.f with level of significance α (5% or 1%).

### 3.4.2 Estimation of Genetic Parameters

#### *a. Genetic Components of Variance*

The phenotypic and genotypic components of the variance were estimated for each character by equating the expected value of the mean squares (MS) with the components of the respective variance (Jain, 1982).

Genotypic Variance (VG) $VG = \frac{MST-MSE}{r}$

Environmental Variance (VE) $VE = MSE$

Phenotypic Variance (VP) $VP = VG + VE$

***b. Coefficient of Variation***

Genotypic, Phenotypic and Environmental Coefficient of Variation were estimated from VP, VG and VE, expressed in percentage for each trait.

i. Genotypic coefficient of variation, $GCV=\frac{\sqrt{VG}}{X} \times 100$

ii. Phenotypic coefficient of variation, $PCV=\frac{\sqrt{VP}}{X} \times 100$

iii. Environmental coefficient of variation, $ECV=\frac{\sqrt{VE}}{X} \times 100$

Where, X = Grand mean

The range of variation was classified as per the scale given by Sivasubramanian and Menon (1973):

| Category | Range |
|---|---|
| Low | Less than 20% |
| Moderate | 10 – 20% |
| High | More than 20% |

***c. Heritability (Broad sense)***

Genetic contribution to the phenotypic expression of traits is reflected by the estimates of heritability. Heritability ($h^2$) in broad sense is a ratio of genotypic variance to the total observed variance in the population, expressed in percent and calculated by the formula suggested by Burton (1952) and Johnson *et al.* (1955).

$$h^2=\frac{VG}{VP} \times 100$$

Range of heritability estimation (Johnson *et al.*, 1955)

| Category | Range |
|---|---|
| Low | 0-30% |
| Medium | 30-60% |
| High | More than 60% |

***d. Genetic Advance***

Genetic advance refers to the expected genetic gain or improvement in the subsequent generation by selecting superior genotype under certain amount of selection pressure. The formula for genetic advance as suggested by Burton and De Vane (1935) and Johnson *et al.* (1955).

$$GA = Kh^2\sqrt{VP}$$

Where, K= selection differential, at 5% selection intensity

K=2.06 (Miller *et al.*, 1958)

$h^2$ = Heritability

Vp = Phenotypic variance

***e. Genetic Advance as Percent of Mean***

$$GAM = GA/X \times 100$$

Where, GA= Genetic Advance

X= Grand Mean

Ranges of genetic advance is classified as per Johnson *et al.* (1955).

| Category | Range |
|---|---|
| Low | Less than 10% |
| Medium | 10-20% |
| High | More than 20% |

***3.3.3. Estimation of Correlation***

A statistical measure which gives the degree and direction of association between two variables is referred to as correlation coefficient. Phenotypic, genotypic and environmental coefficients of correlation were worked out following analysis of covariance involving all possible paired combinations among the characters studied using Falconer (1964) formula.

Genotypic coefficient of correlation ($r_g$) $= r(x_i.x_j)_g = \frac{Cov((xi.xj)g}{\sqrt{v(xi)g.v(xj)g}}$

Phenotypic coefficient of correlation ($r_p$) $= r(x_i.x_j)_p = \frac{Cov((xi.xj)p}{\sqrt{v(xi)p.v(xj)p}}$

Error coefficient of correlation ($r_e$) $= r(x_i.x_j)_e = \frac{Cov((xi.xj)e}{\sqrt{v(xi)e.v(xj)e}}$

### *3.3.4. Path Coefficient Analysis*

Path coefficient is a standardized partial regression coefficient that separates the correlation coefficients into direct and indirect effects (Dewey and Lu, 1959). It measures the cause of association between two characters. Hence path analysis technique is used to estimate the direct and indirect effects of component characters on yield and this method was developed by Wright (1954).

r1y = P1y r11+P2yr12+P3yr13.....+Pnyr1n

r2y = P2y r21+P2yr22+P3yr23.....+Pnyr2n

rny = P1y rn1+P2yrn2+P3yrn3.....+Pnyrnn

Where,

1,2.....n = independent variables

y = dependent variable

r1y, r2y.....rny = coefficient of correlation between independent variables 1 to n on dependent variable y.

P1y, P2y.....Pny = direct effect of character 1 to n on character y.

The above equation can be written in matrix form

$$\begin{bmatrix} r_{1y} \\ r_{2y} \\ . \\ . \\ . \\ r_{ny} \end{bmatrix} \begin{bmatrix} 1 & r_{12} & r_{13} & . & . & r_{1n} \\ r_{21} & 1 & r_{23} & . & . & r_{2n} \\ . & . & . & . & . & . \\ . & . & . & . & . & . \\ . & . & . & . & . & . \\ r_{n1} & r_{n2} & r_{n3} & . & . & 1 \end{bmatrix} \begin{bmatrix} P_{1y} \\ P_{2y} \\ . \\ . \\ . \\ P_{ny} \end{bmatrix}$$

Then $B=C^{-1}A$, where $C^{-1}=\begin{bmatrix} C_{11} & C_{12} & C_{13} & . & . & C_{1n} \\ C_{21} & C_{22} & C_{23} & . & . & C_{2n} \\ . & . & . & . & . & . \\ . & . & . & . & . & . \\ . & . & . & . & . & . \\ C_{n1} & C_{n2} & C_{n3} & . & . & C_{nn} \end{bmatrix}$

Direct effects:

$P_{1y}= \sum_{i=1}^{k} c_{1i}\ r_{iy}$

$P_{2y} = \sum_{i=1}^{k} c_{2i} r_{iy}$

$P_{ny} = \sum_{i=1}^{k} c_{ni} r_{iy}$

Residual effect $PR_y= \sqrt{1 - r^2}$

Where, $r^2 = (P_{1y}r_{1y} + P_{2y}r_{2y} + P_{3y}r_{3y} \dots \dots \dots \dots \dots \dots \dots \dots + P_{ny}r_{ny})$

$P_{iy}$= direct effect of $X_i$ on y

$r_{iy}$= correlation coefficient of $X_i$ on y

i = 1,2,3.....n

### *3.3.5. Genetic Divergence*

Mahalanobis $D^2$ statistics was used to study the genetic divergence present in the given population. Using $D^2$ values, different genotypes were grouped into various clusters following Toucher's method as suggested by Rao (1952).

# *Results*

# 4. RESULTS

The data collected for various biometrical, morphological and biochemical characters were subjected to statistical analysis and the results obtained are presented in this chapter.

## 4.1. EVALUATION OF HORSEGRAM GENOTYPES

### 4.1.1. Variability

Thirty genotypes of horsegram were evaluated for different characters and the data on each character was statistically analyzed separately under open and partially shaded conditions using analysis of variance technique. Pooled analysis was also done to compare the performance of the genotypes under both conditions.

#### *4.1.1.1. Variability in number of days for sprouting*:

The observations on number of days for sprouting are depicted in Table 2.

Under open condition, least number of days for sprouting was recorded for the genotype T11 (2.07) which was on par with other genotypes like T4 (2.13), T7 (2.33), T9 (2.20), T12 (2.20), T13 (2.47), T14 (2.33), T15 (2.40), T16 (2.13), T17 (2.20), T19 (2.40), T24 (2.47) and T29 (2.27) whereas days for sprouting was noticed to be high for the genotype T26 (3.60). Under partially shaded conditions, the genotype T16 (2.00) took less days for sprouting which was on par with genotypes T2 (2.13), T11 (2.13), T29 (2.20), T4 (2.27), T5 (2.27), T8 (2.20), T9 (2.20), T13 (2.33), T15 (2.20) and T17 (2.33), while delayed sprouting was exhibited by the genotype T23 (3.47) and this was on par with genotypes T3 (3.27), T22 (3.33), T26 (3.33) and T30 (3.13).

In pooled analysis, the genotype T16 (2.07) recorded least days for sprouting which was on par with other genotypes like T11 (2.10), T9 (2.20), T17 (2.27), T29 (2.23), T12 (2.30) and T15 (2.30), and the genotype T23 (3.50) took more days for sprouting which significantly differed from all other genotypes except for the two genotypes T22 (3.37) and T26 (3.47).


(a) Open Condition


(b) Shaded Condition

Plate 1. Field view

Table 2. Number of days for sprouting of different genotypes of horsegram under open and partially shaded conditions.

| Genotypes | Number of days for sprouting | | |
|---|---|---|---|
| | Open | Shade | Pooled |
| T1 | 2.93 | 2.73 | 2.83 |
| T2 | 2.73 | 2.13 | 2.43 |
| T3 | 3.13 | 3.27 | 3.20 |
| T4 | 2.13 | 2.27 | 2.20 |
| T5 | 2.53 | 2.27 | 2.40 |
| T6 | 2.40 | 2.47 | 2.43 |
| T7 | 2.33 | 2.40 | 2.37 |
| T8 | 2.53 | 2.20 | 2.37 |
| T9 | 2.20 | 2.20 | 2.20 |
| T10 | 2.67 | 2.53 | 2.60 |
| T11 | 2.07 | 2.13 | 2.10 |
| T12 | 2.20 | 2.40 | 2.30 |
| T13 | 2.47 | 2.33 | 2.40 |
| T14 | 2.33 | 2.40 | 2.37 |
| T15 | 2.40 | 2.20 | 2.30 |
| T16 | 2.13 | 2.00 | 2.07 |
| T17 | 2.20 | 2.33 | 2.27 |
| T18 | 2.60 | 2.73 | 2.67 |
| T19 | 2.40 | 2.40 | 2.40 |
| T20 | 2.80 | 2.87 | 2.83 |
| T21 | 3.07 | 2.93 | 3.00 |
| T22 | 3.40 | 3.33 | 3.37 |
| T23 | 3.53 | 3.47 | 3.50 |
| T24 | 2.47 | 2.67 | 2.57 |
| T25 | 3.20 | 3.00 | 3.10 |
| T26 | 3.60 | 3.33 | 3.47 |
| T27 | 2.73 | 2.53 | 2.63 |
| T28 | 2.67 | 2.53 | 2.60 |
| T29 | 2.27 | 2.20 | 2.23 |
| T30 | 3.20 | 3.13 | 3.17 |
| Mean | 2.64 | 2.58 | 2.61 |
| SE of mean | 0.15 | 0.14 | 0.10 |
| CD (5%) Between genotypes | 0.41 | 0.38 | 0.28 |
| CD (5%) Open x Shade | NS | | |
| CD (5%) Genotype x Condition | NS | | |

### *4.1.1.2. Variability in number of primary branches plant$^{-1}$:*

From Table 3 it is evident that highest number of primary branches plant$^{-1}$ were recorded by genotype T8 in pooled analysis as well as in open and partially shaded conditions. The genotypes exhibited significant difference in their performance over both conditions. Under open condition, genotype T8 (12.47) exhibited maximum number of primary branches per plant which was on par with genotypes T15 (11.97), T18 (10.67), T20 (10.37), T2 (9.77), T4 (10.20), T6 (10.20), T10 (9.78), T12 (10.17), T13 (10.73), T14 (9.83), T21 (9.43), T24 (9.07), T25 (10.03), T29 (9.70) and T30 (11.57) whereas minimum number of primary branches were produced by the genotype T9 (5.60) which was on par with the rest of the genotypes. Under partially shaded condition, more number of primary branches were again produced by T8 (11.73) and this was on par with other genotypes like T12 (11.70), T18 (11.23), T13 (11.53), T30 (10.17), T4 (10.53), T6 (10.07), T15 (10.73), T17 (10.60), T1 (9.57) and T14 (9.47). The genotype T28 (5.33) exhibited minimum number of primary branches followed by genotypes T3 (5.53), T10 (5.67), T7 (6.37), T11 (6.03), T19 (6.93), T22 (6.47), T24 (7.32), T25 (6.73) and T29 (7.30).

In pooled analysis, genotype T8 (12.10) produced more number of primary branches followed by genotypes T13 (11.13), T15 (11.35), T4 (10.37), T6 (10.13), T12 (10.93), T18 (10.95) and T30 (10.87), while less number of primary branches were produced by T28 (5.82) which was on par with genotypes T3 (6.17), T5 (7.67), T7 (6.88), T9 (6.23), T10 (7.72), T11 (7.28), T19 (6.88) and T22 (7.42).

### *4.1.1.3. Variability in number of secondary branches plant$^{-1}$:*

The observations on number of secondary plant$^{-1}$ is depicted in Table 4.

The performance of the genotypes showed no significant difference under open and partially shaded conditions and there existed no interaction between the genotypes and conditions. However, variability between the genotypes was found to be significant in pooled analysis. Highest number of secondary branches plant$^{-1}$ was recorded for the genotype T8 in pooled analysis as well as under open and

Table 3. Number of primary branches plant$^{-1}$ of different genotypes of horsegram under open and partially shaded conditions.

| **Genotypes** | **Number of primary branches plant$^{-1}$** | | |
|---|---|---|---|
| | Open | Shade | Pooled |
| T1 | 8.47 | 9.57 | 9.02 |
| T2 | 9.77 | 8.26 | 9.01 |
| T3 | 6.80 | 5.53 | 6.17 |
| T4 | 10.20 | 10.53 | 10.37 |
| T5 | 8.57 | 6.77 | 7.67 |
| T6 | 10.20 | 10.07 | 10.13 |
| T7 | 7.40 | 6.37 | 6.88 |
| T8 | 12.47 | 11.73 | 12.10 |
| T9 | 5.60 | 6.87 | 6.23 |
| T10 | 9.78 | 5.67 | 7.72 |
| T11 | 8.53 | 6.03 | 7.28 |
| T12 | 10.17 | 11.70 | 10.93 |
| T13 | 10.73 | 11.53 | 11.13 |
| T14 | 9.83 | 9.47 | 9.65 |
| T15 | 11.97 | 10.73 | 11.35 |
| T16 | 8.80 | 8.53 | 8.67 |
| T17 | 6.97 | 10.60 | 8.78 |
| T18 | 10.67 | 11.23 | 10.95 |
| T19 | 6.83 | 6.93 | 6.88 |
| T20 | 10.37 | 8.23 | 9.30 |
| T21 | 9.43 | 8.27 | 8.85 |
| T22 | 8.37 | 6.47 | 7.42 |
| T23 | 7.80 | 8.77 | 8.28 |
| T24 | 9.07 | 7.32 | 8.20 |
| T25 | 10.03 | 6.73 | 8.38 |
| T26 | 7.97 | 8.63 | 8.30 |
| T27 | 8.93 | 8.87 | 8.90 |
| T28 | 6.30 | 5.33 | 5.82 |
| T29 | 9.70 | 7.30 | 8.50 |
| T30 | 11.57 | 10.17 | 10.87 |
| Mean | 9.11 | 8.47 | 8.79 |
| SE of mean | 1.20 | 0.82 | 0.72 |
| CD (5%) Between genotypes | 3.41 | 2.31 | 2.02 |
| CD (5%) Open x Shade | 0.522 | | |
| CD (5%) Genotype x Condition | NS | | |

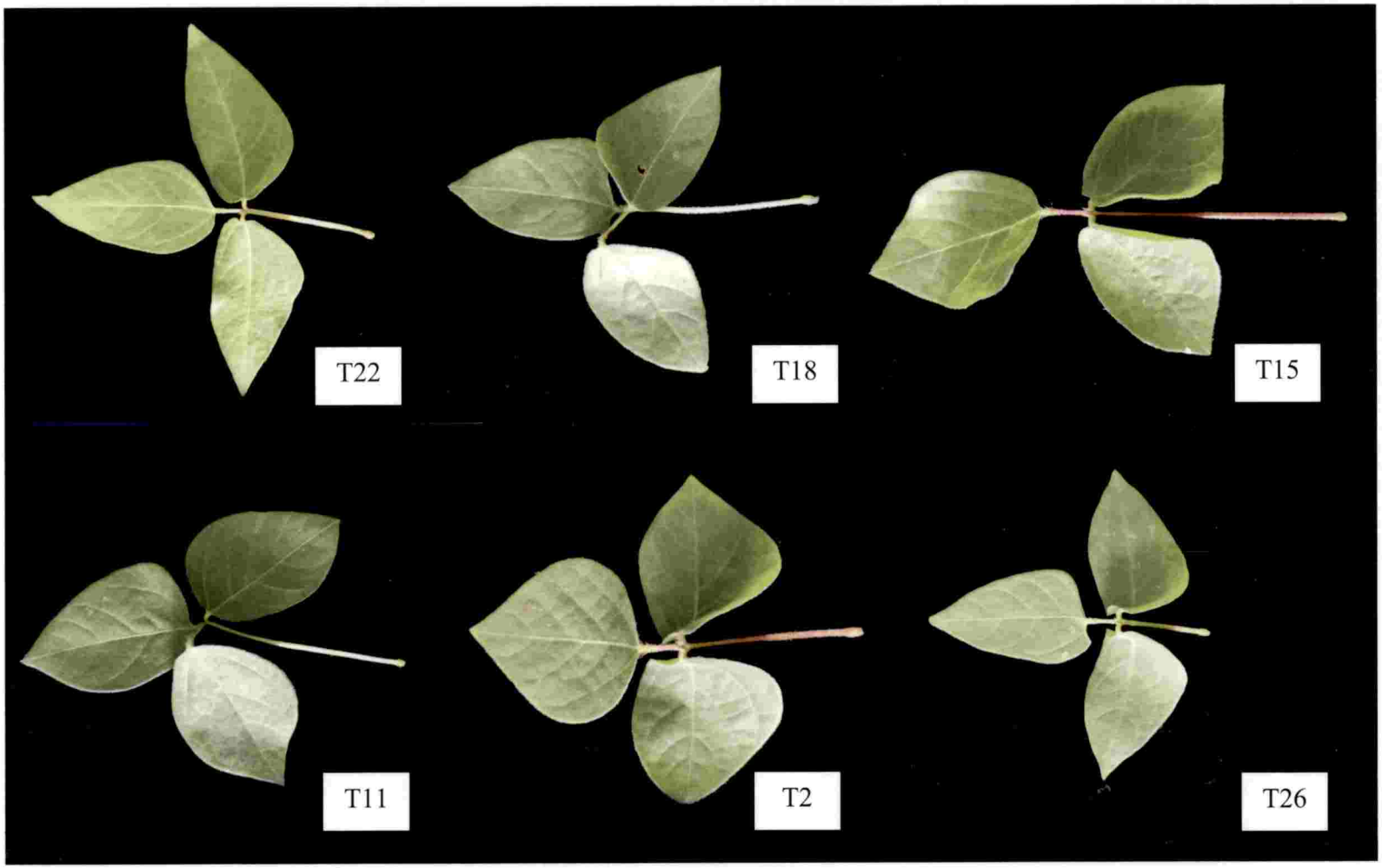



Plate 2. Variability in leaves

partially shaded conditions. In pooled analysis, T8 (18.37) produced highest number of secondary branches plant$^{-1}$ followed by genotypes T13 (17.95), T15 (17.33), T6 (17.18), T4 (16.27), T17 (16.98) and T18 (16.50). Genotype T21 (10.02) produced least number of secondary branches followed by T24 (10.87), T19 (10.40), T28 (10.87), T3 (11.78), T9 (11.37), T16 (11.52), T22 (11.35), T2 (12.53), T10 (12.03), T11 (12.33), T27 (12.03) and T29 (12.00).

#### *4.1.1.4. Variability in days to 50% flowering:*

Table 5 reveals the results of variability in days to 50% flowering in horsegram genotypes under open and partially shaded conditions.

The genotypes performed significantly different under open and partially shaded conditions for this character. From the table, it is also clear that the genotype T30 took the least number of days to attain 50% flowering in pooled analysis as well as under both conditions. Under open condition, genotype T30 (46.33) took less days to attain 50% flowering, and it is significantly different from other genotypes except for T24 (48.33), whereas genotype T7 (80.67) recorded more days for attaining 50% flowering followed by genotypes T6 (78.33), T8 (76.67), T10 (77.67), T4 (74.33), T12 (75.00), T14 (75.67), T17 (74.33) and T19 (74.67). Under partially shaded condition, again genotype T30 (48.67) recorded the least days to 50% flowering followed by T24 (49.00), whereas more days to 50% flowering was given by T6 (81.67), which was on par with genotypes T12 (79.67), T8 (78.00), T17 (78.33), T10 (78.67), T14 (77.00), T19 (76.00), T4 (75.67) and T5 (75.33). In pooled analysis, least days to 50% flowering was observed for genotype T30 (47.50), whereas genotype T7 (80.50) took the highest number of days for 50% flowering. The overall results suggested that genotypes under shaded conditions took more days to reach 50% flowering compared to those under open conditions.

Table 4. Number of secondary branches plant$^{-1}$ of different genotypes of horsegram under open and partially shaded conditions

| Genotypes | Number of secondary branches plant$^{-1}$ | | |
|---|---|---|---|
| | Open | Shade | Pooled |
| T1 | 14.90 | 15.77 | 15.33 |
| T2 | 11.23 | 13.82 | 12.53 |
| T3 | 12.70 | 10.87 | 11.78 |
| T4 | 15.03 | 17.50 | 16.27 |
| T5 | 14.50 | 12.13 | 13.32 |
| T6 | 16.20 | 18.17 | 17.18 |
| T7 | 11.53 | 12.30 | 11.92 |
| T8 | 18.93 | 17.80 | 18.37 |
| T9 | 12.43 | 10.30 | 11.37 |
| T10 | 12.33 | 11.73 | 12.03 |
| T11 | 10.43 | 14.23 | 12.33 |
| T12 | 14.03 | 12.57 | 13.30 |
| T13 | 17.07 | 18.83 | 17.95 |
| T14 | 11.70 | 14.17 | 12.93 |
| T15 | 18.70 | 15.97 | 17.33 |
| T16 | 12.83 | 10.20 | 11.52 |
| T17 | 16.53 | 17.43 | 16.98 |
| T18 | 16.60 | 16.40 | 16.50 |
| T19 | 10.90 | 9.90 | 10.40 |
| T20 | 13.13 | 13.57 | 13.35 |
| T21 | 10.73 | 9.30 | 10.02 |
| T22 | 10.90 | 11.80 | 11.35 |
| T23 | 14.10 | 15.63 | 14.87 |
| T24 | 11.60 | 10.13 | 10.87 |
| T25 | 14.83 | 11.22 | 13.03 |
| T26 | 14.70 | 14.83 | 14.77 |
| T27 | 10.53 | 13.53 | 12.03 |
| T28 | 10.60 | 11.13 | 10.87 |
| T29 | 11.50 | 12.50 | 12.00 |
| T30 | 14.90 | 15.77 | 15.33 |
| Mean | 13.54 | 13.65 | 13.59 |
| SE of mean | 1.49 | 1.20 | 0.98 |
| CD (5%) Between genotypes | 4.24 | 3.40 | 2.75 |
| CD (5%) Open x Shade | NS | | |
| CD (5%) Genotype x Condition | NS | | |

Table 5. Days to 50% flowering of different genotypes of horsegram under open and partially shaded conditions

| Genotypes | Days to 50% flowering | | |
|---|---|---|---|
| | Open | Shade | Pooled |
| T1 | 71.67 | 74.00 | 72.83 |
| T2 | 65.00 | 67.33 | 66.17 |
| T3 | 66.67 | 67.67 | 67.17 |
| T4 | 74.33 | 75.67 | 75.00 |
| T5 | 72.67 | 75.33 | 74.00 |
| T6 | 78.33 | 81.67 | 80.00 |
| T7 | 80.67 | 80.33 | 80.50 |
| T8 | 76.67 | 78.00 | 77.33 |
| T9 | 64.67 | 69.33 | 67.00 |
| T10 | 77.67 | 78.67 | 78.17 |
| T11 | 71.00 | 73.67 | 72.33 |
| T12 | 75.00 | 79.67 | 77.33 |
| T13 | 67.67 | 68.00 | 67.83 |
| T14 | 75.67 | 77.00 | 76.33 |
| T15 | 70.67 | 72.00 | 71.33 |
| T16 | 63.67 | 64.00 | 63.83 |
| T17 | 74.33 | 78.33 | 76.33 |
| T18 | 61.33 | 64.00 | 62.67 |
| T19 | 74.67 | 76.00 | 75.33 |
| T20 | 66.00 | 67.00 | 66.50 |
| T21 | 59.00 | 60.67 | 59.83 |
| T22 | 56.33 | 58.67 | 57.50 |
| T23 | 54.33 | 55.33 | 54.83 |
| T24 | 48.33 | 49.00 | 48.67 |
| T25 | 57.67 | 60.67 | 59.17 |
| T26 | 56.00 | 57.00 | 56.50 |
| T27 | 54.00 | 55.33 | 54.67 |
| T28 | 56.00 | 58.67 | 57.33 |
| T29 | 53.33 | 57.33 | 55.33 |
| T30 | 46.33 | 48.67 | 47.50 |
| Mean | 65.66 | 67.63 | 66.64 |
| SE of mean | 2.30 | 2.33 | 1.63 |
| CD (5%) Between genotypes | 6.53 | 6.60 | 4.56 |
| CD (5%) Open x Shade | 1.18 | | |
| CD (5%) Genotype x Condition | NS | | |

#### *4.1.1.5. Variability in days to maturity:*

The observations on number of days taken for maturity in horsegram are depicted in Table 6.

The character showed significant difference under open and partially shaded conditions but there was no significant interaction between the genotype and the conditions. Under open and partially shaded conditions, the genotype T30 took minimum days to attain maturity (106.60 and 109.40) respectively, while more number of days to maturity was exhibited by genotype T7 under open condition and by genotype T6 under shaded conditions. In pooled analysis, genotype T30 (108.00) matured in least number of days which significantly differed from all other genotypes except T24 (111.90) and highest number of days for maturity was taken by T6 (142.67) which was on par with genotypes T7 (142.43), T19 (141.90) and T1 (138.80).

#### *4.1.1.6. Variability in number of nodes plant$^{-1}$:*

According to Table 7, there exists no significant difference in the behavior of the genotypes under open and partially shaded conditions. Under open condition, genotype T15 (148.40) produced more number of nodes per plant, while genotype T28 (80.60) produced least number of nodes. Under partially shaded condition, highest number of nodes were produced by the genotype T6 (136.10) whereas least nodes were produced by T19 (82.73). But in pooled analysis, highest number of nodes plant$^{-1}$ was recorded for genotype T15 (141.60) followed by T8 (138.42), T13 (136.15) and T6 (135.80), whereas least number of nodes plant$^{-1}$ was produced by the genotype T19 (85.70), which was on par with T28 (87.60) and T21 (92.00). Between the different genotypes studied and the two conditions there was significant interaction for genotypes like T5, T11, T14, T15, T16, T25, T27 and T28.

Table 6. Days to maturity of different genotypes of horsegram under open and partially shaded conditions

| Genotypes | Days to maturity | | |
|---|---|---|---|
| | Open | Shade | Pooled |
| T1 | 137.40 | 140.20 | 138.80 |
| T2 | 123.60 | 125.47 | 124.53 |
| T3 | 126.00 | 127.80 | 126.90 |
| T4 | 124.80 | 126.07 | 125.43 |
| T5 | 139.80 | 143.00 | 141.40 |
| T6 | 141.00 | 144.33 | 142.67 |
| T7 | 142.40 | 142.47 | 142.43 |
| T8 | 134.07 | 136.27 | 135.17 |
| T9 | 125.60 | 126.00 | 125.80 |
| T10 | 136.07 | 137.73 | 136.90 |
| T11 | 123.67 | 125.00 | 124.33 |
| T12 | 132.33 | 134.07 | 133.20 |
| T13 | 125.13 | 126.53 | 125.83 |
| T14 | 133.53 | 135.07 | 134.30 |
| T15 | 132.57 | 133.60 | 133.08 |
| T16 | 127.00 | 127.27 | 127.13 |
| T17 | 141.93 | 143.13 | 142.53 |
| T18 | 129.20 | 131.00 | 130.10 |
| T19 | 141.00 | 142.80 | 141.90 |
| T20 | 128.33 | 128.93 | 128.63 |
| T21 | 121.47 | 123.00 | 122.23 |
| T22 | 113.00 | 116.27 | 114.63 |
| T23 | 114.07 | 114.80 | 114.43 |
| T24 | 111.13 | 112.67 | 111.90 |
| T25 | 123.73 | 125.27 | 124.50 |
| T26 | 116.73 | 119.53 | 118.13 |
| T27 | 112.13 | 113.33 | 112.73 |
| T28 | 115.13 | 115.33 | 115.23 |
| T29 | 115.47 | 116.73 | 116.10 |
| T30 | 106.60 | 109.40 | 108.00 |
| Mean | 126.50 | 128.10 | 127.30 |
| SE of mean | 1.97 | 1.92 | 1.43 |
| CD (5%) Between genotypes | 5.60 | 5.45 | 4.00 |
| CD (5%) Open x Shade | 1.03 | | |
| CD (5%) Genotype x Condition | NS | | |

Table 7. Number of nodes plant$^{-1}$of different genotypes of horsegram under open and partially shaded conditions

| Genotypes | Number of nodes plant$^{-1}$ | | |
|---|---|---|---|
| | Open | Shade | Pooled |
| T1 | 127.70 | 121.67 | 124.68 |
| T2 | 108.40 | 114.83 | 111.62 |
| T3 | 100.00 | 95.63 | 97.82 |
| T4 | 128.17 | 132.50 | 130.33 |
| T5 | 119.70 | 105.70 | 112.70 |
| T6 | 135.50 | 136.10 | 135.80 |
| T7 | 107.57 | 109.20 | 108.38 |
| T8 | 141.13 | 135.70 | 138.42 |
| T9 | 105.73 | 94.60 | 100.17 |
| T10 | 104.27 | 97.77 | 101.02 |
| T11 | 96.30 | 119.47 | 107.88 |
| T12 | 115.53 | 104.83 | 110.18 |
| T13 | 137.43 | 134.87 | 136.15 |
| T14 | 99.53 | 115.80 | 107.67 |
| T15 | 148.40 | 134.80 | 141.60 |
| T16 | 103.30 | 90.00 | 96.65 |
| T17 | 129.60 | 128.00 | 128.80 |
| T18 | 130.43 | 123.03 | 126.73 |
| T19 | 88.67 | 82.73 | 85.70 |
| T20 | 105.43 | 104.23 | 104.83 |
| T21 | 97.07 | 86.93 | 92.00 |
| T22 | 101.57 | 99.60 | 100.58 |
| T23 | 108.37 | 108.73 | 108.55 |
| T24 | 101.60 | 96.33 | 98.97 |
| T25 | 126.60 | 97.47 | 112.03 |
| T26 | 122.03 | 121.37 | 121.70 |
| T27 | 98.97 | 117.27 | 108.12 |
| T28 | 80.60 | 94.60 | 87.60 |
| T29 | 94.97 | 102.40 | 98.68 |
| T30 | 124.87 | 128.37 | 126.62 |
| Mean | 112.98 | 111.15 | 112.07 |
| SE of mean | 4.25 | 4.72 | 3.15 |
| CD (5%) Between genotypes | 12.05 | 13.41 | 8.85 |
| CD (5%) Open x Shade | NS | | |
| CD (5%) Genotype x Condition | 12.51 | | |

### *4.1.1.7. Variability in number of pods plant$^{-1}$:*

The observations taken on number of pods per plant are given in Table 8.

The genotypes differed significantly under open and partially shaded conditions for this character. The number of pods produced per plant was highest for the genotype T12 (105.27) under open conditions and this was on par with other genotypes like T2 (102.00) and T25 (100.47). Least number of pods were produced by the genotype T26 (45.60) followed by genotypes T29 (51.10) and T27 (52.40). Under partially shaded conditions, genotype T12 (98.87) produced more number of pods per plant followed by genotypes T2 (97.33), T21 (95.33), T18 (94.60) and T8 (93.87), whereas minimum number of pods were produced by T26 (41.67) which significantly differed from all other genotypes.

In pooled analysis, highest production of pods plant$^{-1}$ was exhibited by genotype T12 (102.07) and it differed significantly from all other genotypes except T2 (99.67), whereas less production of pods plant$^{-1}$ was shown by genotype T26 (43.63) which is significantly different from all other genotypes taken for the study. Overall, it was observed that more number of pods were produced by the genotypes grown under open conditions than those under partial shade.

### *4.1.1.8. Variability in number of seeds pod$^{-1}$:*

It is clear from Table 9 that there was no significant difference in the performance of the genotypes under open and partially shaded conditions for this character. But in pooled analysis, number of seeds pod$^{-1}$ was observed to be maximum for genotype T12 (7.20) which was on par with genotypes T21 (7.17) and T30 (6.90). Likewise, minimum number of seeds pod$^{-1}$ was exhibited by the genotype T13 (5.20) followed by TT25 (5.37), T19 (5.40), T3 (5.43), T8 (5.50), T29 (5.50), T7 (5.57) and T11 (5.57). The results also showed that there was no significant interaction between the genotypes and condition for the number of seeds per pod.

Table 8. Number of pods plant$^{-1}$of different genotypes of horsegram under open and partially shaded conditions

| Genotypes | Number of pods plant$^{-1}$ | | |
|---|---|---|---|
| | Open | Shade | Pooled |
| T1 | 55.40 | 57.07 | 56.23 |
| T2 | 102.00 | 97.33 | 99.67 |
| T3 | 65.53 | 68.20 | 66.87 |
| T4 | 53.53 | 54.87 | 54.20 |
| T5 | 75.20 | 72.00 | 73.60 |
| T6 | 93.20 | 83.10 | 88.15 |
| T7 | 88.53 | 82.93 | 85.73 |
| T8 | 92.93 | 93.87 | 93.40 |
| T9 | 79.00 | 70.33 | 74.67 |
| T10 | 71.43 | 72.73 | 72.08 |
| T11 | 58.80 | 52.87 | 55.83 |
| T12 | 105.27 | 98.87 | 102.07 |
| T13 | 72.93 | 69.93 | 71.43 |
| T14 | 59.20 | 57.60 | 58.40 |
| T15 | 74.87 | 72.87 | 73.87 |
| T16 | 60.20 | 52.67 | 56.43 |
| T17 | 86.60 | 86.07 | 86.33 |
| T18 | 93.90 | 94.60 | 94.25 |
| T19 | 56.33 | 54.07 | 55.20 |
| T20 | 74.93 | 69.73 | 72.33 |
| T21 | 97.83 | 95.33 | 96.58 |
| T22 | 66.60 | 61.60 | 64.10 |
| T23 | 62.40 | 63.87 | 63.13 |
| T24 | 61.87 | 62.27 | 62.07 |
| T25 | 100.47 | 92.73 | 96.60 |
| T26 | 45.60 | 41.67 | 43.63 |
| T27 | 52.40 | 54.60 | 53.50 |
| T28 | 57.87 | 50.80 | 54.33 |
| T29 | 51.10 | 52.07 | 51.58 |
| T30 | 88.27 | 83.00 | 85.63 |
| Mean | 73.47 | 70.65 | 72.06 |
| SE of mean | 2.45 | 2.10 | 1.61 |
| CD (5%) Between genotypes | 6.95 | 5.97 | 4.51 |
| CD (5%) Open x Shade | 1.17 | | |
| CD (5%) Genotype x Condition | NS | | |

Table 9. Number of seeds pod$^{-1}$of different genotypes of horsegram under open and partially shaded conditions

| Genotypes | Number of seeds pod$^{-1}$ | | |
|---|---|---|---|
| | Open | Shade | Pooled |
| T1 | 6.60 | 6.13 | 6.37 |
| T2 | 7.07 | 6.73 | 6.90 |
| T3 | 5.33 | 5.53 | 5.43 |
| T4 | 6.53 | 6.27 | 6.40 |
| T5 | 5.53 | 6.00 | 5.77 |
| T6 | 6.53 | 6.20 | 6.37 |
| T7 | 5.40 | 5.73 | 5.57 |
| T8 | 5.40 | 5.60 | 5.50 |
| T9 | 6.13 | 6.00 | 6.07 |
| T10 | 5.60 | 6.07 | 5.83 |
| T11 | 5.47 | 5.67 | 5.57 |
| T12 | 7.27 | 7.13 | 7.20 |
| T13 | 5.13 | 5.27 | 5.20 |
| T14 | 6.07 | 6.07 | 6.07 |
| T15 | 6.27 | 6.40 | 6.33 |
| T16 | 5.53 | 5.20 | 5.37 |
| T17 | 6.00 | 5.67 | 5.83 |
| T18 | 6.53 | 6.27 | 6.40 |
| T19 | 5.33 | 5.47 | 5.40 |
| T20 | 5.87 | 5.53 | 5.70 |
| T21 | 7.47 | 6.87 | 7.17 |
| T22 | 6.20 | 6.13 | 6.17 |
| T23 | 6.13 | 6.20 | 6.17 |
| T24 | 6.20 | 5.93 | 6.07 |
| T25 | 5.20 | 5.53 | 5.37 |
| T26 | 6.20 | 5.93 | 6.07 |
| T27 | 5.67 | 5.73 | 5.70 |
| T28 | 6.73 | 6.27 | 6.50 |
| T29 | 5.67 | 5.33 | 5.50 |
| T30 | 6.40 | 6.60 | 6.50 |
| Mean | 6.05 | 5.98 | 6.02 |
| SE of mean | 0.22 | 0.17 | 0.14 |
| CD (5%) Between genotypes | 0.63 | 0.48 | 0.39 |
| CD (5%) Open x Shade | NS | | |
| CD (5%) Genotype x Condition | NS | | |

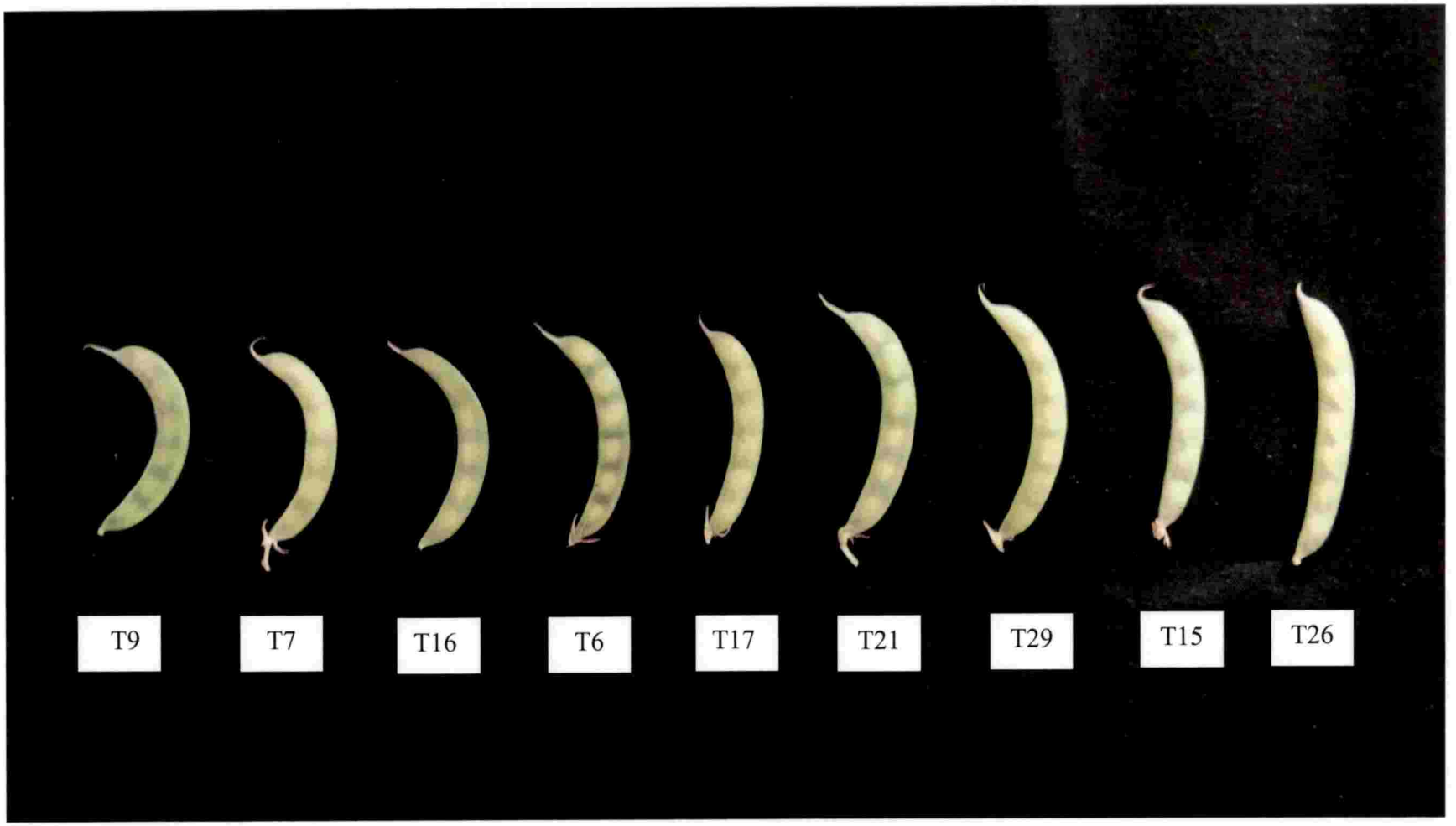



Plate 3. Variability in pod size and shape

#### *4.1.1.9. Variability in pod length:*

The results from Table 10 revealed no significant difference in pod length for horsegram genotypes when grown under open and partially shaded conditions. Also there was no significant interaction between the genotypes and the condition. The genotype T15 (5.68cm) showed highest pod length under open conditions and the least pod length was given by the genotype T9 (4.32cm). Under partially shaded conditions, longer pods were observed for genotype T26 (5.77cm) while shorter pods were produced by the genotype T18 (4.24cm). In pooled analysis, the genotype T26 (5.71cm) recorded the highest pod length followed by genotypes T15 (5.64cm), T25 (5.50cm), T29 (5.57cm) and T21 (5.49cm). Minimum length of pod was exhibited by the genotype T9 (4.35cm) which was on par with other genotypes like T7 (4.40cm), T24 (4.40cm), T18 (4.41cm) and T6 (4.44cm).

#### *4.1.1.10. Variability in 100 seed weight:*

The results of variability in 100 seed weight is depicted in the Table 11.

The genotypes showed no significant difference in their performance for this trait under open and partially shaded conditions. Pooled analysis of the genotypes under the two conditions revealed that high value for 100 seed weight was shown by the genotype T17 (3.69g) which was significantly different from all other genotypes except genotype T12 (3.68g). The least value for 100 seed weight was recorded for the genotype T18 (2.74g) and this was found to be significantly different from all other genotypes included in the study.

#### *4.1.1.11. Variability in Plant height:*

There existed no significant difference in the performance of the genotypes under both conditions. In pooled analysis, maximum plant height was exhibited by the genotype T8 (146.75cm) which differed significantly from all other genotypes except T13 (143.18cm), whereas least plant height was recorded for the genotype T19 (83.68cm) which was on par with the genotype T28 (85.06cm). The results showed that there was significant interaction between genotypes and condition for plant height. (Table 12)

Table 10. Pod length of different genotypes of horsegram under open and partially shaded conditions

| **Genotypes** | **Pod length (cm)** | | |
|---|---|---|---|
| | Open | Shade | Pooled |
| T1 | 5.40 | 5.33 | 5.36 |
| T2 | 5.43 | 5.30 | 5.37 |
| T3 | 5.10 | 4.93 | 5.02 |
| T4 | 5.49 | 5.34 | 5.41 |
| T5 | 5.17 | 5.11 | 5.14 |
| T6 | 4.50 | 4.37 | 4.44 |
| T7 | 4.31 | 4.48 | 4.40 |
| T8 | 5.20 | 5.24 | 5.22 |
| T9 | 4.32 | 4.38 | 4.35 |
| T10 | 4.90 | 4.85 | 4.88 |
| T11 | 4.89 | 4.62 | 4.76 |
| T12 | 5.33 | 5.19 | 5.26 |
| T13 | 5.09 | 5.27 | 5.18 |
| T14 | 5.24 | 5.16 | 5.20 |
| T15 | 5.68 | 5.60 | 5.64 |
| T16 | 4.87 | 4.53 | 4.70 |
| T17 | 4.83 | 4.85 | 4.84 |
| T18 | 4.57 | 4.24 | 4.41 |
| T19 | 5.29 | 5.41 | 5.35 |
| T20 | 5.23 | 5.25 | 5.24 |
| T21 | 5.58 | 5.39 | 5.49 |
| T22 | 4.89 | 5.11 | 5.00 |
| T23 | 5.15 | 5.21 | 5.18 |
| T24 | 4.35 | 4.45 | 4.40 |
| T25 | 5.63 | 5.38 | 5.50 |
| T26 | 5.65 | 5.77 | 5.71 |
| T27 | 5.45 | 5.48 | 5.46 |
| T28 | 5.42 | 5.18 | 5.30 |
| T29 | 5.52 | 5.63 | 5.57 |
| T30 | 5.11 | 4.96 | 5.04 |
| Mean | 5.12 | 5.07 | 5.09 |
| SE of mean | 0.13 | 0.10 | 0.083 |
| CD (5%) Between genotypes | 0.38 | 0.28 | 0.233 |
| CD (5%) Open x Shade | NS | | |
| CD (5%) Genotype x Condition | NS | | |


Plate 4. Variability in grain colour

Table 11. 100 seed weight of different genotypes of horsegram under open and partially shaded conditions

| Genotypes | 100 seed weight (g) | | |
|---|---|---|---|
| | Open | Shade | Pooled |
| T1 | 3.29 | 3.38 | 3.34 |
| T2 | 3.47 | 3.42 | 3.45 |
| T3 | 3.50 | 3.45 | 3.47 |
| T4 | 3.13 | 3.11 | 3.12 |
| T5 | 2.88 | 2.87 | 2.88 |
| T6 | 3.19 | 3.24 | 3.22 |
| T7 | 3.01 | 2.95 | 2.98 |
| T8 | 3.26 | 3.20 | 3.23 |
| T9 | 3.14 | 3.11 | 3.13 |
| T10 | 3.19 | 3.15 | 3.17 |
| T11 | 3.58 | 3.50 | 3.54 |
| T12 | 3.68 | 3.67 | 3.68 |
| T13 | 2.92 | 3.04 | 2.98 |
| T14 | 3.34 | 3.40 | 3.37 |
| T15 | 3.39 | 3.32 | 3.35 |
| T16 | 3.44 | 3.44 | 3.44 |
| T17 | 3.65 | 3.72 | 3.69 |
| T18 | 2.76 | 2.72 | 2.74 |
| T19 | 3.19 | 3.23 | 3.21 |
| T20 | 3.30 | 3.31 | 3.31 |
| T21 | 3.23 | 3.20 | 3.22 |
| T22 | 2.94 | 2.98 | 2.96 |
| T23 | 3.33 | 3.28 | 3.30 |
| T24 | 3.30 | 3.24 | 3.27 |
| T25 | 3.04 | 3.01 | 3.03 |
| T26 | 3.11 | 3.12 | 3.11 |
| T27 | 2.93 | 2.86 | 2.89 |
| T28 | 3.32 | 3.24 | 3.28 |
| T29 | 3.04 | 3.02 | 3.03 |
| T30 | 3.21 | 3.23 | 3.22 |
| Mean | 3.22 | 3.21 | 3.22 |
| SE of mean | 0.04 | 0.02 | 0.02 |
| CD (5%) Between genotypes | 0.12 | 0.05 | 0.07 |
| CD (5%) Open x Shade | NS | | |
| CD (5%) Genotype x Condition | NS | | |

Table 12. Plant height of different genotypes of horsegram under open and partially shaded conditions

| Genotypes | Plant height (cm) | | |
|---|---|---|---|
| | Open | Shade | Pooled |
| T1 | 113.23 | 107.97 | 110.60 |
| T2 | 109.70 | 124.87 | 117.28 |
| T3 | 107.53 | 99.73 | 103.63 |
| T4 | 122.22 | 121.87 | 122.04 |
| T5 | 124.46 | 127.37 | 125.92 |
| T6 | 121.93 | 129.97 | 125.95 |
| T7 | 113.73 | 113.47 | 113.60 |
| T8 | 140.80 | 152.70 | 146.75 |
| T9 | 94.90 | 100.43 | 97.67 |
| T10 | 119.90 | 111.37 | 115.63 |
| T11 | 104.55 | 122.13 | 113.34 |
| T12 | 119.20 | 116.83 | 118.02 |
| T13 | 147.57 | 138.80 | 143.18 |
| T14 | 110.70 | 121.77 | 116.23 |
| T15 | 126.17 | 130.70 | 128.43 |
| T16 | 101.07 | 93.53 | 97.30 |
| T17 | 132.46 | 140.60 | 136.53 |
| T18 | 129.13 | 133.13 | 131.13 |
| T19 | 85.13 | 82.23 | 83.68 |
| T20 | 107.53 | 112.63 | 110.08 |
| T21 | 99.24 | 87.20 | 93.22 |
| T22 | 107.07 | 93.17 | 100.12 |
| T23 | 96.60 | 104.73 | 100.67 |
| T24 | 109.70 | 101.60 | 105.65 |
| T25 | 118.50 | 96.70 | 107.60 |
| T26 | 112.73 | 113.73 | 113.23 |
| T27 | 106.52 | 109.20 | 107.86 |
| T28 | 83.68 | 86.43 | 85.06 |
| T29 | 105.88 | 105.80 | 105.84 |
| T30 | 121.20 | 125.63 | 123.42 |
| Mean | 113.10 | 113.54 | 113.32 |
| SE of mean | 3.80 | 2.92 | 2.41 |
| CD (5%) Between genotypes | 10.78 | 8.28 | 6.76 |
| CD (5%) Open x Shade | NS | | |
| CD (5%) Genotype x Condition | 9.57 | | |

### *4.1.1.12. Variability in Seed yield plant$^{-1}$:*

The data on seed yield plant$^{-1}$ are presented in the Table 13.

There existed significant difference in the performance of genotypes between open and partially shaded conditions for seed yield plant$^{-1}$. Highest yield was recorded for the genotype T12 in pooled analysis as well as under open and partially shaded conditions, whereas least yield was observed for the genotype T26. Under open conditions, T12 (20.08g) gave higher yield plant$^{-1}$ followed by the genotypes T2 (19.82g), T21 (18.22g) and T6 (17.78), while less yield plant $^{-1}$ was exhibited by the genotype T26 (7.76g) which was on par with other genotypes like T19 (8.92g), T27 (9.46g), T29 (9.68g), T13 (9.58g) and T11 (9.62g). Under partially shaded conditions, genotype T12 (18.36g) produced highest yield plant$^{-1}$ and this was on par with genotypes T2 (17.75g), T17 (16.99g), T6 (16.85g), T8 (16.67g) and T18 (16.10) whereas lowest yield plant$^{-1}$ was given by genotype T26 (7.43g) followed by T29 (8.09g), T13 (8.46g), T16 (8.96g) and T19 (9.30g).

In pooled analysis also, the genotype T12 (19.22g) gave the maximum yield plant$^{-1}$, which was significantly different from all other genotypes except T2 (18.79g). Minimum values for yield plant$^{-1}$ was exhibited by the genotype T26 (7.59g) followed by genotypes T29 (8.89g) and T19 (9.11g). The results also show that there was no significant interaction between the genotype and the condition for this trait.

### *4.1.1.13. Variability in Crop duration:*

The genotypes showed significant difference in their performance under open and partially shaded conditions with respect to this character. Minimum crop duration was given by the genotype T30 under open and partially shaded conditions as well as in pooled analysis. Under open conditions, least duration for the crop was exhibited by the genotype T30 (121.40) followed by genotypes like T24 (124.80), T27 (125.00), T22 (125.13) and T28 (127.20). The genotype T19 (153.47) took maximum duration, which was on par with T5 (152.43), T6 (152.53), T7 (152.24),

Table 13. Seed yield plant$^{-1}$ of different genotypes of horsegram under open and partially shaded conditions

| **Genotypes** | **Seed yield plant$^{-1}$** | | |
|---|---|---|---|
| | Open | Shade | Pooled |
| T1 | 11.25 | 10.97 | 11.11 |
| T2 | 19.82 | 17.75 | 18.79 |
| T3 | 12.68 | 12.83 | 12.76 |
| T4 | 12.15 | 10.58 | 11.37 |
| T5 | 13.90 | 10.43 | 12.16 |
| T6 | 17.78 | 16.85 | 17.31 |
| T7 | 13.69 | 11.26 | 12.47 |
| T8 | 14.90 | 16.67 | 15.79 |
| T9 | 13.76 | 12.79 | 13.28 |
| T10 | 11.83 | 11.71 | 11.77 |
| T11 | 9.62 | 10.53 | 10.08 |
| T12 | 20.08 | 18.36 | 19.22 |
| T13 | 9.58 | 8.46 | 9.02 |
| T14 | 11.12 | 10.87 | 11.00 |
| T15 | 14.54 | 14.15 | 14.34 |
| T16 | 11.09 | 8.96 | 10.03 |
| T17 | 17.19 | 16.99 | 17.09 |
| T18 | 15.87 | 16.10 | 15.99 |
| T19 | 8.92 | 9.30 | 9.11 |
| T20 | 13.40 | 11.48 | 12.44 |
| T21 | 18.22 | 14.39 | 16.31 |
| T22 | 10.41 | 10.34 | 10.38 |
| T23 | 12.89 | 11.22 | 12.06 |
| T24 | 11.33 | 10.68 | 11.00 |
| T25 | 16.39 | 13.33 | 14.86 |
| T26 | 7.76 | 7.43 | 7.59 |
| T27 | 9.46 | 10.64 | 10.05 |
| T28 | 13.08 | 10.38 | 11.73 |
| T29 | 9.68 | 8.09 | 8.89 |
| T30 | 17.02 | 13.17 | 15.10 |
| Mean | 13.31 | 12.22 | 12.77 |
| SE of mean | 0.88 | 0.86 | 0.62 |
| CD (5%) Between genotypes | 2.50 | 2.45 | 1.73 |
| CD (5%) Open x Shade | 0.45 | | |
| CD (5%) Genotype x Condition | NS | | |

Fig.1. Comparative mean seed yield performance of 30 horsegram genotypes under open and partially shaded conditions

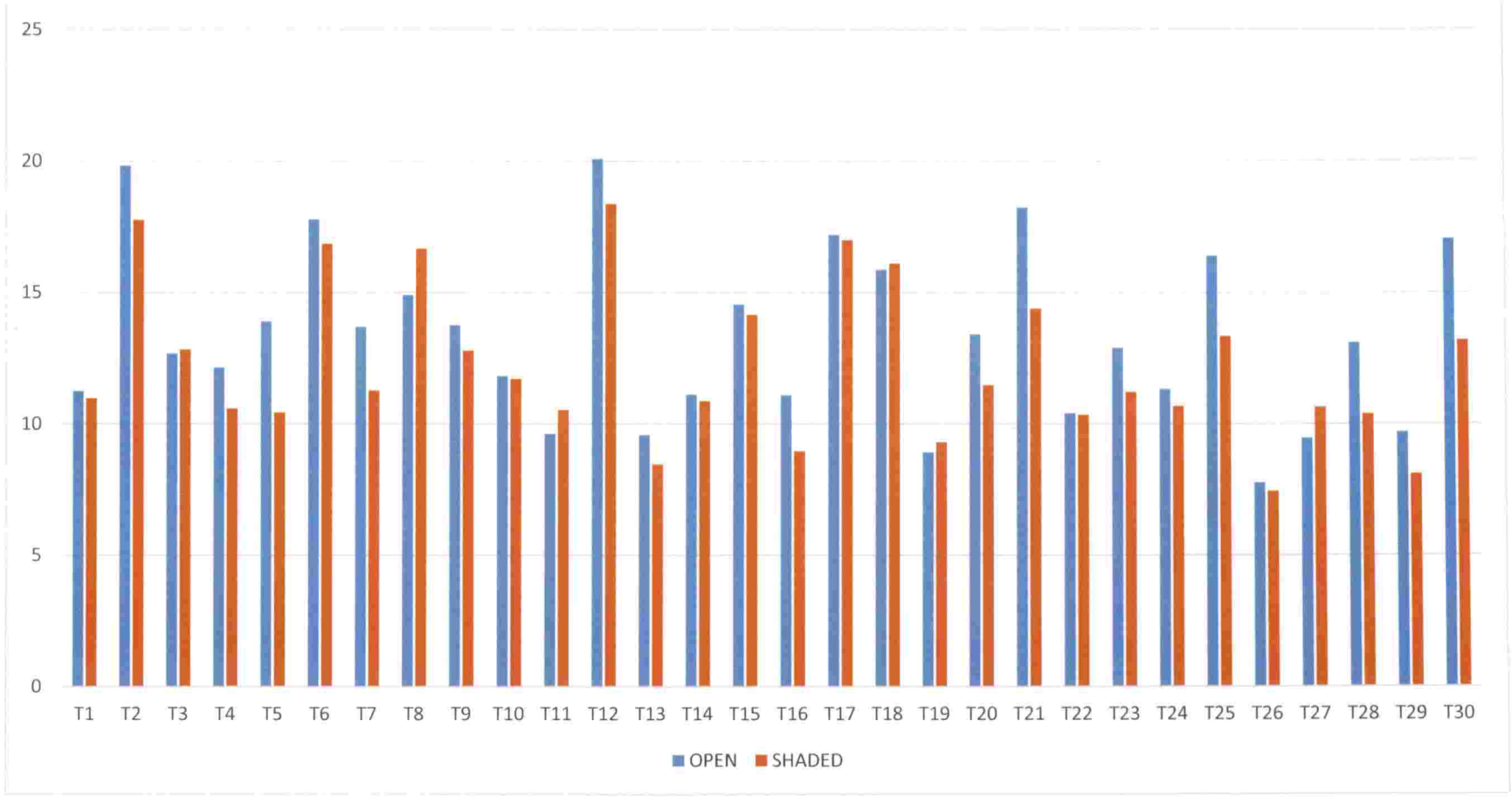


Table 14. Crop duration of different genotypes of horsegram under open and partially shaded conditions

| Genotypes | Crop duration | | |
|---|---|---|---|
| | Open | Shade | Pooled |
| T1 | 148.27 | 150.13 | 149.20 |
| T2 | 135.27 | 136.87 | 136.07 |
| T3 | 138.87 | 140.27 | 139.57 |
| T4 | 137.73 | 140.80 | 139.27 |
| T5 | 152.43 | 153.67 | 153.05 |
| T6 | 152.53 | 155.53 | 154.03 |
| T7 | 152.24 | 153.00 | 152.62 |
| T8 | 144.33 | 148.23 | 146.28 |
| T9 | 138.20 | 140.47 | 139.33 |
| T10 | 148.13 | 148.87 | 148.50 |
| T11 | 135.90 | 136.47 | 136.18 |
| T12 | 141.87 | 144.07 | 142.97 |
| T13 | 135.23 | 137.67 | 136.45 |
| T14 | 146.40 | 149.20 | 147.80 |
| T15 | 144.87 | 144.73 | 144.80 |
| T16 | 140.33 | 142.47 | 141.40 |
| T17 | 152.40 | 155.20 | 153.80 |
| T18 | 145.80 | 149.20 | 147.50 |
| T19 | 153.47 | 154.87 | 154.17 |
| T20 | 140.33 | 141.80 | 141.07 |
| T21 | 133.60 | 137.13 | 135.37 |
| T22 | 125.13 | 127.80 | 126.47 |
| T23 | 127.67 | 129.13 | 128.40 |
| T24 | 124.80 | 125.73 | 125.27 |
| T25 | 135.27 | 138.87 | 137.07 |
| T26 | 128.47 | 130.67 | 129.57 |
| T27 | 125.00 | 127.20 | 126.10 |
| T28 | 127.20 | 127.63 | 127.42 |
| T29 | 126.47 | 129.07 | 127.77 |
| T30 | 121.40 | 122.67 | 122.03 |
| Mean | 138.65 | 140.65 | 139.65 |
| SE of mean | 2.22 | 2.23 | 1.58 |
| CD (5%) Between genotypes | 6.30 | 6.34 | 4.44 |
| CD (5%) Open x Shade | 1.15 | | |
| CD (5%) Genotype x Condition | NS | | |

Plate 5. Superior genotype of horsegram identified (T12 - Palakkad Local)

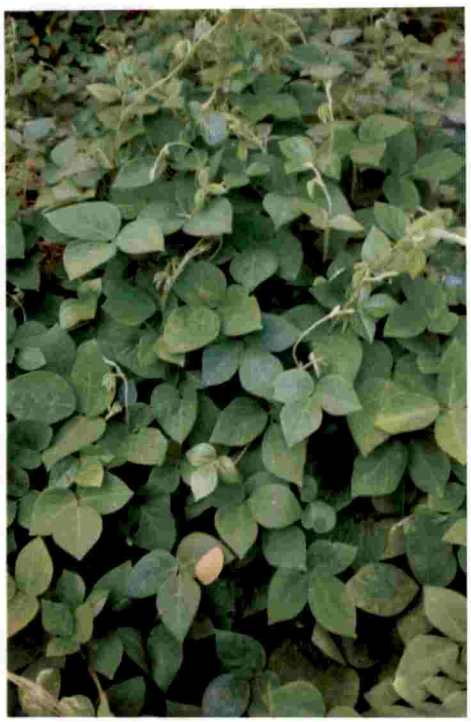


Plate 6. Superior genotype of horsegram identified (T2 - Chintada Local)

Plate 7. Superior genotype of horsegram identified (T21 – IC22762)

T17 (152.40) and T1 (148.27). Minimum days for the completion of the crop in the field was taken by T30 (122.67) under partially shaded conditions as well, followed by T27 (125.00), T22 (125.13), T24 (124.80) and T28 (127.20), while maximum number of days was taken by the genotype T6 (155.53).

In pooled analysis, shortest crop duration was given by the genotype T30 (122.03) which was on par with T24 (125.27), T27 (126.10) and T22 (126.47), whereas longest crop duration was exhibited by genotype T19 (154.17) followed by T6 (154.03), T17 (153.80), T5 (153.05) and T7 (152.62).

Table 14 reveals the data on the duration of different horsegram genotypes.

***4.1.1.14. Variability in Harvest Index:***

From Table 15 it is clear that there was significant difference in the performance of the genotype under the two conditions. Under open conditions, highest harvest index was recorded for the genotype T12 (25.71) followed by genotypes T2 (24.29), T30 (23.94), T6 (23.09), T17 (22.70), T18 (21.01) and T21 (21.97), whereas least harvest index was recorded for the genotype T10 (12.27). Under partially shaded conditions, the genotype T17 (25.34) recorded the highest harvest index, which was on par with other genotypes such as T21 (23.01), T12 (22.04), T2 (21.04) and T18 (21.73), while the lowest harvest index was observed for the genotype T16 (9.24).

From pooled analysis, highest harvest index was observed for the genotype T17 (24.02), which was on par with genotypes T12 (23.88), T6 (21.55), T2 (22.66), T21 (22.49) and T18 (21.37), whereas lowest value for harvest index was exhibited by the genotype T10 (11.08).

Table 15. Harvest index of different genotypes of horsegram under open and partially shaded conditions

| Genotypes | Harvest index (%) | | |
|---|---|---|---|
| | Open | Shade | Pooled |
| T1 | 15.76 | 16.48 | 16.12 |
| T2 | 24.29 | 21.04 | 22.66 |
| T3 | 16.37 | 19.12 | 17.75 |
| T4 | 17.15 | 15.74 | 16.45 |
| T5 | 16.87 | 14.09 | 15.48 |
| T6 | 23.09 | 20.01 | 21.55 |
| T7 | 17.53 | 13.69 | 15.61 |
| T8 | 19.02 | 22.79 | 20.90 |
| T9 | 16.13 | 14.94 | 15.54 |
| T10 | 12.27 | 9.88 | 11.08 |
| T11 | 14.19 | 14.91 | 14.55 |
| T12 | 25.71 | 22.04 | 23.88 |
| T13 | 19.65 | 15.15 | 17.40 |
| T14 | 15.31 | 10.82 | 13.07 |
| T15 | 18.52 | 14.76 | 16.64 |
| T16 | 13.00 | 9.24 | 11.12 |
| T17 | 22.70 | 25.34 | 24.02 |
| T18 | 21.01 | 21.73 | 21.37 |
| T19 | 14.71 | 16.11 | 15.41 |
| T20 | 17.94 | 14.73 | 16.33 |
| T21 | 21.97 | 23.01 | 22.49 |
| T22 | 16.57 | 19.27 | 17.92 |
| T23 | 18.21 | 16.32 | 17.27 |
| T24 | 16.98 | 16.89 | 16.94 |
| T25 | 19.01 | 11.51 | 15.26 |
| T26 | 14.15 | 13.56 | 13.85 |
| T27 | 13.01 | 14.37 | 13.69 |
| T28 | 15.65 | 13.89 | 14.77 |
| T29 | 15.25 | 15.08 | 15.17 |
| T30 | 23.94 | 19.78 | 21.86 |
| Mean | 17.87 | 16.54 | 17.20 |
| SE of mean | 1.67 | 1.64 | 1.16 |
| CD (5%) Between genotypes | 4.74 | 4.64 | 3.26 |
| CD (5%) Open x Shade | 0.84 | | |
| CD (5%) Genotype x Condition | NS | | |

Table 16. Crude protein content of different genotypes of horsegram under open and partially shaded condition

| Genotypes | Crude protein (%) | | |
|---|---|---|---|
| | Open | Shade | Pooled |
| T1 | 25.52 | 26.73 | 26.13 |
| T2 | 24.15 | 25.63 | 24.89 |
| T3 | 22.92 | 24.92 | 23.92 |
| T4 | 26.33 | 26.54 | 26.44 |
| T5 | 27.19 | 27.31 | 27.25 |
| T6 | 25.17 | 24.04 | 24.61 |
| T7 | 26.42 | 25.69 | 26.05 |
| T8 | 26.53 | 27.13 | 26.83 |
| T9 | 24.56 | 24.69 | 24.63 |
| T10 | 22.60 | 23.63 | 23.11 |
| T11 | 27.75 | 27.08 | 27.42 |
| T12 | 25.40 | 25.77 | 25.59 |
| T13 | 25.85 | 27.00 | 26.42 |
| T14 | 28.92 | 29.04 | 28.98 |
| T15 | 23.93 | 22.23 | 23.08 |
| T16 | 26.30 | 25.98 | 26.14 |
| T17 | 22.83 | 23.15 | 22.99 |
| T18 | 24.41 | 25.48 | 24.95 |
| T19 | 27.33 | 28.40 | 27.86 |
| T20 | 26.52 | 27.33 | 26.93 |
| T21 | 28.21 | 27.79 | 28.00 |
| T22 | 26.10 | 26.58 | 26.34 |
| T23 | 27.27 | 29.17 | 28.22 |
| T24 | 26.36 | 26.07 | 26.21 |
| T25 | 24.91 | 24.81 | 24.86 |
| T26 | 25.95 | 25.60 | 25.78 |
| T27 | 28.76 | 28.21 | 28.48 |
| T28 | 25.59 | 25.85 | 25.72 |
| T29 | 24.09 | 24.04 | 24.07 |
| T30 | 23.37 | 23.33 | 23.35 |
| Mean | 25.71 | 25.97 | 25.84 |
| SE of mean | 0.92 | 0.85 | 0.63 |
| CD (5%) Between genotypes | 2.61 | 2.40 | 1.75 |
| CD (5%) Open x Shade | NS | | |
| CD (5%) Genotype x Condition | NS | | |

#### *4.1.1.15. Variability in Crude protein content:*

The results of protein content analysis are given in the Table 16.

The results revealed no significant difference in the crude protein content for horsegram seeds under open and partially shaded conditions. But in pooled analysis, maximum protein content was observed for the genotype T14 (28.98) followed by the genotypes T23 (28.22), T27 (28.48), T21 (28.00) and T19 (27.86). Genotype T17 (22.99) recorded the lowest protein content, which was on par with genotypes like T15 (23.08), T3 (23.92), T10 (23.11), T30 (23.35), T29 (24.07) and T9 (24.63).

## 4.2. STATISTICAL ANALYSIS

### 4.2.1 Genetic Parameters

The different genetic parameters such as range, phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance for yield and yield attributing characters under open and partially shaded conditions are given in the Table 17 and 18, respectively.

#### 4.2.1.1. *Under open condition:*

The results showed that there existed wide range of variation among all the characters included in the study under open condition. Characters like number of nodes plant$^{-1}$ (80.60 – 148.40), plant height (83.68 – 147.57) and number of pods plant$^{-1}$ (45.60 – 105.27) exhibited wide range of variation. However, the range of characters such as days to sprouting (2.07 - 3.60), pod length (4.32 – 5.68) and 100-seed weight (2.76 – 3.68) were found to be generally low.

High GCV and PCV were noticed for characters like yield plant$^{-1}$(23.98, 26.57) followed by number of pods plant$^{-1}$(23.66, 24.35) whereas moderate GCV and PCV were recorded for characters like days to sprouting, days to 50% flowering, number of nodes plant$^{-1}$ and plant height. Days to maturity, number of seeds pod$^{-1}$, pod length, 100-sed weight, crop duration and crude protein content

Table 17. Estimates of genetic parameters for yield and yield contributing characters of horsegram under open condition

| Characters | Mean | Range | PCV | GCV | Heritability | GA (5%) |
|---|---|---|---|---|---|---|
| No. of days for sprouting | 2.64 | 2.07 - 3.60 | 18.18 | 15.51 | 72.80 | 27.26 |
| No of primary branches plant$^{-1}$ | 9.11 | 5.60 – 12.47 | 26.17 | 12.82 | 23.99 | 12.93 |
| No. of secondary branches plant$^{-1}$ | 13.54 | 10.53 – 18.93 | 24.04 | 14.59 | 36.84 | 18.24 |
| Days to 50% flowering | 65.66 | 46.33 – 80.67 | 15.54 | 14.30 | 84.73 | 27.12 |
| Days to maturity | 126.49 | 106.60 – 142.40 | 8.42 | 7.98 | 89.70 | 15.56 |
| No. of nodes plant$^{-1}$ | 112.98 | 80.60 – 148.40 | 15.88 | 14.49 | 83.20 | 27.22 |
| No. of pods plant$^{-1}$ | 73.47 | 45.60 – 105.27 | 24.35 | 23.66 | 94.39 | 47.35 |
| No. of seeds pod$^{-1}$ | 6.05 | 5.13 – 7.47 | 11.47 | 9.53 | 69.04 | 16.32 |
| Pod length | 5.12 | 4.32 – 5.68 | 8.69 | 7.43 | 73.19 | 13.10 |
| 100 seed weight | 3.23 | 2.76 – 3.68 | 7.35 | 6.97 | 89.85 | 13.61 |
| Plant height | 113.10 | 83.68 – 147.57 | 13.69 | 12.39 | 81.92 | 23.10 |
| Yield plant$^{-1}$ | 13.31 | 7.76 – 20.08 | 26.57 | 23.98 | 81.44 | 44.58 |
| Harvest index | 17.87 | 12.27 – 25.71 | 23.99 | 17.73 | 54.56 | 26.97 |
| Crop duration | 138.65 | 121.40 – 153.47 | 7.42 | 6.89 | 86.06 | 13.16 |
| Crude protein | 25.71 | 22.60 – 28.92 | 8.33 | 5.57 | 44.65 | 7.67 |

Fig.2. GCV and PCV for 15 characters in horsegram genotypes under open condition.

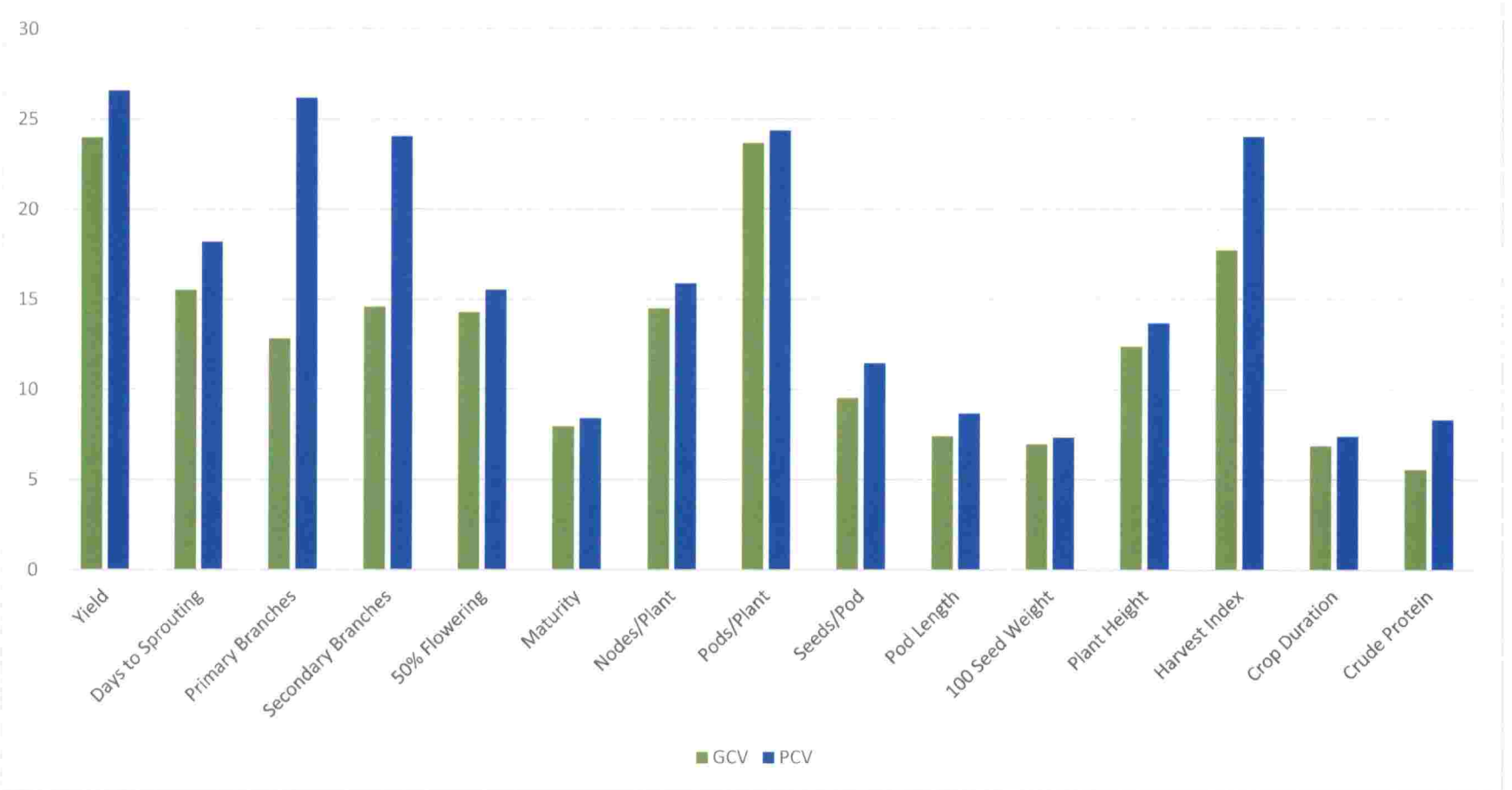
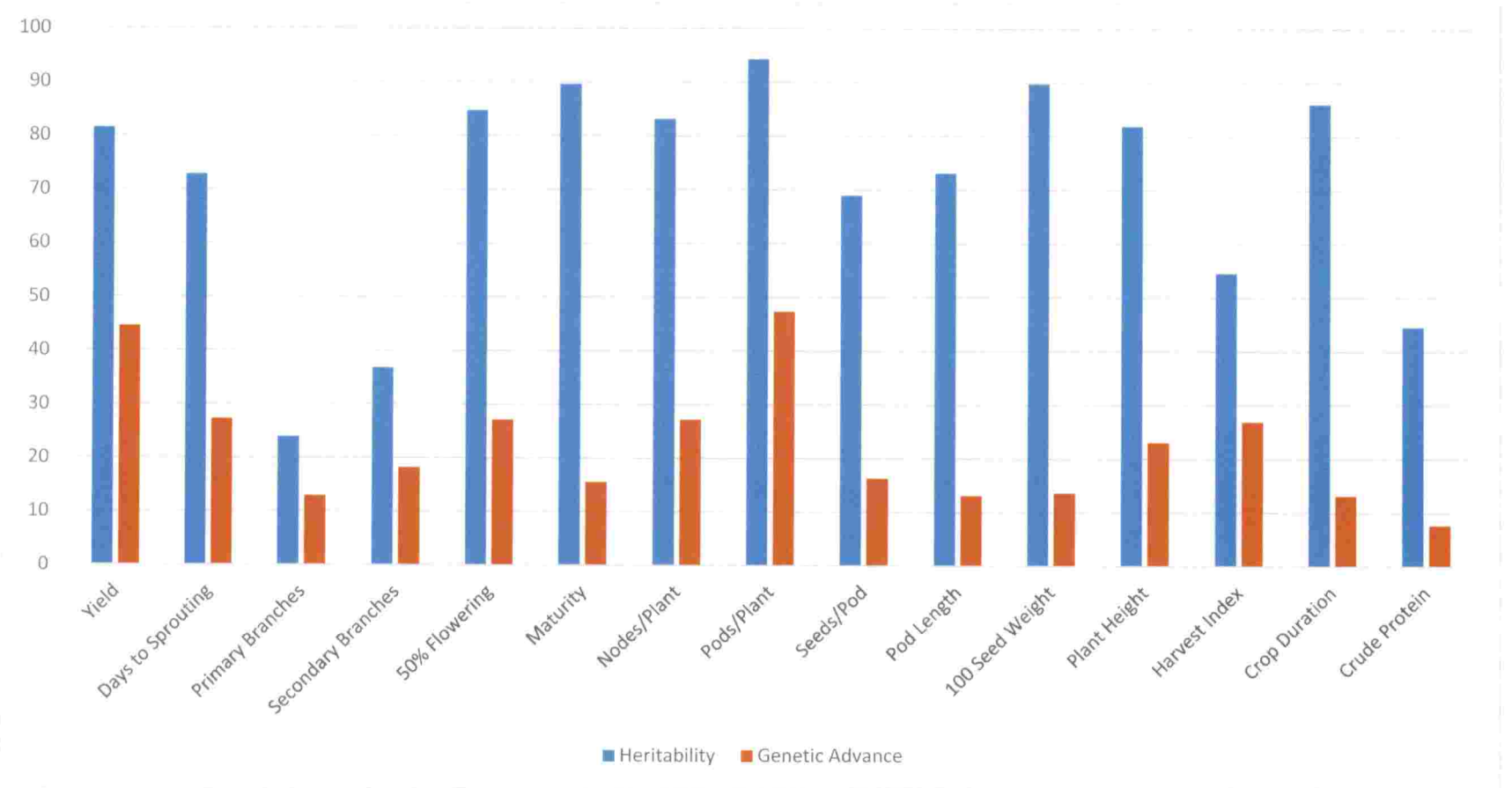


Fig.3. Heritability and genetic advance for 15 characters in horsegram genotypes under open condition



recorded the lowest GCV and PCV. All other characters in the study exhibited moderate PCV. It was also observed that the PCV values were generally higher than their corresponding GCV values for all the characters studied. (Fig.2)

Heritability was high for most of the characters, with number of pods plant$^{-1}$(94.39) recording the highest heritability under open conditions followed by 100-seed weight (89.85), days to maturity (89.70) and crop duration (86.06). Moderate heritability was exhibited by characters like harvest index (54.56), crude protein content (44.65) and number of secondary branches plant$^{-1}$ whereas low heritability was shown by number of primary branches plant$^{-1}$(23.99).

Genetic advance expressed as percentage of mean was found to be highest for number of pods plant$^{-1}$(47.35) followed by seed yield plant$^{-1}$(44.58), days to sprouting (27.26), days to 50% flowering (27.12), number of nodes plant$^{-1}$(27.22), plant height (23.10) and harvest index (26.97). Low genetic advance as percentage of mean was recorded for the character crude protein content (7.67), while all other characters showed moderate genetic advance. (Fig.3)

Characters like days to sprouting, days to 50% flowering, number of nodes plant$^{-1}$, number of pod plant$^{-1}$ and plant height exhibited high heritability coupled with high genetic advance and hence direct phenotypic selection could be used for the improvement of these traits. Also it is evident from the Table 17 that two characters namely, yield plant$^{-1}$ and number of pods plant$^{-1}$ recorded high GCV, PCV, heritability and genetic advance which indicates their importance in further selection of the genotypes.

***4.2.1.2. Under partial shade:***

From Table 18, it is evident that under partially shaded conditions, wide range of variation existed for characters like plant height (82.23 – 152.70), number of pods plant$^{-1}$(41.67 – 98.87) and number of nodes plant$^{-1}$ (82.73 – 136.10),

Table 18. Estimates of genetic parameters for yield and yield contributing characters of horsegram under partially shaded condition

| Characters | Mean | Range | PCV | GCV | Heritability | GA (5%) |
|---|---|---|---|---|---|---|
| No. of days for sprouting | 2.58 | 2.00 – 3.47 | 17.58 | 15.08 | 73.57 | 26.65 |
| No of primary branches plant$^{-1}$ | 8.47 | 5.33 – 11.73 | 27.11 | 21.35 | 62.06 | 35.65 |
| No. of secondary branches plant$^{-1}$ | 13.65 | 9.30 – 17.80 | 23.84 | 18.35 | 59.27 | 29.11 |
| Days to 50% flowering | 67.81 | 48.67 – 81.67 | 15.05 | 13.83 | 84.46 | 26.17 |
| Days to maturity | 128.10 | 109.40 – 144.33 | 8.36 | 7.95 | 90.33 | 15.56 |
| No. of nodes plant$^{-1}$ | 111.15 | 82.73 – 136.10 | 15.61 | 13.76 | 77.76 | 25.00 |
| No. of pods plant$^{-1}$ | 70.65 | 41.67 – 98.87 | 23.86 | 23.30 | 95.33 | 46.86 |
| No. of seeds pod$^{-1}$ | 5.98 | 5.20 – 7.13 | 8.89 | 7.39 | 69.20 | 12.67 |
| Pod length | 5.07 | 4.24 – 5.77 | 8.59 | 7.88 | 84.15 | 14.89 |
| 100 seed weight | 3.21 | 2.72 – 3.72 | 7.21 | 7.15 | 98.19 | 14.59 |
| Plant height | 113.54 | 82.23 – 152.70 | 15.72 | 15.08 | 91.98 | 29.79 |
| Yield plant$^{-1}$ | 12.22 | 7.43 – 18.36 | 26.38 | 23.38 | 78.59 | 42.71 |
| Harvest index | 16.54 | 9.24 – 25.34 | 28.28 | 22.51 | 63.33 | 36.90 |
| Crop duration | 140.65 | 122.67 – 155.53 | 7.38 | 6.85 | 86.12 | 13.09 |
| Crude protein | 25.97 | 22.23 – 29.04 | 8.17 | 5.91 | 52.21 | 8.79 |

Fig.4. GCV and PCV for 15 characters of horsegram genotypes under partially shaded condition

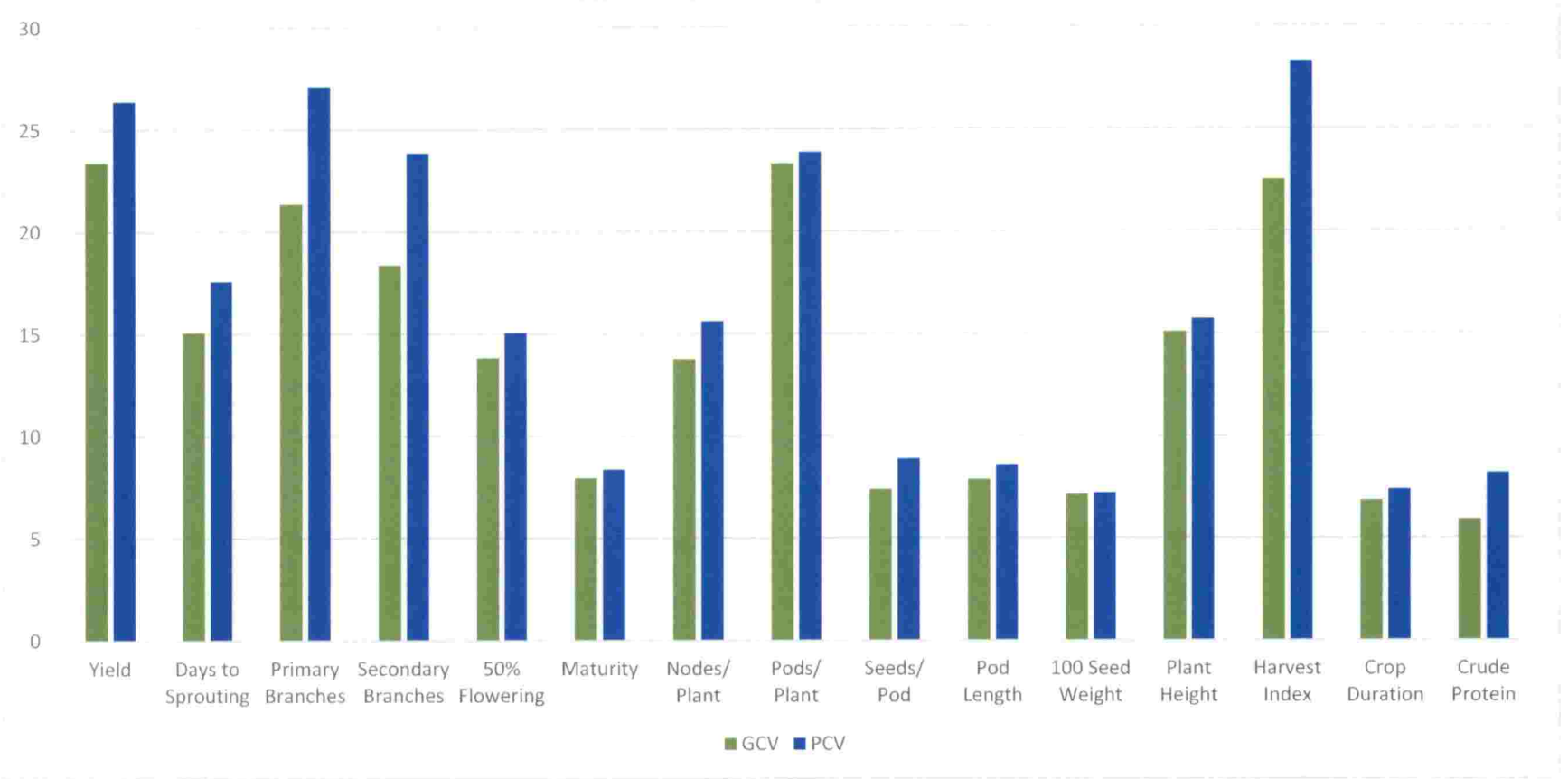
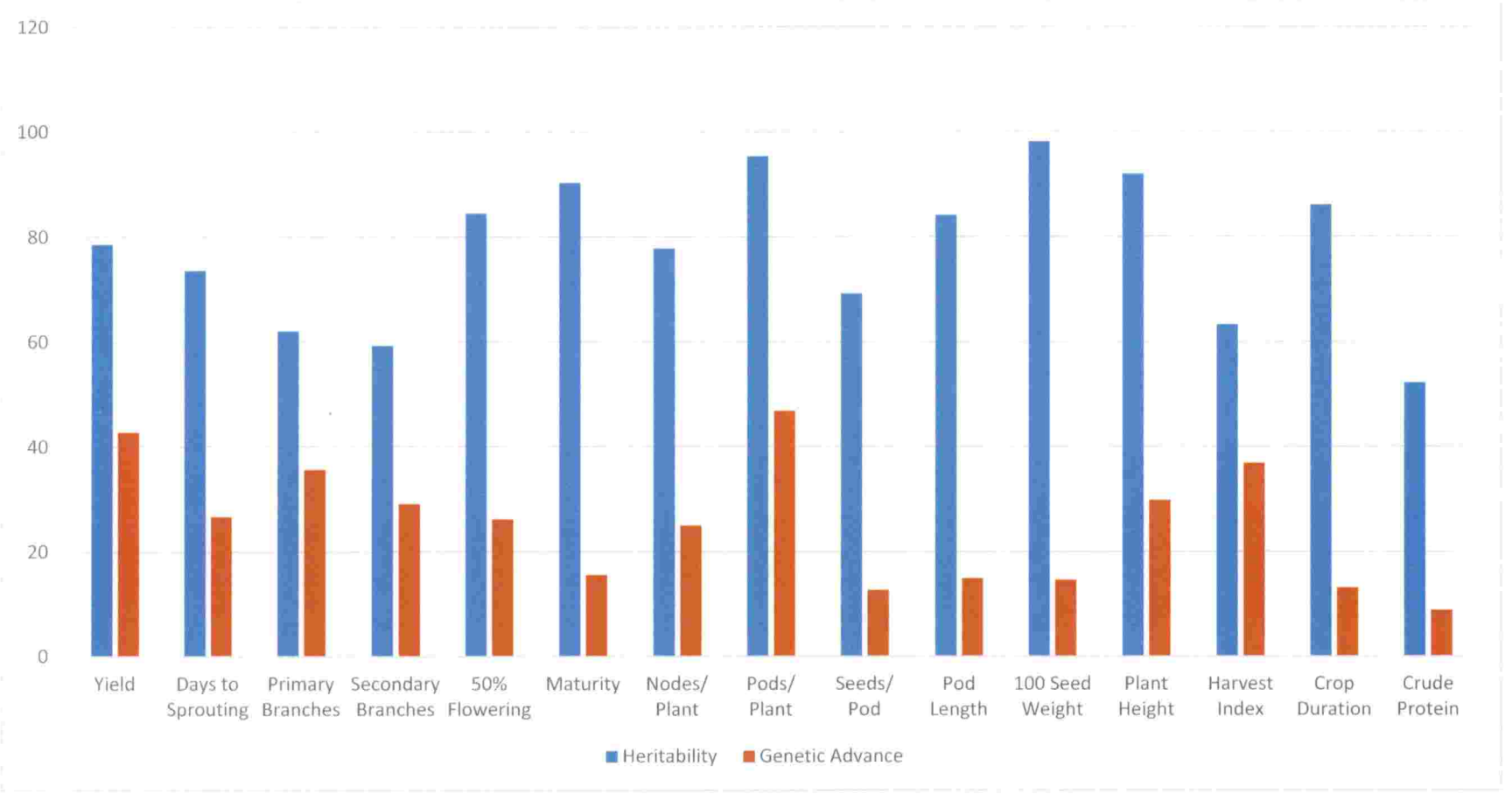


Fig.5. Heritability and genetic advance for 15 characters in horsegram under partially shaded condition



whereas characters like pod length (4.24 – 5.77), 100-seed weight (2.72 – 3.72) and number of seeds pod$^{-1}$(5.20 – 7.13) exhibited narrow range of variation.

Characters like yield plant$^{-1}$(23.38), number of pods plant$^{-1}$(23.30), harvest index (22.51) and number of primary branches plant$^{-1}$(21.35) showed high values for GCV, while high PCV was exhibited by harvest index (28.28), number of primary branches plant$^{-1}$(27.11), yield plant$^{-1}$ (26.38), number of pods plant$^{-1}$ (23.86) and number of secondary branches plant$^{-1}$ (23.84).

The characters such as days to maturity (7.5 and 8.36), number of seeds pod$^{-1}$(7.39 and 8.89), pod length (7.88 and 8.59), 100-seed weight (7.15 and 7.21), crop duration (6.85 and 7.38) and crude protein content (5.91 and 8.17) showed lower GCV and PCV values, while all other characters showed moderate GCV and PCV.

High heritability was reported for 100-seed weight (98.19) followed by number of pods plant$^{-1}$(95.33), plant height (91.98) and days to maturity (90.33). Almost all the characters exhibited high heritability values except for characters like number of secondary branches plant$^{-1}$(59.27) and crude protein (52.21), which showed moderate heritability.

Characters like days to maturity (15.56), pod length (14.89), 100-seed weight (14.59), number of seeds pod$^{-1}$(12.67) and crop duration (13.09) exhibited moderate genetic advance expressed as percentage of mean, while lowest genetic advance was shown by crude protein (8.79). Number of pods plant$^{-1}$(46.86) recorded the highest genetic advance followed by yield plant$^{-1}$(42.71).

From Table 18, it is clear that yield plant$^{-1}$, number of primary branches plant$^{-1}$, number of pods plant$^{-1}$ and harvest index recorded high GCV, PCV, heritability and genetic advance under partially shaded conditions.

Characters such as yield plant$^{-1}$, days to sprouting, days to 50% flowering, number of nodes plant$^{-1}$, number of pods plant$^{-1}$ and plant height exhibited high heritability coupled with high genetic advance under both the conditions, which reveals the importance of these characters during selection.

### 4.2.2. Correlation Studies

#### *4.2.2.1. Under open condition*

The genotypic and phenotypic correlation coefficients of different characters with seed yield and between themselves when grown under open conditions are given in Table 19 and Table 20, respectively.

Genotypic correlation studies revealed a strong positive correlation of yield with characters like number of pods plant$^{-1}$(0.934), number of nodes plant$^{-1}$(0.360), number of primary branches plant$^{-1}$(0.359), number of secondary branches plant$^{-1}$(0.326) and plant height (0.276), while crude protein content (-0.425) was found to be negatively correlated with seed yield.

Association of number of seeds pod$^{-1}$ (0.304) and pod length (0.410) with number of days for sprouting was found to be highly significant and positive, while days to 50% flowering (-0.593), days to maturity (-0.506) and crop duration (-0.515) had high negative correlation with days for sprouting.

The character number of primary branches plant$^{-1}$ exhibited a strong positive correlation with number of secondary branches plant$^{-1}$ (0.955), plant height (0.957) and number of nodes plant$^{-1}$ (0.864) whereas it was negatively correlated with 100-seed weight (-0.218).

A strong positive correlation was observed between number of secondary branches plant$^{-1}$ with characters like number of nodes plant$^{-1}$ (0.231), plant height (0.021), crop duration (0.472), days to maturity (0.419), number of pods plant$^{-1}$ (0.389) and days to 50% flowering (0.370).

Days to 50% flowering had high positive significant correlation with days to maturity (0.950), crop duration (0.936), plant height (0.356) and number of nodes plant$^{-1}$ (0.285) and a strong negative correlation with number of seeds pod$^{-1}$ (-0.469).

Table 19. Genotypic correlation of yield and yield contributing characters of horsegram under open condition

| | X1 | X2 | X3 | X4 | X5 | X6 | X7 | X8 | X9 | X10 | X11 | X12 | X13 | X14 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **X1** | 1 | | | | | | | | | | | | | |
| **X2** | -0.059 | 1 | | | | | | | | | | | | |
| **X3** | 0.359** | -0.175 | 1 | | | | | | | | | | | |
| **X4** | 0.326** | 0.035 | 0.955** | 1 | | | | | | | | | | |
| **X5** | 0.137 | -0.593** | 0.023 | 0.370** | 1 | | | | | | | | | |
| **X6** | 0.215* | -0.506** | -0.066 | 0.419** | 0.950** | 1 | | | | | | | | |
| **X7** | 0.360** | -0.022 | 0.864** | 0.231** | 0.285** | 0.332** | 1 | | | | | | | |
| **X8** | 0.934** | -0.030 | 0.524** | 0.389** | 0.209* | 0.289** | 0.402** | 1 | | | | | | |
| **X9** | 0.244* | 0.302** | 0.076 | -0.232* | -0.469** | -0.456** | -0.056 | -0.005 | 1 | | | | | |
| **X10** | -0.067 | 0.401** | 0.451** | 0.126 | -0.216* | -0.261* | 0.078 | -0.214* | 0.251* | 1 | | | | |
| **X11** | 0.260* | -0.177 | -0.218* | -0.051 | 0.205 | 0.131 | -0.147 | 0.033 | -0.113 | 0.039 | 1 | | | |
| **X12** | 0.276** | -0.148 | 0.957** | 0.021** | 0.356** | 0.311** | 0.900** | 0.412** | -0.221* | -0.041 | -0.188 | 1 | | |
| **X13** | 0.221* | -0.515** | -0.087 | 0.472** | 0.936** | 0.013** | 0.324** | 0.275** | -0.403** | -0.302** | 0.106 | 0.301** | 1 | |
| **X14** | -0.425** | -0.045 | -0.114 | -0.436** | -0.003 | -0.092 | -0.394** | -0.349** | 0.209* | 0.121 | -0.230* | -0.374** | -0.105 | 1 |

**X1** Yield
**X2** Days to Sprouting
**X3** No. of Primary Branches Plant$^{-1}$
**X4** No. of Secondary Branches Plant$^{-1}$
**X5** Days to 50 % flowering
**X6** Days to Maturity
**X7** No. of Nodes Plant$^{-1}$
**X8** No. of Pods Plant$^{-1}$
**X9** No. of Seeds Pod$^{-1}$
**X10** Pod Length
**X11** 100 Seed Weight
**X12** Plant Height
**X13** Crop Duration
**X14** Crude Protein

Table 20. Phenotypic correlation of yield and yield contributing characters of horsegram under open conditions

| | X1 | X2 | X3 | X4 | X5 | X6 | X7 | X8 | X9 | X10 | X11 | X12 | X13 | X14 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **X1** | 1 | | | | | | | | | | | | | |
| **X2** | 0.002 | 1 | | | | | | | | | | | | |
| **X3** | 0.247* | 0.062 | 1 | | | | | | | | | | | |
| **X4** | 0.244* | -0.091 | 0.297** | 1 | | | | | | | | | | |
| **X5** | 0.143 | -0.458** | 0.068 | 0.154 | 1 | | | | | | | | | |
| **X6** | 0.198 | -0.424** | 0.012 | 0.231* | 0.856** | 1 | | | | | | | | |
| **X7** | 0.266* | -0.008 | 0.404** | 0.671** | 0.257* | 0.279** | 1 | | | | | | | |
| **X8** | 0.847** | -0.020 | 0.239* | 0.242* | 0.181 | 0.260* | 0.354** | 1 | | | | | | |
| **X9** | 0.219* | 0.207 | 0.070 | -0.023 | -0.355** | -0.348** | -0.019 | 0.026 | 1 | | | | | |
| **X10** | -0.063 | 0.279** | 0.180 | 0.077 | -0.205 | -0.229* | 0.052 | -0.178 | 0.104 | 1 | | | | |
| **X11** | 0.217* | -0.160 | -0.133 | -0.071 | 0.197 | 0.115 | -0.117 | 0.035 | -0.074 | 0.032 | 1 | | | |
| **X12** | 0.199 | -0.125 | 0.434** | 0.575** | 0.272** | 0.295** | 0.761** | 0.353** | -0.184 | -0.026 | -0.174 | 1 | | |
| **X13** | 0.185 | -0.394** | 0.040 | 0.180 | 0.809** | 0.951** | 0.283** | 0.256* | -0.333** | -0.239* | 0.095 | 0.264* | 1 | |
| **X14** | -0.252* | -0.014 | -0.004 | -0.269* | 0.009 | -0.067 | -0.224* | -0.248* | 0.026 | 0.110 | -0.172 | -0.205 | -0.053 | 1 |

**X1** Yield
**X2** Days to Sprouting
**X3** No. of Primary Branches Plant $^{-1}$
**X4** No. of Secondary Branches Plant $^{-1}$
**X5** Days to 50 % flowering
**X6** Days to Maturity
**X7** No. of Nodes Plant $^{-1}$
**X8** No. of Pods Plant $^{-1}$
**X9** No. of Seeds Pod $^{-1}$
**X10** Pod Length
**X11** 100 Seed Weight
**X12** Plant Height
**X13** Crop Duration
**X14** Crude Protein

Days to maturity was found to be strongly and positively correlated with characters like crop duration (0.013), number of nodes plant$^{-1}$ (0.332), plant height (0.311) and number of pods plant$^{-1}$ (0.289).

Association between plant height (0.912), crop duration (0.324) and number of pods plant$^{-1}$(0.402) with number of nodes plant$^{-1}$ was highly significant and positive. Crude protein (-0.394) exhibited a strong negative correlation with number of nodes plant$^{-1}$.

Characters like plant height (0.412) and crop duration (0.275) showed highly significant positive correlation with number of pods plant$^{-1}$, while crude protein (-0.349) gave a strong negative correlation with number of pods plant$^{-1}$.

A strong negative correlation was observed for seeds pod$^{-1}$ with crop duration (-0.403). Pod length was negatively correlated with crop duration (-0.302) and 100-seed weight gave a negative correlation with crude protein content (-0.230). Plant height was also found to be negatively correlated to crude protein content (-0.374).

***4.2.2.2. Under partial shade***

The genotypic and phenotypic correlation coefficients of different characters with seed yield and between themselves under partially shaded conditions are given in Tables 21 and 22.

Under partially shaded conditions, the genotypic correlation with yield was highly significant and positive for characters like number of pods plant$^{-1}$(0.902), number of primary branches plant$^{-1}$ (0.520), plant height (90.464), crop duration (0.367), days to 50% flowering (0.362), days to maturity (0.334), number of secondary branches plant$^{-1}$ (0.293) and number of seeds pod$^{-1}$ (0.293). Pod length (-0.300) and crude protein content (-0.370) were found to exhibit a strong negative correlation with yield.

Association of days to sprouting with seeds pod (0.245) and pod length (0.266) was significant and positive, while characters like days to 50% flowering (-0.581), days to maturity (-0.452), plant height (-0.344) and crop duration (-0.447) had high negative correlation with days to sprouting.

Primary branches plant$^{-1}$ was strongly and positively correlated with number of secondary branches plant$^{-1}$ (0.915), number of nodes plant$^{-1}$ (0.830), plant height (0.741) and number of pods plant$^{-1}$ (0.390) whereas, secondary branches plant$^{-1}$ was strongly correlated with number of nodes plant$^{-1}$ (0.141), plant height (0.944) and days to 50% flowering (0.319).

Characters such as days to maturity (0.954), crop duration (0.932), plant height (0.403) and 100 seed weight (0.248) were found to have strong positive significant correlation with days to 50% flowering, while seeds pod$^{-1}$(-0.294) and pod length (-0.229) gave a strong negative correlation.

Days to maturity was positively correlated to crop duration (0.013), plant height (0.360) and number of pods plant$^{-1}$ (0.300) while a strong negative correlation of days to maturity was observed with seeds pod$^{-1}$ (-0.335) and pod length (-0.243).

Association of nodes plant$^{-1}$ with plant height (0.919) was found to be positive and highly significant as opposed to crude protein (-0.218) which had a negative correlation with nodes plant$^{-1}$.

Number of pods plant$^{-1}$ exhibited significant positive correlation with plant height (0.405) and crop duration (0.321), whereas it had strong negative correlation with crude protein content (-0.304).

A strong negative correlation was observed for number of seeds pod$^{-1}$ with correlation with crop duration (-0.334) and 100-seed weight (-0.243), while crop duration (0.354) exhibited strong positive correlation with plant height.

Table 21. Genotypic correlation of yield and yield contributing characters of horsegram under partially shaded conditions

| | X1 | X2 | X3 | X4 | X5 | X6 | X7 | X8 | X9 | X10 | X11 | X12 | X13 | X14 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **X1** | 1 | | | | | | | | | | | | | |
| **X2** | -0.133 | 1 | | | | | | | | | | | | |
| **X3** | 0.520** | -0.204 | 1 | | | | | | | | | | | |
| **X4** | 0.293** | -0.104 | 0.915** | 1 | | | | | | | | | | |
| **X5** | 0.362** | -0.581** | 0.203 | 0.319** | 1 | | | | | | | | | |
| **X6** | 0.334** | -0.452** | 0.186 | 0.214* | 0.954** | 1 | | | | | | | | |
| **X7** | 0.295** | -0.157 | 0.830** | 0.141** | 0.260* | 0.178 | 1 | | | | | | | |
| **X8** | 0.902** | -0.049 | 0.390** | 0.166 | 0.256* | 0.300** | 0.157 | 1 | | | | | | |
| **X9** | 0.293** | 0.245* | 0.142 | 0.074 | -0.294** | -0.335** | 0.215* | 0.168 | 1 | | | | | |
| **X10** | -0.300** | 0.266* | 0.192 | 0.107 | -0.229* | -0.243* | 0.093 | -0.257* | 0.140 | 1 | | | | |
| **X11** | 0.261* | -0.067 | 0.018 | -0.001 | 0.248* | 0.155 | -0.023 | -0.014 | -0.243* | -0.042 | 1 | | | |
| **X12** | 0.464** | -0.344** | 0.741** | 0.944** | 0.403** | 0.360** | 0.919** | 0.405** | 0.013 | -0.089 | 0.000 | 1 | | |
| **X13** | 0.367** | -0.447** | 0.207* | 0.207 | 0.932** | 0.013** | 0.161 | 0.321** | -0.334** | -0.312** | 0.120 | 0.354** | 1 | |
| **X14** | -0.370** | 0.134 | -0.112 | -0.203 | -0.074 | -0.077 | -0.218* | -0.304** | 0.019 | 0.216* | -0.138 | -0.255* | -0.079 | 1 |

**X1** Yield
**X2** Days to Sprouting
**X3** No. of Primary Branches Plant $^{-1}$
**X4** No. of Secondary Branches Plant $^{-1}$
**X5** Days to 50 % flowering
**X6** Days to Maturity
**X7** No. of Nodes Plant $^{-1}$
**X8** No. of Pods Plant $^{-1}$
**X9** No. of Seeds Pod $^{-1}$
**X10** Pod Length
**X11** 100 Seed Weight
**X12** Plant Height
**X13** Crop Duration
**X14** Crude Protein

Table 22. Phenotypic correlation of yield and yield contributing characters of horsegram under partially shaded conditions

| | X1 | X2 | X3 | X4 | X5 | X6 | X7 | X8 | X9 | X10 | X11 | X12 | X13 | X14 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **X1** | 1 | | | | | | | | | | | | | |
| **X2** | -0.099 | 1 | | | | | | | | | | | | |
| **X3** | 0.311** | -0.111 | 1 | | | | | | | | | | | |
| **X4** | 0.202 | -0.068 | 0.547** | 1 | | | | | | | | | | |
| **X5** | 0.306** | -0.467** | 0.127 | 0.164 | 1 | | | | | | | | | |
| **X6** | 0.311** | -0.380** | 0.143 | 0.164 | 0.830** | 1 | | | | | | | | |
| **X7** | 0.243* | -0.172 | 0.572** | 0.705** | 0.219* | 0.145 | 1 | | | | | | | |
| **X8** | 0.798** | -0.023 | 0.310** | 0.112 | 0.224* | 0.292** | 0.151 | 1 | | | | | | |
| **X9** | 0.209* | 0.170 | 0.071 | 0.078 | -0.272** | -0.272** | 0.135 | 0.119 | 1 | | | | | |
| **X10** | -0.265* | 0.206 | 0.070 | 0.064 | -0.210* | -0.234* | 0.065 | -0.222* | 0.096 | 1 | | | | |
| **X11** | 0.255* | -0.049 | 0.025 | 0.002 | 0.231* | 0.149 | -0.024 | -0.013 | -0.205 | -0.047 | 1 | | | |
| **X12** | 0.381** | -0.312** | 0.595** | 0.681** | 0.385** | 0.321** | 0.791** | 0.357** | -0.021 | -0.089 | 0.004 | 1 | | |
| **X13** | 0.300** | -0.387** | 0.186 | 0.165 | 0.795** | 0.936** | 0.131 | 0.304** | -0.227* | -0.274** | 0.106 | 0.309** | 1 | |
| **X14** | -0.277** | 0.099 | 0.043 | -0.018 | -0.018 | -0.093 | -0.203 | -0.233* | 0.053 | 0.089 | -0.112 | -0.182 | -0.027 | 1 |

**X1** Yield
**X2** Days to Sprouting
**X3** No. of Primary Branches Plant $^{-1}$
**X4** No. of Secondary Branches Plant $^{-1}$
**X5** Days to 50 % flowering
**X6** Days to Maturity
**X7** No. of Nodes Plant $^{-1}$
**X8** No. of Pods Plant $^{-1}$
**X9** No. of Seeds Pod $^{-1}$
**X10** Pod Length
**X11** 100 Seed Weight
**X12** Plant Height
**X13** Crop Duration
**X14** Crude Protein

### 4.2.3. Path Analysis

The association among various yield contributing characters were partitioned into direct and indirect effects using path analysis. It was carried out using the data from open conditions and the results are presented in the Table 23 and Fig.6.

The path analysis was done using 10 yield contributing characters which had high correlation with yield. The direct and indirect effect of each of these characters on yield are presented in the Table 23.

#### *4.2.3.1. Direct effects:*

From Table 23, it is clear that number of pods plant$^{-1}$ (1.9535) exhibited highest positive direct effect on yield plant$^{-1}$ followed by number of seeds pod$^{-1}$ (0.7683), number of nodes plant$^{-1}$ (0.6409) and 100-seed weight (0.5585) while, number of primary branches plant$^{-1}$ (0.1934) exhibited low positive direct effect on yield. Characters like plant height (-0.2600), crude protein content (-0.2860) and number of secondary branches plant$^{-1}$ (-0.1768) showed negative direct effect on yield.

#### *4.2.3.2. Indirect effects:*

Highest positive indirect effect was recorded by primary branches plant$^{-1}$ (1.0234) on seed yield through number of pods plant$^{-1}$, followed by number of secondary branches plant$^{-1}$ (0.7605), days to maturity (0.5643), number of nodes plant$^{-1}$ (0.7857) and plant height (0.8056) while, crude protein (-0.6814) had high negative indirect effect on yield through number of pods plant$^{-1}$.

Characters like number of primary branches plant$^{-1}$ (0.5539), number of secondary branches plant$^{-1}$ (0.7892) and plant height (0.5769) showed a high indirect effect on yield through number of nodes plant$^{-1}$, while days to maturity (0.2125) and number of pods plant$^{-1}$ (0.2578) had moderate indirect effect on yield through number of nodes plant$^{-1}$.

Number of secondary branches plant$^{-1}$ (0.1847), number of nodes plant$^{-1}$(0.1672), number of pods plant$^{-1}$ (0.1013) and plant height (0.1852) recorded low positive indirect effects on yield through number of primary branches plant$^{-1}$.

Low negative indirect effect on yield was observed for number of primary branches plant$^{-1}$ (-0.1689), number of nodes plant$^{-1}$(-0.2177) and plant height (-0.1805) through number of secondary branches plant$^{-1}$.

Days to maturity (-0.3505) had high negative indirect effect on yield through number of seeds pod$^{-1}$ whereas, number of secondary branches plant$^{-1}$ (-0.1780) and plant height (-0.1694) had low negative indirect effect. Low positive indirect effect for crude protein (0.1604) on yield was observed through number of seeds pod$^{-1}$.

Crude protein (0.6814) recorded high negative indirect effect on yield through number of pods plant$^{-1}$, while characters like number of primary branches plant$^{-1}$(-0.1217), plant height (-0.1053) and crude protein (-0.1285) had low negative indirect effect on yield through 100-seed weight.

Number of primary branches plant$^{-1}$ (-0.2490), number of secondary branches plant$^{-1}$ (-0.2654) and number of nodes plant (-0.2341) had moderate negative indirect effect on yield through plant height, while number of pods plant$^{-1}$ (-0.1072) showed low negative indirect effects.

Low positive indirect effect was exhibited by characters like number of secondary branches plant$^{-1}$ (0.1247), number of nodes plant$^{-1}$ (0.1128) and plant height (0.1068) on yield through crude protein.

### 4.2.4. Genetic Divergence Analysis

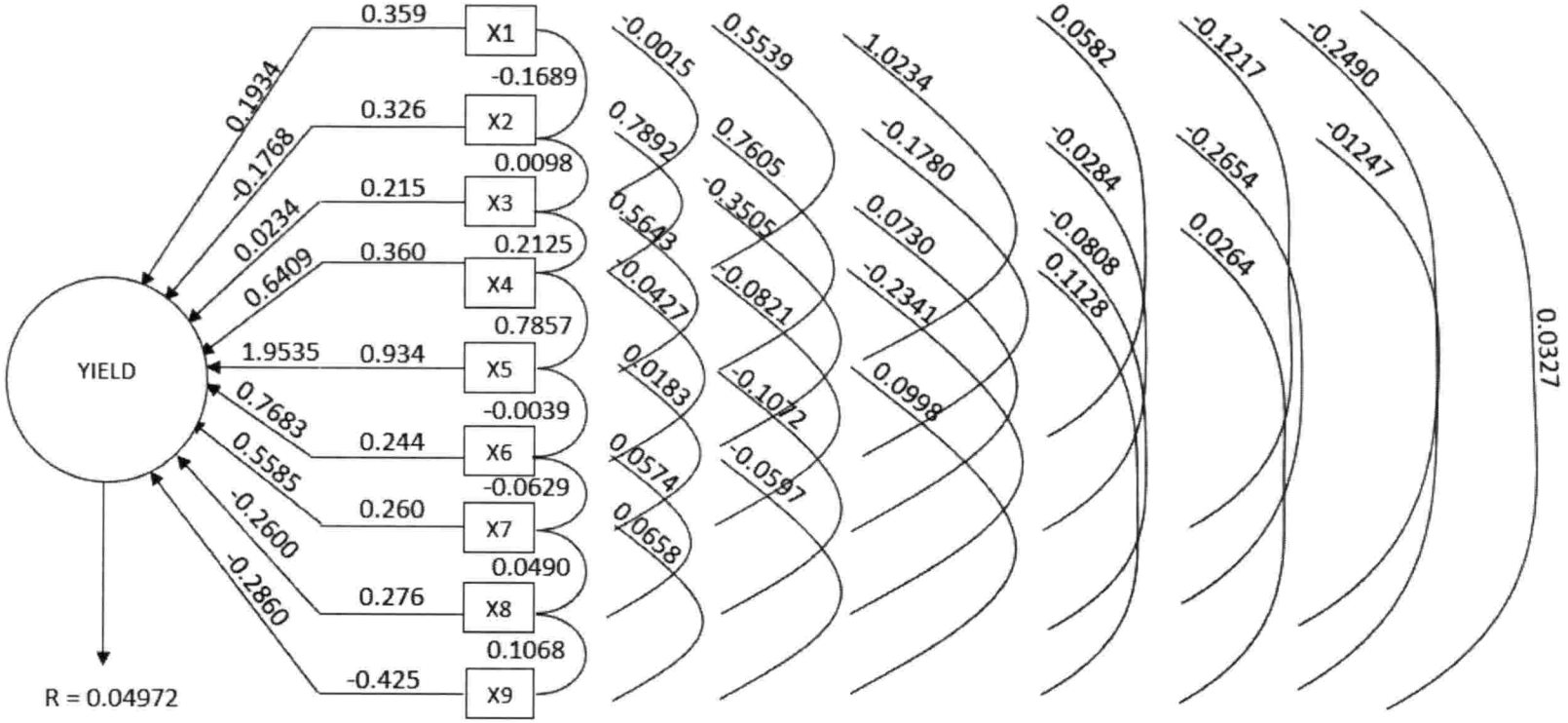
The genotypes selected for the study was subjected to Mahalanobis $D^2$ analysis based on 10 prominent characters such as yield plant$^{-1}$, number of primary branches plant$^{-1}$, number of secondary branches plant$^{-1}$, days to maturity, number of nodes plant$^{-1}$, number of pods plant$^{-1}$, number of seeds pod$^{-1}$, 100-seed weight, plant height and crude protein. Using Tochers' method of clustering, the thirty

Table 23. Direct and indirect effects of different characters on yield under open conditions

| | X1 | X2 | X3 | X4 | X5 | X6 | X7 | X8 | X9 | Genotypic correlation |
|---|---|---|---|---|---|---|---|---|---|---|
| **X1** | **0.1934** | -0.1689 | -0.0015 | 0.5539 | 1.0234 | 0.0582 | -0.1217 | -0.2490 | 0.0327 | 0.359 |
| **X2** | 0.1847 | **-0.1768** | 0.0098 | 0.7892 | 0.7605 | -0.1780 | -0.0284 | -0.2654 | 0.1247 | 0.326 |
| **X3** | -0.0127 | -0.0742 | **0.0234** | 0.2125 | 0.5643 | -0.3505 | 0.0730 | -0.0808 | 0.0264 | 0.215 |
| **X4** | 0.1672 | -0.2177 | 0.0078 | **0.6409** | 0.7857 | -0.0427 | -0.0821 | -0.2341 | 0.1128 | 0.360 |
| **X5** | 0.1013 | -0.0688 | 0.0068 | 0.2578 | **1.9535** | -0.0039 | 0.0183 | -0.1072 | 0.0998 | 0.934 |
| **X6** | 0.0147 | 0.0410 | -0.0107 | -0.0356 | -0.0100 | **0.7683** | -0.0629 | 0.0574 | -0.0597 | 0.244 |
| **X7** | -0.0422 | 0.0090 | 0.0031 | -0.0942 | 0.0641 | -0.0865 | **0.5585** | 0.0490 | 0.0658 | 0.260 |
| **X8** | 0.1852 | -0.1805 | 0.0073 | 0.5769 | 0.8056 | -0.1694 | -0.1053 | **-0.2600** | 0.1068 | 0.276 |
| **X9** | -0.0221 | 0.0771 | -0.0022 | -0.2527 | -0.6814 | 0.1604 | -0.1285 | 0.0971 | **-0.2860** | -0.425 |

**X1** No. of Primary Branches Plant $^{-1}$
**X2** No. of Secondary Branches Plant $^{-1}$
**X3** Days to Maturity
**X4** No. of Nodes Plant $^{-1}$
**X5** No. of Pods Plant $^{-1}$
**X6** No. of Seeds Pod $^{-1}$
**X7** 100 Seed Weight
**X8** Plant Height
**X9** Crude protein

Fig. 6. Path Diagram showing direct and indirect effects of components of yield




| | | |
|---|---|---|
| **X1** No. of Primary Branches Plant $^{-1}$ | **X4** No. of Nodes Plant $^{-1}$ | **X7** 100 Seed Weight |
| **X2** No. of Secondary Branches Plant $^{-1}$ | **X5** No. of Pods Plant $^{-1}$ | **X8** Plant Height |
| **X3** Days to Maturity | **X6** No. of Seeds Pod $^{-1}$ | **X9** Crude Protein |

genotypes were grouped into eight clusters. The clustering pattern is depicted in Table 24 and Fig.7.

Cluster I had the highest number of genotypes (12) followed by Cluster II (6), Cluster III (5), Cluster IV and Cluster V with two genotypes each and Cluster VI, VII, VIII were solitary. Cluster I accommodated genotypes T6, T18, T30, T21, T1, T4, T12, T5, T2, T29, T3 and T26. The genotypes T22, T24, T11, T7, T14 and T27 constituted Cluster II, while T16, T19, T9, T28 and T20 were in Cluster III. Cluster IV had the genotypes T23 and T25, whereas T13 and T17 were included in Cluster V. The genotypes T8, T10 and T15 were left out as divergent genotypes which cannot be included in any of these clusters and hence each of them remained as a separate cluster.

When the relative contribution of each character towards divergence was calculated, it was observed that yield plant$^{-1}$ (21.38) contributed maximum percentage towards genetic diversity followed by number of primary branches plant$^{-1}$ (18.85), days to maturity (17.01) and number of pods plant$^{-1}$ (13.56). (Table 24).

Based on the total $D^2$ values, the average inter cluster and intra cluster distances were calculated and the results are presented in the Table 26. Maximum intra cluster distance was recorded for the cluster V (16.18), followed by cluster I (15.27). The inter cluster distances varied from 21.04 (between clusters III and VI) to 481.99 (between cluster V and VIII). Maximum divergence was reported between clusters V and VIII, while minimum between clusters III and VI.

From the cluster diagram (Fig.7) it is clear that cluster I is at a maximum distance from cluster VIII followed by cluster V, cluster IV, cluster III, cluster VI, cluster VII and cluster II. Cluster II is highly diverse from cluster VIII followed by cluster IV, cluster III, cluster VI, cluster V and cluster VII. Cluster III had maximum distance from cluster V followed by cluster VII, cluster VIII, cluster IV and cluster VI. Cluster IV was at maximum distance from cluster V followed by cluster VII,

Table 24. Clustering pattern of horsegram genotypes

| Cluster No | No. of genotypes | Name of genotypes |
|---|---|---|
| **I** | 12 | T6, T18, T30, T21, T1, T4, T12, T5, T2, T29, T3, T26 |
| **II** | 6 | T22, T24, T11, T7, T14, T27 |
| **III** | 5 | T16, T19, T9, T28, T20 |
| **IV** | 2 | T23, T25 |
| **V** | 2 | T13, T17 |
| **VI** | 1 | T8 |
| **VII** | 1 | T10 |
| **VIII** | 1 | T15 |

Table 25. Relative contribution of each character to divergence

| Sl No. | Character | Contribution (%) |
|---|---|---|
| 1 | Yield (g) | 21.38 |
| 2 | Primary branches plant$^{-1}$ | 18.85 |
| 3 | Secondary branches plant$^{-1}$ | 8.74 |
| 4 | Days to maturity | 17.01 |
| 5 | Number of nodes plant$^{-1}$ | 10.34 |
| 6 | Number of pods plant$^{-1}$ | 13.56 |
| 7 | Number of seeds pod$^{-1}$ | 4.37 |
| 8 | 100 seed weight (g) | 3.68 |
| 9 | Plant height (cm) | 1.38 |
| 10 | Crude protein (%) | 0.69 |
| | **TOTAL** | **100** |

cluster VI and cluster VIII. The distance between cluster V and cluster VIII was the highest and cluster VI was at maximum distance from cluster VII.

Cluster means for yield and yield contributing characters were worked out and are presented in Table 25. Cluster means were high in cluster VI for characters like number of primary branches plant$^{-1}$, number of secondary branches plant$^{-1}$, number of pods plant$^{-1}$ and plant height. Cluster I had high cluster means for yield and number of seeds pod$^{-1}$. Number of nodes plant$^{-1}$ and 100-seed weight showed maximum cluster means in cluster VIII. Days to maturity which contributed 17.01 percent for divergence exhibited high cluster means in cluster VII and crude protein had high mean value in cluster II.

Table 26. Average intra and inter cluster distance among eight clusters

| Cluster | I | II | III | IV | V | VI | VII | VIII |
|---|---|---|---|---|---|---|---|---|
| **I** | 15.27 | 29.45 | 58.05 | 126.54 | 129.83 | 47.46 | 40.08 | 132.36 |
| **II** | | 4.70 | 118.28 | 223.65 | 62.55 | 117.02 | 34.54 | 243.14 |
| **III** | | | 8.96 | 31.47 | 314.48 | 21.04 | 109.81 | 40.42 |
| **IV** | | | | 11.73 | 448.12 | 33.15 | 226.52 | 26.97 |
| **V** | | | | | 16.18 | 279.06 | 135.22 | 481.99 |
| **VI** | | | | | | 0.00 | 110.66 | 31.34 |
| **VII** | | | | | | | 0.00 | 194.05 |
| **VIII** | | | | | | | | 0.00 |

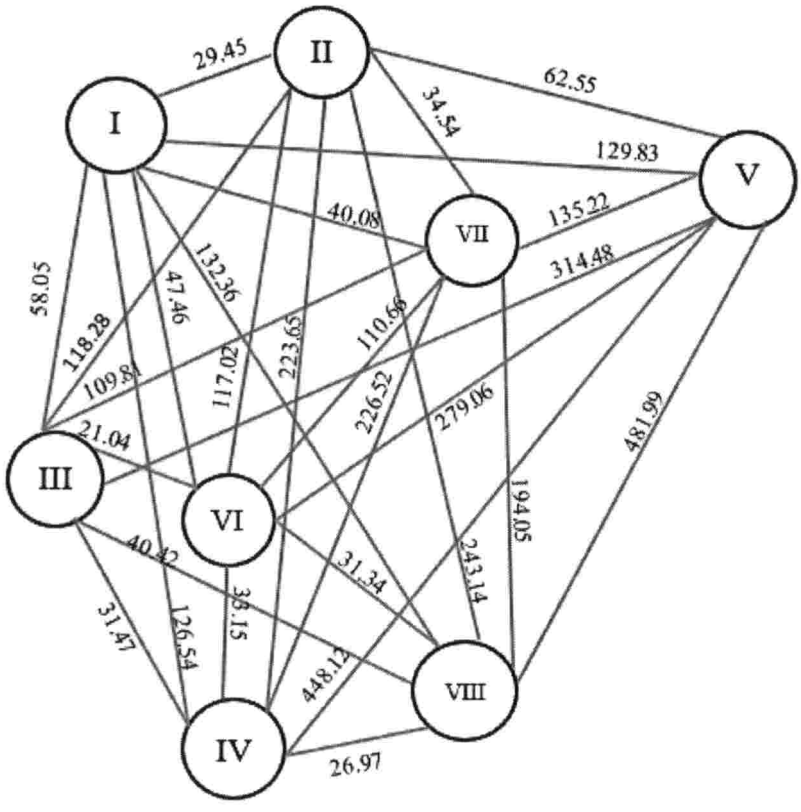



Fig.7. Cluster diagram under open conditions

Table 27. Cluster means of yield and yield contributing characters

| Cluster No. | X1 | X2 | X3 | X4 | X5 | X6 | X7 | X8 | X9 | X10 |
|---|---|---|---|---|---|---|---|---|---|---|
| I | 14.686 | 9.46 | 13.92 | 126.15 | 107.28 | 77.24 | 6.29 | 3.20 | 115.54 | 25.23 |
| II | 10.939 | 8.69 | 11.12 | 122.64 | 100.92 | 64.57 | 6.10 | 3.18 | 108.71 | 27.39 |
| III | 12.050 | 7.58 | 11.98 | 127.41 | 96.75 | 65.67 | 5.92 | 3.28 | 94.45 | 26.06 |
| IV | 14.640 | 8.92 | 14.47 | 118.90 | 117.49 | 81.44 | 5.67 | 3.19 | 107.55 | 26.09 |
| V | 13.385 | 8.85 | 16.80 | 133.53 | 133.52 | 79.77 | 5.57 | 3.30 | 140.02 | 24.34 |
| VI | 14.90 | 12.47 | 18.93 | 134.07 | 141.13 | 92.93 | 5.40 | 3.26 | 140.8 | 26.53 |
| VII | 11.83 | 9.78 | 12.33 | 136.07 | 104.27 | 71.43 | 5.60 | 3.19 | 119.9 | 22.60 |
| VIII | 14.54 | 11.97 | 18.70 | 132.57 | 148.40 | 74.87 | 6.27 | 3.39 | 126.17 | 23.93 |

**X1** Yield
**X2** No. of Primary Branches Plant $^{-1}$
**X3** No. of Secondary Branches Plant $^{-1}$
**X4** Days to Maturity
**X5** No. of Nodes Plant $^{-1}$
**X6** No. of Pods Plant $^{-1}$
**X7** No. of Seeds Pod $^{-1}$
**X8** 100 Seed Weight
**X9** Plant Height
**X10** Crude Protein

# *Discussion*

# 5. DISCUSSION

Horsegram (*Macrotyloma uniflorum (Lam.) Verdc.)* is an important drought hardy pulse crop adapted to a wide range of Indian agricultural regimes. Apart from being a rich source of dietary proteins, it also possesses immense medicinal values which makes it a potential food source for the future generations. Since land is a highly limiting factor in Kerala, intercropping is the best alternative to boost the income of the farmers. Hence identification of cultivars that performs well even under shaded conditions has become the need of the hour.

In accordance with the above scenario, the present investigation was undertaken to assess the variability and performance of horsegram genotypes collected from different regions under open and partially shaded conditions, for yield and protein content. The results of the study based on analysis of genetic parameters of horsegram genotypes under open and partially shaded conditions are discussed in this chapter.

## 5.1. VARIABILITY ANALYSIS

The extent of variability present in a population is of paramount importance for a plant breeder as it provides a basis for effective selection. The total observable variation in a population arises due to the genotypic and environmental effects. However, only the genetic component of the total variability is useful for exploitation in selection and hybridization. Hence, knowledge on the magnitude and nature of genetic variation which governs the inheritance of quantitative characters is highly important.

In the present study, 30 horsegram genotypes were evaluated and wide range of variation was observed for all the characters studied.

### 5.1.1. Mean Performance

In the present study, fourteen biometric characters along with one biochemical analysis (crude protein) were studied for 30 genotypes of horsegram under open and partially shaded conditions simultaneously. There was significant

variation among the genotypes for all the characters studied which confirms that the material selected for the study was appropriate. Variability for different characters was previously observed by Mathew (1991), Dogra (2004), Sahoo*et al.* (2010), Varma (2013) and Vijayakumar *et al.* (2016).

There were significant differences among the genotypes for number of days for sprouting and it ranged from 2.07to 3.60 under open conditions and from 2.00 to 3.47 under partially shaded conditions. However, the overall performance of the genotypes under the two growing conditions was on par for this character.

In pooled analysis, it was observed that the number of primary branches in the present study ranged from 5.82 to 12.10 with an average of 8.79 and number of secondary branches ranged from 10.02 to 18.37, with an average of 13.59. Highest number of primary and secondary branches plant$^{-1}$ was observed for the genotype T8 (Vadakarapalli local). The variation in the production of branches among the genotypes observed in the present study was in accordance with the findings of Mathew (1991), Dogra (2004) and Bhagwat (2015). The production of branches was on par for the genotypes under the two conditions, which indicates the minimum effect of the environmental conditions on this character.

Days to 50 per cent flowering ranged between 46.33 and 80.67 under open conditions, while it was between 48.67 and 81.67 under partially shaded conditions. There existed significant differences in days to 50 per cent flowering between horsegram genotypes. The genotype T30 (IC 22759) took minimum days for flowering, while the genotype T7 (Chittur local) took more days to attain 50 per cent flowering under open conditions. Similar findings for the variation in this trait were reported by Dogra (2004) and Vijayakumar (2016). Most of the genotypes flowered earlier under open conditions and there was considerable difference for this trait between the two growing conditions. Under partial shade, more vegetative growth was observed due to the ambient environmental conditions, thereby delaying the reproductive stage and hence genotypes took more time to attain 50 per cent flowering. Delaying of flowering under shade has also been reported by Jiang (1993) in soybean.

Days to maturity of different genotypes ranged from 106.60 to 142.40 under open conditions with an average of 126.50, which was in agreement with the findings of Mathew (1991), Dogra (2004) and Sahoo (2010). Under partially shaded conditions, days to maturity ranged from 109.40 to 144.33 days, which clearly indicates that genotypes took more days to attain maturity under partial shade compared to open conditions. However, these results are in contradiction to the findings of Bhagwat (2015) who reported that light intensity had no effect on flowering and maturity in black gram.

Number of nodes plant$^{-1}$ was maximum for the genotype T15 (Vanjangipeta local) under open conditions, while it was maximum for genotype T6 (Agali local) under partially shaded conditions. The results showed that the genotypes produced more number of nodes under open conditions compared to partially shaded conditions. This may be due to the fact that the plants subjected to low light intensities often grow rapidly producing longer internodes (Sumner, 1922).

Number of pods plant$^{-1}$ varied significantly among the genotypes under the two growing conditions. The present study recorded number of pods plant$^{-1}$ in a range of 45.60 to 105.27 with an average of 73.47 under open conditions, while it ranged from 41.67 to 98.87 with an average of 70.65 under partially shaded conditions. Under both conditions, the genotype T12 (Palakkad local) reported the highest number of pods plant$^{-1}$, even though there was difference in the average number of the pods produced by the genotype under both conditions. Mathew (1991), Dogra (2004), Sahoo (2010) and Gomashe (2018) also reported similar variations for number of pods plant$^{-1}$ in horsegram, but the range was smaller than that obtained in the present study.

From the results it is evident that there existed no variation in the characters like number of seeds pod$^{-1}$, pod length and 100 seed weight under open and partially shaded conditions. Pooled analysis showed that the number of seeds pod$^{-1}$ ranged from 5.20 to 7.20, pod length from 4.35 to 5.71cm and 100-seed weight from 2.74 to 3.69g. Variations observed in these characters were in accordance with the

findings of Dogra (2004), Varma (2013), Vijayakumar (2016) and Gomashe *et al.* (2018).

Plant height ranged from 83.68 to 147.57cm under open conditions while it was from 82.23 to 152.70cm under partially shaded conditions. Similar variations were reported by Mathew (1991), Dogra (2004), Poornima (2016) and Gomashe *et al.* (2018), but their results showed a lower range for plant height in horsegram. In general, genotypes exhibited more plant height under partial shade which may be due to the higher vegetative growth and longer internodal length under shaded conditions. Moreover, all the genotypes showed significant interaction with the environment for this character.

The highest variability was recorded for seed yield plant$^{-1}$ which can be used as selection criteria for crop improvement in horsegram. Yield plant$^{-1}$ was high for Palakkad local (20.08 and 18.36g plant$^{-1}$) under open and partially shaded conditions, respectively. Gomashe (2018) had earlier reported a similar trend in the yield of horsegram. Similar variations in seed yield plant$^{-1}$, but with lower range were reported by Mathew (1991), Dogra (2004), Ram *et al.* (2005) and Poornima (2016).

In the present study, harvest index was found to range from 12.27 per cent to 25.71 per cent under open conditions and from 9.24 per cent to 25.34 per cent under partial shade. The genotypes showed significant difference in their performance under both conditions for this character. Since the character showed high positive correlation with yield, an increasing trend for harvest index with increase in yield was observed in the study. A slightly lower range for harvest index in horsegram was earlier reported by Dogra (2004).

Crop duration of horsegram genotypes was found to vary from 121.40 days to 153.47 days with an average of 138.65 days under open conditions, while it varied from 122.67 to 155.53 days with an average of 140.65 days under partially shaded conditions. Genotypes under partial shade took slightly longer time to complete their crop duration compared to those which were grown under full

sunlight. This may be attributed to their longer vegetative phase which further delayed their flowering and hence increased the duration of the crop in the field. Minimum crop duration was reported for the genotype T30 (IC22759) under both conditions in the current study. Similar variation in crop duration was reported by Dogra (2004), but the range was relatively lower.

There was significant variability for crude protein content among the different genotypes, but their overall performance with respect to this trait was not significant over the two conditions. In pooled analysis, the protein content in the genotypes was found to vary from 22.99 per cent to 28.98 per cent. Lower range of protein content in horsegram seeds were earlier reported by Gupta *et al.* (2001) and Poornima (2015).

### 5.1.2. Variability Components

Variability present in a population can also be expressed as coefficients of variation. The coefficients of variation, genotypic (GCV) and phenotypic (PCV) give an idea about the magnitude of variability present in the population. PCV measures the extent of total variation present in a population while GCV provides a valid basis for the assessment and comparison of the genetic variability for the characters. A close relationship between genotypic and phenotypic coefficients of variation suggests a low environmental influence and reflected the reliability of selection based on phenotypic performance of the genotypes.

In the current study it was observed that the values of genotypic coefficient of variation were smaller than the corresponding phenotypic coefficient of variation for almost all the characters studied. The narrow difference between GCV and PCV for characters like days to 50 per cent flowering, days to maturity, number of pods plant$^{-1}$, pod length, 100-seed weight and plant height under both conditions indicated the minimum influence of the environment on the expression of these characters and hence their phenotypic values will be reliable for selection. These observations were supported by the findings of Sood *et al.* (1994) and Prakash and Khanure (2000) based on their studies in horsegram.

The value of genotypic coefficient of variation (GCV) ranged from 5.57 per cent to 23.99 per cent under open conditions and 5.91 per cent to 23.38 per cent under partially shaded condition. Highest GCV was recorded for yield plant$^{-1}$ followed by number of pods plant$^{-1}$, while lowest was for crude protein under both conditions. This was in accordance with the studies of Khulbe *et al.* (2013) who reported that number of pods plant$^{-1}$ and yield plant$^{-1}$ exhibited high values for genotypic coefficient of variation in horsegram genotypes. The low GCV for crude protein under both conditions has also been reported by Bhagwat (2015) in black gram genotypes. The present study indicated a higher contribution of yield plant$^{-1}$ and number of pods plant$^{-1}$ towards variability suggesting that parents selected on the basis of these characters may be utilized in breeding programmes to obtain good segregants.

Highest GCV and PCV was observed for yield plant$^{-1}$ under open conditions which was in agreement with the studies of Sood *et al.* (1994), Dogra (2004), Ram *et al.* (2005), Vijayakumar *et al.* (2016) and Priyanka *et al.* (2019).Days to maturity, days to 50 per cent flowering, pod length, 100-seed weight, crop duration, crude protein, number of seeds pod$^{-1}$, number of nodes plant$^{-1}$ and plant height recorded low to moderate GCV and PCV under open and partially shaded conditions, indicating less scope for their improvement through selection. Similar findings were reported by Nagaraja (1997), Nehru *et al.* (2000), Ram *et al.* (2005) and Priyanka *et al.* (2019).

### 5.1.3. Heritability and Genetic Advance

The extent of contribution of genotype to the phenotypic variation for a trait in a population is known as heritability. It is the heritable portion of phenotypic variance of the characters and is a good index for the transmission of characters from parents to their off springs. The estimates of heritability guide the plant breeder in the selection of elite genotypes from diverse genetic populations. However, heritability alone may fail to indicate the response to selection. Hence heritability estimates along with genetic advance are more useful in predicting the gain under selection.

In the present study, heritability estimates ranged from 23.99 per cent for number of primary branches plant$^{-1}$ to 94.39 per cent for number of pods plant$^{-1}$under open conditions and from 52.21 per cent for crude protein to 98.19 per cent for 100-seed weight under partially shaded conditions. Highest heritability percent was recorded for the character number of pods plant$^{-1}$ (94.39 per cent), followed by 100-seed weight (89.85 per cent), days to maturity (89.70 per cent), crop duration (86.06), days to 50 per cent flowering (84.73 per cent), number of nodes plant$^{-1}$ (83.20), yield plant$^{-1}$ (81.44 per cent) and plant height (81.92) under open conditions. Hence selection for these characters is most likely to be effective. Most of the characters studied exhibited high heritability except for number of secondary branches plant$^{-1}$ (36.84 per cent), harvest index (54.56 per cent) and crude protein (44.65 per cent) which showed moderate heritability, while lowest heritability was recorded for number of primary branches plant$^{-1}$ (23.99 per cent).

High heritability estimates for days to 50 per cent flowering, days to maturity, pods plant$^{-1}$, yield plant$^{-1}$ and 100-seed weight were earlier reported by Sood *et al.* (1994), Tripathi (1999), Venkateswarlu (2000) and Sahoo *et al.* (2010) in horsegram. Primary branches plant$^{-1}$ showed low heritability, in accordance with the results obtained by Senapathi *et al.* (1998) and Durga (2012)

Almost all the characters exhibited high heritability under partially shaded conditions too except for number of secondary branches plant$^{-1}$ and crude protein, which showed moderate heritability, and these results were in agreement with the studies of Bhagwat (2015) in black gram.

In the present investigation, genetic advance as percent of mean was reported to be high for number of pods plant$^{-1}$ under both conditions followed by yield plant$^{-1}$. This was in contradiction to the results obtained by Nehru *et al.* (2000), who reported lower values of genetic advance for number of pods plant$^{-1}$ and moderate values for yield plant$^{-1}$. Characters like number of branches plant$^{-1}$, days to maturity, seeds pod$^{-1}$, pod length, 100-seed weight, and crop duration exhibited moderate genetic advance while, crude protein gave the lowest values. This implies

that these characters may be controlled by non-additive genes and heterosis breeding may be useful for their improvement.

High heritability coupled with high genetic advance expressed as percent of mean was recorded for characters like yield plant$^{-1}$, days to sprouting, days to 50 per cent flowering, number of nodes plant$^{-1}$, number of pods plant$^{-1}$ and plant height. This was in accordance with Sreekantaradya *et al.* (1975) and Sahoo *et al.* (2010) in horsegram. This indicates that these characters are most likely governed by additive gene action and hence direct phenotypic selection may be effective.

**5.1.4. Correlation Studies**

Correlation measures the nature and extent of association between two or more characters. It helps the plant breeder to understand the relative importance of different plant traits and provide an effective basis for selection. Correlation may be positive or negative based on the nature of the characters under study. It not only determines the total association existing between a pair of character but also measures the inter relationship between pairs of characters. So when selection is carried out for a particular trait of interest in a population, it gets naturally associated with the improvement of other traits which are correlated with the trait of interest and hence simultaneous improvement of more than one character which moves in the same direction of selection occurs.

In the present investigation, genotypic and phenotypic correlation coefficients were worked out for 14 quantitative characters of the horsegram genotypes. Almost all the characters showed positive significant correlation with yield under both conditions. Correlation analysis revealed that the genotypic correlation coefficients were higher than the phenotypic correlation coefficients for all the characters which suggest a strong association between these characters genetically, but the phenotypic value is lessened by the significant interaction of the environment.

In general, most of the component traits like number of pods plant$^{-1}$, number of primary branches plant$^{-1}$, number of secondary branches plant$^{-1}$, days to maturity,

number of nodes plant$^{-1}$, number of seeds pod$^{-1}$ and 100-seed weight showed strong positive correlation with yield plant$^{-1}$, which implies that an improvement in any one of these characters will simultaneously result in the amelioration of yield.

Number of pods plant$^{-1}$ recorded the maximum positive significant correlation with yield plant$^{-1}$, number of primary branches plant$^{-1}$ and number of nodes plant$^{-1}$. These findings were in agreement with Savithramma (1994), Poornima (2015).

Significant positive correlation of number of seeds pod$^{-1}$ and 100-seed weight on seed yield was earlier reported by Samal and Senapati (1997), Lad *et al.* (1999), Nehru *et al.* (2000) and Roopadevi *et al.* (2002).

Plant height and number of branches plant$^{-1}$ were positively correlated to yield plant$^{-1}$ at genotypic level. However, at phenotypic level, plant height showed positive but non-significant correlation with yield. Similar results were reported by Prakash and Khanure (2000).

Days to 50 per cent flowering and pod length were found to have no significant correlation with yield under open conditions, while they exhibited positive significant correlation with yield under partially shaded conditions. This may be due to the fluctuations in the environmental conditions. These results were in contradiction to the findings of Vijayakumar *et al.* (2016), who reported a negative correlation of days to 50 per cent flowering with yield and Prabha *et al.* (2010), who reported a positive correlation of yield with length of pod.

Crude protein content exhibited a negative correlation with yield which suggests that an increase in yield plant$^{-1}$ may reduce the protein content in the seeds marginally. This was in agreement with the results obtained by Mello Filho *et al.* (2004) and Singh *et al.* (2016) in soybean.

Based on these values of phenotypic and genotypic correlations, it would be easier for the plant breeder to develop efficient breeding strategies so that the useful associations could be effectively exploited.

### 5.1.5. Path Analysis

Correlation of yield and its contributing characters does not provide an exact picture of the relative significance of various yield attributes. Path analysis helps in the partitioning of correlation coefficients into measures of direct and indirect effects of the component characters on yield. It provides information about the cause and effect of association between two variables. Hence it is done to confirm whether the correlation of component characters with the dependant character is due to their direct effect or is a consequence of their indirect effect *via* some other character. If the correlation between yield and a component character is due to the direct effect of the character, it indicates a true relationship between them and so direct selection for that particular trait will be rewarding for crop improvement. However, if the correlation is due to the indirect effect of the trait through another component character, indirect selection through such trait will help in yield improvement.

Based on genotypic correlation, ten yield components like number of primary branches plant$^{-1}$, number of secondary branches plant$^{-1}$, days to maturity, number of nodes plant$^{-1}$, number of pods plant$^{-1}$, number of seeds pod$^{-1}$, 100-seed weight, plant height and crude protein content which were highly correlated with yield has been selected as independent characters for path analysis. This measures the direct and indirect contribution of independent characters on dependant character. (Fig.6.)

In the current study, the highest positive direct effect on yield plant$^{-1}$ was shown by number of pods plant$^{-1}$ followed by number of seeds pod$^{-1}$, number of nodes plant$^{-1}$ and 100-seed weight. All these characters were found to exhibit significant positive correlation with yield. Hence direct selection for these traits will definitely result in improvement of yield in horsegram. This was in accordance with the study by Yarguntappa (1987) who reported that number of pods plant$^{-1}$ exerted maximum direct and positive effect on seed yield. Similar findings were reported by Prakash and Khanure (2000), Khulbe *et al.* (2013) and Priyanka *et al.* (2019).

The characters like number of secondary branches plant$^{-1}$, plant height and crude protein exhibited direct, significant negative effect on yield, which implies that selection for these characters will result in reduction of yield in horsegram. Khulbe *et al.* (2013) had also previously reported that plant height has direct negative effect on yield.

Number of primary branches plant$^{-1}$ had direct positive effect on yield in the present study. It also exerted the maximum indirect effect on yield through number of pods plant$^{-1}$. This was in agreement with Paliwal *et al.* (2005), who also reported that primary branches had direct positive effect on yield. Number of seeds pod$^{-1}$ and 100-seed weight recorded high positive direct effect on yield and through plant height, they also exerted high indirect effect. This was in accordance with the findings of Yarguntappa (1987), Kabir and Sen (1989) and Savithramma (1994).

A low residual effect (0.049) was noticed in the study, which indicates the contribution of the traits towards variability.

### 5.1.6. Divergence Analysis

The multivariate analysis using Mahalanobis $D^2$ statistics is one of the potent techniques of measuring genetic divergence. For any crop improvement programme, knowledge regarding the nature and extent of genetic diversity within a population is essential in order to identify specific parents for realizing useful recombinants. It helps the breeder to assess the magnitude of dissimilarity among the genotypes and subsequently group them based on their phenotypic expression.

In the present study, Mahalanobis $D^2$ statistics was used to group the 30 genotypes into eight clusters. During this process, certain genotypes belonging to the same locality got separated into different clusters while, some genotypes of different places got assembled into the same cluster. This proves that factors other than geographical diversity may be responsible for the clustering pattern of the population. Dobhal and Rana (1994) and Dasgupta *et al.* (2005), on getting similar

results had earlier suggested that selection and genetic drift may be the prime cause for genetic diversity in a population rather than geographical isolation.

In the present study, out of the eight clusters obtained, cluster I was the largest comprising of twelve genotypes, cluster II with six genotypes, cluster III with five genotypes, cluster IV and cluster V with two genotypes and clusters VI, VII and VIII were solitary clusters. Cluster with maximum number of genotypes were highly diverse as most of the genotypes present in them were collected from diverse locations.

Highest inter cluster distance was observed between the clusters V and VIII followed by clusters IV and V. The distance between the clusters is a measure of the degree of diversification. The greater the distance between the clusters, the greater will be the genetic divergence among the genotypes present. Highest intra cluster distance was recorded for the cluster V followed by cluster I, which shows that the genotypes present in the same cluster exhibits significant variability among themselves. Hence, selection within a cluster may be practiced on the basis of the highest mean performance of the genotype for desirable traits.

The study showed that yield plant$^{-1}$ contributed maximum toward genetic divergence at genotypic level, followed by primary branches plant$^{-1}$ and days to maturity. This was in accordance with the findings of Dogra (2004) and Kalia and Dogra (2007) who also reported that yield gave the maximum contribution towards genetic diversity.

Cluster VI exhibited high mean values for characters like number of pods plant$^{-1}$, plant height, number of primary branches plant$^{-1}$ and number of secondary branches plant$^{-1}$. Cluster I had high means for yield and number of seeds pod$^{-1}$. Cluster VIII had highest average number of pods plant$^{-1}$ and maximum 100-seed weight. These results implied that the selection of genotypes with high mean values for a particular trait can be done and they can be employed in further crop improvement programmes.

# *Summary*

## 6. SUMMARY

The present study on variability in horsegram [*Macrotyloma uniflorum* (Lam.) Verdc.] under open and partially shaded conditions was carried out at the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani, during 2017-19 with an objective to assess the variability and performance of horsegram genotypes collected from different regions under open and partially shaded conditions, for yield and protein content.

The current investigation was conducted as two experiments simultaneously, under open and partially shaded conditions. Thirty genotypes of horsegram collected from different regions of the state and outside were assessed for their variability and performance under both conditions in a Randomized Block Design (RBD) with three replications during 2018-19. The seeds were dibbled in the field at a spacing of 30cm×25cm during September, 2018. A total of 25 plants were maintained in each experimental plot and each genotype was considered as individual treatments.

The thirty genotypes were evaluated for 15 different quantitative characters and their mean performance were recorded. Various studies which includes variability studies, estimation of genetic parameters such as GCV, PCV, heritability and genetic advance, correlation analysis, path coefficient analysis and genetic divergence analysis were conducted.

Analysis of variance showed significant difference among the 30 genotypes for all the 15 traits studied. Pooled analysis was also conducted for all the characters to compare the performance of the genotypes under open and partially shaded conditions.

It revealed significant difference between genotypes averaged over two conditions for characters such as number of primary branches plant$^{-1}$, days to 50% flowering, days to maturity, number of pods plant$^{-1}$, harvest index, crop duration and seed yield plant$^{-1}$.

Variability studies in horsegram revealed the presence of considerable amount of variability in characters like seed yield plant$^{-1}$, number of pods plant$^{-1}$,

number of nodes plant$^{-1}$, harvest index, plant height, days to sprouting, day to 50% flowering, number of primary branches plant$^{-1}$ and number of secondary branches plant$^{-1}$under both open and partially shaded conditions.

The character seed yield plant$^{-1}$(23.98 and 23.38) recorded the highest genotypic coefficient of variation (GCV) under both open and partially shaded conditions, respectively followed by number of pods plant$^{-1}$(23.66 and 23.29) while, characters like primary branches plant$^{-1}$, secondary branches plant$^{-1}$, pods plant$^{-1}$, seed yield and harvest index exhibited high values for phenotypic coefficient of variation (PCV). Moderate GCV and PCV were recorded for days to sprouting, days to 50% flowering, number of nodes plant and plant height., while characters like days to maturity, pod length, 100-seed weight, crop duration and crude protein content exhibited lowest GCV and PCV. High heritability coupled with high genetic advance was observed for seed yield plant$^{-1}$, days to sprouting, days to 50% flowering, nodes plant$^{-1}$, pods plant$^{-1}$ and plant height under both conditions whereas, under partially shaded conditions, two more characters such as primary branches plant$^{-1}$ and harvest index also showed high heritability with high genetic gain.

Seed yield plant$^{-1}$ was found to be significantly and positively correlated with number of primary branches plant$^{-1}$, number of secondary branches plant$^{-1}$, nodes plant$^{-1}$, pods plant$^{-1}$, seeds pod$^{-1}$ and 100-seed weight both at genotypic and phenotypic levels under open and partially shaded conditions. Path analysis revealed that number of pods plant$^{-1}$, seeds pod$^{-1}$, nodes plant$^{-1}$ and 100-seed weight had high positive direct effect on seed yield plant$^{-1}$.

Genetic divergence studies using Mahalanobis' $D^2$ statistics grouped the thirty genotypes into eight clusters. The highest inter cluster distance was recorded between Clusters V and VIII, while Cluster V also exhibited maximum intra cluster distance. Among the individual traits, seed yield plant$^{-1}$contributed highest towards genetic divergence.

The results of the study revealed the presence of wide variability among the thirty horsegram genotypes under open and partially shaded conditions. The genotype T12 (Palakkad local) from Kerala was found to be superior in yield

performance both under open and partially shaded conditions, followed by the genotype T2 (Chintada local) from Andhra Pradesh. When protein content was assessed, maximum value was recorded for genotype T14 (Dharmapuri local) under open conditions and genotype T23 (IC15735) under partially shaded conditions. The superior genotypes identified in the present study can be utilized for further crop improvement programmes to develop high yielding varieties.

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# Variability in horsegram [*Macrotyloma uniflorum* (Lam.) Verdc.] under open and partially shaded conditions

*by*

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## ABSTRACT

The present study entitled "Variability in horsegram [*Macrotyloma uniflorum* (Lam.) Verdc.] under open and partially shaded conditions" was carried out in the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani during 2017-2019. The study was undertaken to assess the variability and performance of horsegram genotypes collected from different regions under open and partially shaded conditions, for yield and protein content.

Thirty genotypes of horsegram were collected from different regions of state and outside and were raised under open and partially shaded conditions, simultaneously for variability analysis. The partial shade was provided by coconut garden, planted at a spacing of 7.8 x 7.8 m, where the average shade percent was 24. These accessions were evaluated in a Randomized Block Design (RBD) with three replications during September 2018 to February 2019.

Analysis of variance revealed significant difference among the genotypes for all the fifteen characters studied. Pooled analysis was also conducted for all the characters to compare the performance of genotypes under open and partially shaded conditions. The genotypes exhibited significant difference for characters such as number of primary branches plant$^{-1}$, days to 50% flowering, days to maturity, number of pods plant$^{-1}$, harvest index, crop duration and seed yield plant$^{-1}$ under the two conditions.

Under both conditions, genotypic coefficient of variation (GCV) was high for seed yield plant$^{-1}$ and number of pods plant$^{-1}$ while, characters like primary branches plant$^{-1}$, secondary branches plant$^{-1}$, pods plant$^{-1}$, seed yield and harvest index exhibited high values for phenotypic coefficient of variation (PCV). High heritability coupled with high genetic advance was observed for seed yield plant$^{-1}$, days to sprouting, days to 50% flowering, nodes plant$^{-1}$, pods plant$^{-1}$ and plant height under both conditions whereas, under partially shaded conditions, two more characters such as primary branches plant$^{-1}$ and harvest index also showed high heritability with high genetic gain.

Seed yield plant$^{-1}$ was found to be significantly and positively correlated with number of primary branches plant$^{-1}$, number of secondary branches plant$^{-1}$, nodes plant$^{-1}$, pods plant$^{-1}$, seeds pod$^{-1}$ and 100-seed weight both at genotypic and phenotypic levels under open and partially shaded conditions. An improvement in these characters would lead to an enhancement in the seed yield plant$^{-1}$. Path analysis was carried out using seed yield plant$^{-1}$ as the dependent character and other characters as independent variables. It revealed that number of pods plant$^{-1}$, seeds pod$^{-1}$, nodes plant$^{-1}$, 100-seed weight, days to maturity and number of primary branches plant$^{-1}$ were the primary yield contributing characters due to their high direct effect on seed yield plant$^{-1}$.

Genetic divergence was studied under open conditions using Mahalanobis' $D^2$ statistics and based on this analysis, the thirty genotypes were grouped into eight clusters. The maximum number of genotypes were accommodated in Cluster I (12), followed by Cluster II (6), Cluster III (5), Cluster IV & Cluster V with two genotypes each and Clusters VI, VII and VIII were solitary. Among the eight clusters, the highest inter cluster distance was recorded between Clusters V and VIII, while Cluster V also exhibited maximum intra cluster distance. It was observed that among the individual traits, seed yield plant$^{-1}$ contributed highest for divergence followed by primary branches plant$^{-1}$ and days to maturity.

The results of the study revealed the presence of wide variability among the thirty horsegram genotypes under open and partially shaded conditions. The genotype T12 (Palakkad local) was found to be superior in yield performance both under open (20.08 g) and partially shaded conditions (18.36g), followed by the genotype T2 (Chintada local) from Andhra Pradesh (19.82g, 17.75g). Also the genotype T21 (IC22762) (18.22g) was found to be a high yielder under open conditions and genotype T17 (Attapadi local) (16.99g) under partially shaded conditions. When protein content was assessed, maximum value (28.92%) was recorded for genotype T14 (Dharmapuri local) under open conditions and genotype T23 (IC15735) (29.17%) under partially shaded conditions. The superior genotypes identified in the present study can be utilized for further crop improvement programmes to develop high yielding varieties.