GENETIC DIVERSITY ANALYSIS OF HORSE GRAM [*Macrotyloma uniflorum* (Lam.) Verdc.] FOR MOISTURE STRESS TOLERANCE IN SOUTH CENTRAL LATERITES OF KERALA

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(2019-11-111)

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KERALA, INDIA
2021

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by

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(2019-11-111)

THESIS

Submitted in partial fulfilment of the
requirement for the degree of

MASTER OF SCIENCE IN AGRICULTURE

Faculty of Agriculture
Kerala Agricultural University

DEPARTMENT OF PLANT BREEDING AND GENETICS
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KERALA, INDIA
2021

DECLARATION

I, hereby declare that this thesis entitled "**Genetic diversity analysis of horse gram [*Macrotyloma uniflorum* (Lam.) Verdc.] for moisture stress tolerance in south central laterites of Kerala**" 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 “**Genetic diversity analysis of horse gram [*Macrotyloma uniflorum* (Lam.) Verdc.] for moisture stress tolerance in south central laterites of Kerala**” is a record of research work done independently by Mr. **VISAKH R L (2019-11-111)** 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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We, the undersigned members of the advisory committee of **Mr. Visakh R L (2019-11-111)**, a candidate for the degree of **Master of Science in Agriculture** with major in Plant Breeding and Genetics, agree that the thesis **"Genetic diversity analysis of horse gram [*Macrotyloma uniflorum* (Lam.) Verdc.] for moisture stress tolerance in south central laterites of Kerala"** may be submitted by **Mr. Visakh R L (2019-11-111)**, in partial fulfilment of the requirement for the degree.

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Acknowledgement

At the very outset, I praise and thank ***God*** *with a grateful heart****,*** *who kindly imbued the energy and enthusiasm through the thick and thins of my endeavours.*

As the end of my post-graduation is insight, a sudden discernment makes me ponder over the last two years of my life. Indeed, this is my opportunity to offer deep gratitude and words of appreciation to all those who wished me success and helped me to conduct my current study.

First of all, I consider myself as lucky to be able to carry out the research work under dynamic and masterful guidance. The words at my disposal are inadequate to convey the depth of my feeling and gratitude to my honourable major advisor ***Dr. Bindu M. R.****, Professor, Farming Systems Research Station, Sadanandapuram, for her insightful guidance, endless encouragement, constructive and reasonable criticism and supervision and the care that she has given me from day one and throughout this investigation. Thank you, madam.*

I express my deep sense of regard and unforgettable indebtedness to ***Dr. Arya K.,*** *Professor and Head, Department of Plant Breeding and Genetics and member of the advisory committee for her valuable advice and support from the very beginning, which helped me in the successful completion of the thesis.*

I acknowledge with due respect and thanks to my other committee members ***Dr. Roy Stephen****, Professor, Department of Plant Physiology and* ***Dr. Poornima Yadav****, Assistant Department of Agronomy, KVK, Kollam for their valuable suggestions, constant attention and help throughout the investigation.*

I also appreciate tremendous help and unparalleled affection received from ***Dr. Lekha Rani. C.*** *(Retd. Prof.),* ***Dr. Mareen Abraham*** *(Retd. Prof.),* ***Dr. Beena Thomas*** *(Asst. Prof.) and* ***Dr. Gayathri G.*** *(Asst. Prof.) and other staff members of the Department of Plant Breeding and Genetics during this study.*

I extend my sincere gratitude to ***Dr. Roshini Vijayan,*** *Assistant Professor, RARS Pattambi, KAU,* ***Dr. Krishna,*** *Assistant Professor, UAS Bengaluru,* ***Dr. Ganga Prasad,*** *Professor and Head, UAHS Shivamooga and* ***Dr. Manubhai Patel,*** *Research scientist, SDAU, Gujarat, for providing me seeds of different horse gram genotypes for my study.*

I would like to express my gratitude and heartfelt thanks to ***Mr. Shinoj P.****, Farm Officer, FSRS, Sadanandapuram and other* ***office staffs*** *and* ***labourers*** *of FSRS, Sadanandapuram namely* ***Monisha chechi****,* ***Anchu chechi, Viji chechi****,* ***Shihab ikka, Ganesh chettan, Suresh chettan and Sreehari*** *for their support and help rendered during the endeavour.*

At this moment, I render my gratitude to my seniors ***Darshana chechi, Reshma chechi, Mythri chechi, Swathy chechi, Ankitha chechi, Arya chechi, Anju chechi, Shahiba chechi, Niji chechi, Chippy chechi, Rehana chechi, Anand ettan, Arun ettan and Bhaskar ettan*** *for their kind guidance and cordial support.*

I owe it to overwhelming happiness to express my deepest awe to my beloved friends, ***Parth, Sindhav, Mayank, Som, Aravind, Anandhu, Akhil, Arya, Revathi, Amritha, Bindhya, Priyanka*** *and* ***Priti*** *who accompanied me during tough times, cheered me and celebrated each accomplishment. I extend a special thanks to my* ***juniors*** *for their cheerful company and constant support.*

Without my parent's affection, encouragement, unlimited love, tireless inspiration and selfless willingness to sacrifice, I would not be who I am today. I thank my father Shri. ***Ravindran Nair*** *and mother Smt.* ***Lalithambika****, for their love, blessings and constant moral support, without which this research would have been possible. All my success is attributed to them.*

Visakh R L

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LIST OF ABBREVIATIONS AND SYMBOLS USED

et al.	And others
cm^2	Square centimeters
CD	Critical Difference
°C	Degree Celsius
d.f.	Degrees of freedom
FCRD	Factorial Completely Randomized Design
Fig.	Figure
FSRS	Farming Systems Research Station
GAM	Genetic advance as per cent of mean
g	Gram
GCV	Genotypic coefficient of variation
KAU	Kerala Agricultural University
LAI	Leaf area index
mg	milligram
No.	Number
%	Per cent
PCV	Phenotypic coefficient of variation
RBD	Randomized Block Design
RARS	Regional agricultural research station
RWC	Relative Water Content
SDAU	Sardarkrushinagar Dantiwada Agricultural University
SE	Standard Error
SV I	Seedling vigour index I
SV II	Seedling vigour index II
Sl.	Serial
SLA	Specific leaf area
UAHS	University of Agriculture and Horticulture Sciences
µmol	Micromole
viz.	Namely

Introduction

1. INTRODUCTION

The earth is bestowed with more than 30,000 edible plants. Even though we are blessed with such a huge crop diversity, at present about 40% of our calorie intake is contributed by just three crops- rice, wheat and maize (FAO, 2018). Dependency on limited number of crops to feed the growing population can make our food system susceptible to serious pests and diseases. There are thousands of underutilized crop species which can safeguard agriculture and food security. These neglected crops not only enrich our diet but also keep the traditional knowledge alive, combat climate change and also increase the income of small-scale farmers. With increased health consciousness among the people with the onset of COVID-19 pandemic, there is a demand for more balanced diet and these underutilised crops can be the right choice.

Sustaining agriculture is the need of the hour for addressing the growing food insecurity raised by the exploding population. But various challenges like abiotic stress including drought, cold and salinity stresses etc. and the biotic stress including pest and diseases are causing hindrance to sustain agricultural development. Among abiotic stresses, drought is one of the major constraints affecting the plants, animals, humans and water resources (Bhardwaj and Yadav, 2012b).

Moisture stress affects growth, yield, osmotic adjustment and photosynthetic activity in crops (Benjamin and Nielsen, 2006). With increasing aridity due to climate change and growing animal and human population, water will become a scarce resource in near future. Diversification of food resources and aligning underutilized climate resilient crops as the possible future crops in the cropping systems can be undertaken to combat water scarcity (Mabhaudhi *et al.*, 2017).

Horse gram [*Macrotyloma uniflorum* (Lam.) Verdc., formerly *Dolichos biflorus* L.] is one such underutilized climate resilient crop belonging to the family Fabaceae. It is a versatile crop which is cultivated for food and fodder purpose. This sturdy crop is famous for its considerable drought tolerance. It is an annual or perennial legume vernacularly known by the names Kulthi (Hindi), Muthira (Malayalam), Kollu or

Kaanam (Tamil), Hurali (Kannada), Ulavalu (Telugu) etc. The crop has earned its common name as it is used to feed horses. It's also known as poor man's food as it is mostly consumed by poor sections of the society.

Horse gram is reported to be photosensitive and a short-day plant; however, some day-neutral lines are also noted. Horse gram is a diploid species with chromosome number 2n=20, 22, 24 (Bhardwaj *et al*. 2013). Four subspecies has been reported under *Macrotyloma uniflorum* viz- *M. uniflorum* var. *stenocarpum* (Brenan) Verdc., *M. uniflorum* var. *verrucosum* Verdc., *M. uniflorum* var. *uniflorum* and *M. uniflorum* var. *benadirianum* (Choiv.) Verdc.

According to Indiastat (2019), the crop is cultivated in an area of 457.43 thousand hectares with a production of 296.86 thousand tonnes and productivity is 649 kg ha^{-1} in India. Horse gram is mostly cultivated in Karnataka, Tamil Nadu, Telangana, Andhra Pradesh, Maharashtra, hilly slopes of Uttarakhand, Madhya Pradesh, Jharkhand, Odisha etc. The crop is mainly grown as rabi crop but is also grown in kharif season for green manure and fodder purposes. The cultivation of crop in marginal land, lack of improved varieties, non-adoption of scientific cultivation methods and low consumer preference among public are the chief reasons for low production of horse gram compared to other pulses in India. In Kerala, the area and production of this crop are very low.

Horse gram is a therapeutically and nutritionally potential pulse crop included under super food as it is excellent source of protein, carbohydrate, dietary fibre, vitamins and minerals like iron, calcium which can help in removing malnutrition from the society. Apart from nutritional aspect, the horse gram has ethnomedicinal values too. The crop is used for treating insulin resistance and curing kidney stone. Various bioactive compounds present in horse gram seeds like phenols, tannins, phytic acids etc are now considered as anti-oxidants having many health benefits such as anti-hypercholesterolemic effects. Being a legume, it also enriches soil with atmospheric nitrogen through symbiotic association with the bacteria, rhizobium. Thus, horse gram can be a potential future crop due to its immense nutritional qualities and endurance to harsh climate.

Being a minor pulse, the crop has not got any due attention for its genetic upliftment. The Kerala Agricultural University has yet to release a high yielding variety in horse gram. Hence a systematic screening of the genotypes collected from diverse agro ecological conditions may identify cultivars with high yield, quality and tolerance to moisture stress.

In this context, the present study entitled “Genetic diversity analysis of horse gram [*Macrotyloma uniflorum* (Lam.) Verdc.] for moisture stress tolerance in south central laterites of Kerala” was undertaken with the following objectives.

- To evaluate and select moisture stress tolerant horse gram genotypes suited to the south-central laterites of Kerala.
- To evaluate the genotypes for physiological characters associated with moisture stress tolerance
- To evaluate inter-relationship between yield and yield contributing characters under moisture stress.
- To identify the superior parental lines for future breeding programmes.

Review of Literature

2. REVIEW OF LITERATURE

2.1. HORSE GRAM AND IMPORTANCE OF MOISTURE STRESS TOLERANCE

Horse gram, popularly considered as poor man's food is a hardy, multi-functional legume of semi-arid tropics. Seeds contain 18–29% protein, 57.2% carbohydrate, 3.2% minerals, 5.3% crude fibre and various vitamins such as thiamine, riboflavin, niacin and vitamin C (Gopalan *et al.*, 2006). It has been recognized as a potential food source for the future by the U.S. National Academy of Sciences in 1978.

Lately, climate change has brought back-to-back drought conditions in Kerala. The year 2016 faced one of the extreme droughts in the recent past. Even after the devasting floods of 2018, there were reports of drought overshadowing in the state with reduced streamflow and drying of wells at an alarming rate (Madhusoodhanan and Sreeja, 2019).

Shaji *et al.* (2009) reported a declining trend in groundwater availability over the past decades. Mainly rainfed system of agriculture is followed in Kerala with less than 30% of agricultural land under irrigation. Prolonged meteorological drought can severely affect agricultural activity in the state (Abhilash *et al.* 2019).

Among minor legumes, horse gram has a special status as a legume of indemnity under harsher environmental conditions. It is an underutilized pulse crop having considerable tolerance against various abiotic stresses like drought, heat, salinity, etc. (Sharma *et al.*, 2015) along with insurmountable pest resistance (Kawsar *et al.*, 2008). Farmers of Karnataka practice Panch Dhani, the cultivation of a mixture of five crops - horse gram, cowpea, indian bean, castor and niger to combat water deficit conditions (Kumar, 2006). Among different legumes, horse gram is a suitable candidate for studying moisture stress tolerance and is a potential source of genes/QTL for the same (Yasin, 2014). It is a crop that flourishes in a wide range of geographical locations with varying water availability and offers the basis to search for genetic variability and the mechanism of stress tolerance. However, only a few works of literature, dealing with the genetic mechanism of stress tolerance and physiological and biochemical responses of horse gram to moisture stress are available.

2.2. THE EFFECT OF PEG INDUCED MOISTURE STRESS ON MORPHO-PHYSIOLOGICAL PARAMETERS OF SEEDLINGS

Selection of drought-tolerant lines at seedling stage can be made by determining early vigour in terms of various seedling characters (Nagarajan and Rane, 2000).

The study of differences in pigeon pea cultivars under PEG induced moisture stress during seedling stage by Kumar *et al.* (2011) revealed decrease in germination percentage, root and shoot length, seedling dry weight and vigour index.

According to Kaur *et al.* (2017), a substantial reduction in germination, shoot and root length and their corresponding dry weight with increased concentrations of PEG was observed in green gram genotypes. In the study, drought-tolerant genotypes were scrutinized on the basis of germination percentage and vigour index.

A significant reduction was noted for germination percentage, shoot length, root length, seedling dry weight and seedling vigour in chickpea under PEG-induced moisture stress (Meena, 2017).

Jincy (2019) reported a significant decline in germination percentage, radicle length and vigour index at lower water potential concentration of PEG in mungbean.

The effect of PEG-induced moisture stress on 28 genotypes of black gram varieties at the seedling stage was studied by Shobanadevi *et al.* (2021) and a considerable decrease in germination percentage, length of radicle and plumule along with delay in initiation and completion of germination was observed.

2.3. EFFECT OF MOISTURE STRESS ON IMPORTANT BIOMETRIC CHARACTERS

Pawar (2006) reported that leaf area, leaf area index, leaf dry weight, root dry weight, pods per plant, biological yield and grain yield per plant showed higher sensitivity to moisture stress in horse gram.

2.3.1. Number of primary branches per plant

Yasin *et al.* (2014) observed a reduction in the number of primary branches per plant in horse gram under water stressed condition.

The performance of green gram and black gram genotypes under moisture stress condition was assessed by Pandiyan *et al.* (2017) and reported a reduction in number of branches per plant under stressed condition.

In a study conducted to compare the effects of water stress applied at different phenological phases of chickpea revealed that the number of primary branches was significantly lower when water stress was imposed at vegetative stage than at seed filling stage (Mekonnen, 2020).

2.3.2. Days to 50% flowering

Mwanamwenge *et al.* (1999) studied the effect of water stress during floral initiation, flowering and podding stage in three varieties of Fafa bean and reported that water stress caused considerable delay in flowering compared to the non-stressed environment.

Asfaw and Blair (2014) observed a highly significant varietal difference under water stress and non-stress condition for days to 50% flowering in Ethiopian common bean varieties.

Earliness in days to 50 % flowering by two-three days was observed in short and medium duration varieties of pigeon pea under drought stress imposed in the reproductive stage (Vanaja *et al.,* 2015).

2.3.3. Days to maturity

Ulemale *et al.* (2013) suggested early maturity as a remarkable character to avoid drought with the onset of severe water deficits.

The effect of water stress on the yield of cowpea was investigated by Dadson *et al.* (2005) and variations in days to maturity was noted. Earliness in maturity under water stress was noted in varieties viz. California Blackeye 5, Texas Cream 8, White

Acre and Two Crop Brown. However, the maturity was delayed in Quick Pinkeye, Mississippi Silver, Big Boy and Six Week Browneye genotypes by 2–10 days.

Urrea *et al.* (2009) and Belko *et al.* (2014) reported a reduction in days to maturity in dry bean and cowpea respectively under drought stress compared to well-watered conditions.

2.3.4. Plant height

Mafakheri *et al.* (2010) reported a significant effect of drought on plant height in chickpea when drought was induced during the vegetative phase and the anthesis stage.

In an experiment conducted by Ranawake *et al.* (2011) to study the effect of water stress on growth and yield of mung bean revealed that the plant height was significantly shortened due to stress applied at 3 weeks and 6 weeks after planting but not at 8 weeks after planting.

A pot culture study by Yasin *et al.* (2014) revealed a significant decrease in plant height under unirrigated conditions compared to irrigated conditions in horse gram.

Pandiyan *et al.* (2017) observed that the plant height was reduced when drought was imposed in the growth and reproductive stage in black gram and green gram.

2.3.5. Number of pods per plant

Mwanamwenge *et al.* (1999) evaluated the effect of water stress on the growth and yield of faba bean and observed that number of pods per plant was reduced in variety Icarus under moisture stress imposed at floral initiation, flowering and podding stage, while in varieties viz. ACC286 and Fiord, decline in the number of pods per plant was observed only when moisture stress was imposed at the podding stage.

Nleya *et al.* (2001) and Vanaja *et al.* (2015) also reported fewer pods in common bean and pigeon pea respectively under varying levels of soil moisture.

A severe decline in the number of pods per plant was observed under drought stress imposed at vegetative and reproductive stages in mungbean by Bangar *et al.* (2019).

2.3.6. Number of seeds per pod

Biradar *et al*. (2010) reported a reduction in the number of seeds per pod in green gram due to moisture stress.

Pandiyan *et al.* (2017) revealed a decrease in seeds per pod when drought was imposed in both black gram and green gram varieties under study.

A significant decline in the number of seeds per pod was observed when drought stress was imposed at vegetative and reproductive stages in mungbean (Bangar *et al.*, 2019).

2.3.7. 100 seed weight

Low hundred seed weight in mungbean was recorded under moisture stressed condition. This was attributed to shorter grain filling duration and decreased photosynthate mobilization to grains due to water stress at the pod filling stage (Sadeghipour, 2008).

Urrea *et al.* (2009) reported a significant reduction of 100 seed weight in dry beans under moisture stress.

In the study on drought tolerance in short-and medium-duration cowpeas, Belko *et al.* (2014) reported drought-tolerant genotypes had comparatively less decrease in 100 seed weight.

2.3.8. Seed yield per plant

The seed yield is noticeably determined by the timing, intensity and duration of drought stress (Blair *et al.*, 2012).

Pawar (2006) studied the physiological evaluation of drought resistance in horse gram and observed that grain yield per plant is considerably decreased under stress due to negative impact of drought on other morpho-physiological characters.

The seed yield was identified as a notable criterion of drought tolerance in common bean. Compared to non-stressed conditions, grain yield was significantly low in moisture stressed conditions in dry bean (Urrea *et al.*, 2009).

Under drought stressed condition, yield in green gram is greatly influenced by its ability to grow vigorously during the vegetative stage along with a better accumulation of dry matter (Biradar *et al.*, 2010).

Vanaja *et al.* (2015) observed varietal difference and considerably low seed yield per plant in pigeon pea under water stressed condition due to increased flower drops and decreased flower to pod conversion.

Mekonnen (2020) ascribed reductions in dry biomass, pod number per plant and 100 seed weight for the drop in seed yield per plant under drought in chickpea.

2.3.9. Haulm yield per plant

Moisture deficit has been reported to have a severe effect on peanut haulm yield when stress was imposed during the vegetative stage and pegging to pod formation stage, compared to stress during pod formation to pod maturity stage (Shinde and Pawar, 1984). Bacharou Falke *et al.* (2019) also reported a significant reduction in haulm yield per plant under drought stress in groundnut.

2.3.10. Seed yield per plot

Zaman and Mallick (1991) reported that horse gram seed yield was critically influenced by irrigation applied at the flowering stage and resulted in 34% more yield.

A study on the effect of water stress on the yield of cowpea was conducted by Dadson *et al.* (2005) in the Delmarva region of the United States in two seasons (2001 and 2002). It was concluded that seed yield in irrigated conditions was higher compared to a stressed condition in both seasons. The difference in seed yield within the same genotype was also noted in the two seasons.

Under water stress, Sudhakar *et al.* (2006) observed severe reduction in yield by 62% in black gram and 29% in green gram genotypes when compared to well-watered conditions. The decline in stomatal conductance and leaf area resulted in a reduction in dry matter accumulation and consequently low yield.

Mafakheri *et al.* (2010) reported that water stress imposed at the flowering stage resulted in 10% less yield when compared to that at the vegetative stage in chickpea. The genotypes identified as drought-tolerant ones gave the highest seed yield compared to the sensitive ones.

Drought imposed at the flowering and pod filling stage caused a significant decline in seed yield per plot in green gram compared to irrigated control ha(Rambabu, 2014).

2.3.11 Haulm yield per plot

In soybean highest haulm yield was obtained in the irrigated plot while water stress at flowering and pod filling stage brought a significant shortfall in haulm yield by 44% (Sridhara *et al.,* 1997).

Higher haulm yield in groundnut was reported under irrigated conditions compared to water deficit condition by Sounda *et al.* (2006). Similarly, in a study by Hamidou *et al.* (2012) to select drought-tolerant lines of groundnut, a reduction in haulm yield by 8-55% under water stress was observed.

Swetha and Hussain (2017) also observed similar results in chickpea due to higher vegetative growth and dry matter accumulation under irrigation.

2.3.12. Harvest index

According to Dadson *et al.* (2005), considerable variation for harvest index was noted among cowpea genotypes grown under water-stressed and non-stressed conditions. Higher harvest index was given by genotypes with lower biological yields and vice versa.

Moisture stress during the vegetative stage adversely affected the harvest index than stress imposed during the seed filling stage in chickpea. A decline in harvest index during the vegetative stage was attributed to loss of leaves by senescence under severe stress (Mekonnen, 2020).

2.3.13. Leaf area

Anbessa and Bejiga (2002) reported that drought-tolerant Ethiopian chickpea is characterized by smaller leaf size and diminished leaf area expansion to minimize transpiration under drought.

A significant decrease in leaf area was observed due to reduced leaf area expansion and premature leaf senescence under drought stress imposed at flowering and pod maturation stages by withdrawing irrigation in red gram (Nagajothi *et al.,* 2014).

According to Rambabu (2014) the negative effect of water stress on leaf area was more at vegetative stage than at flowering and pod filling stage in green gram.

2.3.13. Leaf weight

About 34% and 31% reduction in leaf fresh weight and dry weight respectively were reported in common bean by Ghanbari *et al.* (2013) under moisture stressed condition.

Abhari and Gholinezhad (2019) also observed a decrease in leaf dry weight by 24% and 10% in chickpea, when a water deficit was imposed in 2016 and 2017.

In comparison to control, imposition of drought for 7 and 14 days significantly reduced the fresh and dry leaf weight in green gram (Uddin *et al.,* 2021).

2.3.14. Root parameters - Root length and Root dry weight

In plants, roots are the first organs to detect and respond to moisture stress. Improved adaptation of crops to water stress can be achieved by studying the root parameters like root length, root architecture etc. (Vadez, 2014).

Blum (1996) and Maseda and Fernández (2006) reported the accumulation of abscisic acid in the roots under drought stress condition. This resulted in an increased root biomass which in turn enhanced hydraulic conductivity and thereby provided drought tolerance.

A marginal reduction in root dry weight and root length under moisture stress was reported by Anbessa and Bejiga (2002) in Ethiopian chickpea genotypes. But in the susceptible variety ‘Mariye’, reduction in these characters was significant.

Ranawake *et al.* (2011) studied the effect of drought stress on growth, yield and root characters of green gram at three different growth stages and observed that length of taproot was significantly affected by 10-day stress given at 6 weeks after planting, while stress given at 3 weeks and 8 weeks after planting didn’t significantly affect root characters.

The outcome of water stress on root growth differed among species with the intensity of stress imposed. Under a water deficit environment horse gram, common bean, faba bean and soybean genotypes showed reduction in root length (Yasin *et al.,* 2014; Polania *et al.,* 2017; Belachew *et al.,* 2018; Gao *et al.,* 2020), while in chickpea and some species of genus *Vigna,* an increase in root length was observed (Ramamoorthy *et al.,* 2017; Iseki *et al.,* 2018).

Similarly, Prakash *et al.* (2018) evaluated black gram genotypes for drought tolerance based on root dynamics and observed higher values in root parameters viz. root length and dry weight of root under severe water stress.

Santos *et al.* (2020) reported that when subjected to moisture stress, drought tolerant cowpea genotypes recorded increased root dry weight of 24.57 %.

2.4. PHYSIOLOGICAL STUDY

2.4.1. Relative water content (RWC)

Under moisture stress, the genotypes with high RWC are identified as drought-tolerant because many physiological processes of the plants that contribute to growth and yield are affected by leaf water levels. Thus, RWC is considered a true indicator of drought stress in plants (Kramer, 1969).

Bhardwaj and Yadav (2012a) evaluated drought tolerant variety (HPK 4) and sensitive variety (HPKC 2) of horse gram under water stress. The study revealed that RWC was found to be significantly higher in the tolerant variety under drought stress. However, in a study by Yasin *et al.* (2014), the RWC was found to be maintained in both control and water-stressed genotypes of horse gram. Due to osmoregulation linked with anatomical changes, the RWC was found to be unaltered under moisture stress conditions.

Similarly, Verma *et al.* (2019) observed that under moisture stress at 50% flowering stage in chickpea, RWC of leaves was less compared to irrigated control. The reduction in RWC is more in drought susceptible genotypes, while tolerant genotypes maintained better water relations.

2.4.2. Leaf area index (LAI)

Bastos *et al.* (2011) reported that under a water deficit condition the LAI was found to be reduced by 20% in cowpea genotypes. Similarly, Ghanbari *et al.* (2013) observed a considerable reduction in LAI under moisture stress in common beans.

In green gram and black gram, a significant reduction in LAI under water deficit was attributed to smaller leaf expansion and this was regarded as a strategy to maintain water content inside the cell under stress (Baroowa and Gogoi, 2015).

2.4.3. Specific leaf area (SLA)

Specific leaf area is a key character for plant performance in response to environmental changes (Zhou *et al.*, 2020).

The effect of moisture stress on leaf area development in pigeon pea investigated by Lopez *et al.* (1997) revealed SLA under stress condition wasn't significantly lower than the control.

Berova and Zlatev (2002) reported a reduction in SLA under drought conditions in *Phaseolus vulgaris* due to a significant decrease in leaf area.

Wellstein *et al.* (2017) reported reduced SLA under moisture stress is associated with increased water use efficiency.

2.4.4. Drought tolerance indices- Stress tolerance index (STI), Geometric mean productivity (GMP), Mean productivity (MP) and Yield stability index (YSI)

The drought-tolerant genotypes have greater values of drought indices like MP, YSI and STI (Fernandez, 1992; Gholinezhad *et al*., 2014; Darkwa *et al*., 2016). Gholinezhad *et al*. (2014) proposed to use indices STI, GMP, MP to select drought-tolerant genotypes under moisture stress conditions as these indices support stable and high yield in both non-stress and stress conditions.

According to Sen *et al.* (2019) drought indices - MP, GMP and STI are the best selection criterion under late sown conditions and are the best-fit parameters for lentil breeding.

2.5. BIOCHEMICAL STUDY

2.5.1. Proline content

Several pieces of literature are available on the role of proline under drought stress. According to Stewart and Hanson (1980) proline is formed as a metabolite but not as an adaptive response to water stressed condition. While Aspinall and Paleg (1981) reported increased content of proline as a signal of drought resistance in crops. Chiang and Dandekar (1995) reported proline level in tissue as an indicator of the degree of water deficit.

Under moisture stress, proline protects and stabilizes essential cell components, photosynthetic apparatus and detoxifies reactive oxygen species and thus plays an important role in cellular osmotic adjustments (Ashraf and Foolad, 2007).

In a study conducted to compare biochemical enzymes in drought tolerant and sensitive horse gram variety under drought stress, the proline content was found to be higher in the tolerant variety (Bhardwaj and Yadav, 2012a).

Baroowa and Gogoi (2015) reported that proline content in leaf was significantly high in black gram and green gram under water deficit conditions.

2.5.2. Chlorophyll content

Zhang and Kirkham (1996) reported that the chlorophyll content was reduced based on the duration and severity of drought level. The reactive oxygen species formed during moisture stress by excess energy absorbed by photosynthetic apparatus reduces total chlorophyll level and thus lower the capacity of plants for light-harvesting (Herbinger *et al.*, 2002).

Anjum *et al.* (2011) suggested lesser chlorophyll content under drought stress as a typical sign of chlorophyll degradation and pigment photo-oxidation.

According to Jincy *et al.* (2020), chlorophyll A, chlorophyll B and total chlorophyll decreased in green gram genotypes under water stress compared to the control. The genotype ‘VGG 17010’ genotype recorded high chlorophyll content which was attributed to the increased content of PS I and PS II subunits that protect chlorophyll proteins from proteasomal degradation.

2.6. SEED QUALITY PARAMETER

2.6.1. Crude protein

Peterson *et al.* (1992) found that under water deficit conditions in legumes, the changes in crude protein concentration was inconsistent.

Alghamdi (2009) observed an increase in protein content of faba bean seeds under lower irrigation levels compared to higher irrigation treatment. This was attributed to the fact that in plants grown under higher moisture levels, the distribution of photosynthetic substrates was higher and so these plants had higher seed yield but less protein content.

However, Choukri *et al.* (2020) reported a decrease in the protein content in lentil seeds under drought stress.

2.6.2. Total phenol content in seed

Sreerama *et al.* (2012) evaluated the nutritional qualities in cowpea, horse gram and chickpea flour and reported that the contents of total polyphenols were significantly higher in horse gram than in cowpea and chickpea.

The overall nutritional profile of horse gram seeds is affected by environmental as well as the agricultural condition and also by variety. Further, the acceptance of horse gram for human consumption is challenged by the high levels of anti-nutritional compounds like polyphenols, phytic acid and tannins in dry horse gram seeds. (Goswami**,** 2017).

Sharma *et al.* (2019) also reported raw horse gram seeds are rich in polyphenols, flavonoids, proteins and major antioxidants.

2.7. STATISTICAL ANALYSIS

The literature available on various characters are reviewed under the following headings:

1. Variability
2. Heritability and Genetic advance
3. Correlation analysis
4. Path coefficient analysis
5. Divergent Analysis

2.7.1. VARIABILITY

The success of the plant breeding programme chiefly depends on the extent of phenotypic and genotypic variability present in the gene pool. The existence of sufficient genetic variability enables the breeders to create new gene combinations through hybridisation.

The variability study in horse gram by Durga (2012) revealed sufficient variation in genotypes under study. A high difference between PCV and GCV was recorded for the number of primary branches per plant and the plant height. Whereas the difference between PCV and GCV was less among test weight, seed yield per plant and pod haulm per plant, pointing to lower environmental influence on the expression of the above-said traits.

Vanaja *et al.* (2015) assessed the genetic variability in three red gram genotypes under drought conditions and reported there existed significant variability between the genotypes for seed yield under moisture stress in comparison to well-watered conditions.

Langat *et al.* (2019) evaluated the variability present in sixteen progeny lines of common beans under moisture stressed condition and noticed high phenotypic and genotypic coefficient of variation estimates for the number of pods per plant, hundred seed weight, yield per plant and days to maturity, under stress condition.

Priyanka *et al.* (2019) investigated the existence of genetic variability in 252 horse gram genotypes. The genotypes showed wide variation and the difference between the PCV and GCV was small, signalling lesser influence of environment on expression of traits under study.

2.7.2. HERITABILITY AND GENETIC ADVANCE

Heritability and genetic advance are the two important selection indices. Estimation of heritability provides an idea about the inheritance of traits from parents to progeny. While genetic advance gives information about the superiority of the selected individuals over the parental population. Effective selection can be achieved by choosing traits showing high heritability and genetic advance.

In horse gram, traits like the number of branches per plant, seeds per pod, yield per plant and yield per plot expressed high heritability (BS) and high genetic advance reflecting additive gene action on these traits, while days for 50 % flowering, plant height, days to maturity and protein content exhibited high heritability and low genetic advance (Bhadait, 2005).

In common beans under water deficit condition, high heritability was estimated for all traits under study; but only days to maturity, number of pods per plant, number of grains per pod, yield per plant and harvest index had high heritability and high GAM revealing that selection of these traits lead to improved traits under drought (Langat *et al.,* 2019).

In horse gram, high heritability coupled with high GAM was noted for seed yield per ha (65.28%, 41.93) and high heritability with moderate GAM was found for days to 50% flowering (99.42%, 10.52) indicating the prevalence of additive gene action for these traits (Vijayakumar *et al.,* 2016). But days to maturity exhibited high heritability with low GAM signalling nonadditive gene action and the high heritability effecting from the favourable environment (Neelima *et al.,* 2021).

2.7.3. CORRELATION ANALYSIS

Correlation analysis between different plant character pairs provides an idea of the extent and direction of their association and thus helps in the selection of those characters which increases the yield.

Correlation analysis aids in understanding the degree of relationship between related characters with yield and yield contributing characters at the genetic level and also in selection for improvement of correlated traits in horse gram (Singh *et al.,* 2020).

Vanaja *et al.* (2015) studied the extent of association between various physiological and biochemical parameters with seed yield under water deficit condition in pigeon pea. A significant positive association of seed yield was recorded with proline content, seed number and hundred seed weight in the study.

Correlation analysis in horse gram by Alle *et al.* (2016) revealed positive and significant association of 100 seed weight, plant height, number of primary branches, number of seeds per pod and number of pods per plant with seed yield per plant. But days to 50% flowering recorded positive non-significant association with yield.

Mohanlal *et al.* (2018) performed correlation analysis in 21 black gram genotypes under water stress and reported positive correlation was noted between seed yield per plant with the number of branches, plant height, number of pods per plant and number of seeds per pod. However, a negative and considerable association was observed between seed yield per plant with leaf chlorophyll content.

Under moisture stress in green gram, a negative correlation was recorded between proline, protein content, RWC and yield parameters. Chlorophyll content showed a significant association with proline and protein content. Plant height was strongly associated with the leaf area, the number of seeds per pod and the number of pods per plant. Leaf area was negatively associated with proline, but exhibited a positive correlation with RWC, protein content and yield components (Bangar *et al.,* 2019).

2.7.4. PATH COEFFICIENT ANALYSIS

Path coefficient analysis discloses the association of yield contributing character on yield by breaking the total correlation coefficient into direct and indirect effects and thus helps in indirect selection.

In a trait association study by Asfaw *et al.* (2017) in the Andean common bean accessions, days to flowering, leaf chlorophyll content and harvest index showed the positive and negative direct effect towards seed yield under water stress and irrigated condition respectively. Days to maturity exhibited negative direct effect under drought stress and a positive direct effect under non-stressed condition.

In a cause-and-effect relationship study in horse gram by Priyanka *et al.* (2019) a positive and high direct effect on seed yield by number of pods per plant, number of seeds per pod, days to maturity and hundred seed weight was observed.

Singh and Salam (2021) estimated the direct and indirect effects of various characters on seed yield of horse gram and reported that on genotypic level, highest direct effect was recorded by pods per plant followed by primary branches per plant, days to 50% flowering and seeds per pod.

2.7.5. DIVERGENT ANALYSIS

For the genetic improvement of any crop, knowledge about the magnitude of existing diversity and the heritability of characters attributing to the divergence in the population is a must. A superior progeny can be developed by crossing genetically divergent parents rather than closely related ones as such crossings lead to more heterosis. D^2 statistics developed by P.C. Mahalanobis in 1928, aids in the identification of genetically divergent parents for use in hybridisation programmes (Singh and Narayanan, 2013).

Based on D^2 statistics, hundred accessions of horse gram were classified into sixteen clusters by Geetha *et al.* (2011) and it was found that seed yield, number of pods per plant, number of branches per plant and plant height contributed more towards genetic divergence.

Varma *et al.* (2013) assessed genetic diversity among 23 accessions of horse gram using Mahalanobis D^2 statistics and grouped them into seven clusters. Among yield component traits, test weight (8.7 %) followed by seed yield per plant (5.5 %) and pod length (2.4 %) offered utmost contribution towards genetic divergence.

Genetic diversity in 48 horse gram genotypes were assessed by Sahoo *et al.* (2014) and reported that days to maturity and days to flowering made a major contribution towards divergence in horse gram.

To select drought-tolerant genotypes among 25 black gram genotypes Kumar *et al.* (2021) performed divergence analysis and classified them into 6 clusters. The greatest inter-cluster distance was between cluster II and IV (160.19) indicating the suitability of genotypes in these clusters for hybridisation programme. Highest contribution to genetic diversity was made by plant height followed by grain yield per plant and days to 50% flowering.

Materials and Methods

3. MATERIALS AND METHODS

The present investigation entitled “Genetic diversity analysis of horse gram [*Macrotyloma uniflorum* (Lam.) Verdc.] for moisture stress tolerance in south central laterites of Kerala” was conducted at Farming Systems Research Station, Sadanandapuram during 2019-2021. The information on materials and methods adopted for the study are described below.

3.1. EXPERIMENTAL MATERIALS

Thirty horse gram accessions, collected from RARS Pattambi under Kerala Agricultural University and various research stations of other State Agricultural Universities were used for evaluation in the laboratory and field. List of genotypes along with their source, used in present study is enlisted in Table 1.

3.2. EXPERIMENTAL SITE

The project involving laboratory and field studies was conducted at Farming Systems Research Station, Sadanandapuram which is located at a latitude of 8.99° N, longitude of 76.82°E and an altitude of 76 m above mean sea level.

3.3. EXPERIMENTAL DESIGN

Experiment was conducted as laboratory and field study.

3.3.1. Laboratory experiment

Laboratory experiment was conducted during October, 2020 in Factorial Completely Randomized Design with thirty accessions of horse gram in three replications. Ten surface sterilized seeds of each accession were subjected to various osmotic potential by raising them in rolled paper towel at 10% and 20% concentration of PEG-6000. These concentrations for screening was fixed, based on studies made by Meena (2017) in chickpea and Roy *et al.* (2020) in lentil. The genotypes were taken as factor A and the two different PEG 6000 concentrations as factor B, considering both genotypes and PEG concentrations as treatments. A control treatment without moisture stress was also maintained. Various morpho-physiological parameters were recorded at 10 days after sowing.

3.3.2. Field Experiment

The field study was conducted from November 2020 to March 2021 in Randomized Block Design with 30 genotypes in three replications. Seeds soaked overnight in water were dibbled at a spacing of 30 × 30 cm into raised beds of 2.25m^2 area. The “Package of Practices Recommendations Crops 2016” recommendation of Kerala Agricultural University (KAU, 2016) was adopted to raise the crop. The moisture stress was imposed in the field by withdrawing irrigation for 15 days at critical stages of growth viz. flowering and podding stage of the crop (reproductive stage). The soil moisture was also measured during this period at weekly interval by following gravimetric method. One control block with all genotypes was maintained under irrigated conditions.

3.4. OBSERVATIONS RECORDED

3.4.1. Morpho-physiological observations of laboratory experiment

3.4.1.1. Germination percentage

Germination percentage was computed as,

$$\text{Germination (\%)} = \frac{\text{Number of seeds germinated}}{\text{Total number of seeds tested}} \times 100$$

3.4.1.2. Shoot length (cm)

Shoot length from the base to the tip of shoot of ten days old seedlings was measured using thread and a scale and recorded in centimetre.

3.4.1.3. Root length (cm)

Root length from the base to the tip of root of ten days old seedlings was measured using thread and a scale and recorded in centimetre.

Table 1: List of horse gram [*Macrotyloma uniflorum* (Lam.) Verdc.] genotypes used in the evaluation

Genotypes	Name of genotype	Source
T_1	IC145300	RARS Pattambi, KAU
T_2	IC71841	RARS Pattambi, KAU
T_3	IC139464	RARS Pattambi, KAU
T_4	IC120753	RARS Pattambi, KAU
T_5	IC39353	RARS Pattambi, KAU
T_6	HG 34 L	UAHS, Shivamooga
T_7	IC15730	RARS Pattambi, KAU
T_8	IC392329	RARS Pattambi, KAU
T_9	HG 26 L	UAHS, Shivamooga
T_{10}	IC277671	RARS Pattambi, KAU
T_{11}	IC406382	RARS Pattambi, KAU
T_{12}	IC22785	RARS Pattambi, KAU
T_{13}	IC26138	RARS Pattambi, KAU
T_{14}	HG 31 L	UAHS, Shivamooga
T_{15}	GDH-1	SDAU, Gujarat

Genotypes	Name of genotype	Source
T_{16}	HG 27 L	UAHS, Shivamooga
T_{17}	IC139470	RARS Pattambi, KAU
T_{18}	IC139435	RARS Pattambi, KAU
T_{19}	IC139554	RARS Pattambi, KAU
T_{20}	IC88926	RARS Pattambi, KAU
T_{21}	IC67011	RARS Pattambi, KAU
T_{22}	HG 18 L	UAHS, Shivamooga
T_{23}	IC139453	RARS Pattambi, KAU
T_{24}	IC22759	RARS Pattambi, KAU
T_{25}	IC26132	RARS Pattambi, KAU
T_{26}	IC123030	RARS Pattambi, KAU
T_{27}	IC283202	RARS Pattambi, KAU
T_{28}	IC22827	RARS Pattambi, KAU
T_{29}	IC221105	RARS Pattambi, KAU
T_{30}	HG 24 L	UAHS, Shivamooga

3.4.1.4. Seedling dry weight (g)

Five seedlings were selected randomly, oven dried at 80°c for 2 days to attain constant weight and average weight was recorded in grams.

3.4.1.5. Seedling vigour index

Seedling vigour index I (SV I) and II (SV II) were estimated as suggested by Abdul-Baki and Anderson (1973),

SV I = [germination percentage × mean (root length + shoot length)]
SV II = [germination percentage × Seedling dry weight

3.4.2. Biometric observations of field experiment

3.4.2.1. Days to 50% flowering

Number of days taken from sowing to flowering of 50 per cent of plants in each plot was recorded.

For recording of following observations, five plants were randomly selected from each plot and recorded.

3.4.2.2. Number of primary branches per plant

Total number of branches on the main of stem of the selected plants were counted and recorded at maturity stage.

3.4.2.3. *Days to maturity*

Days to maturity was counted from the date of sowing to the date of attaining maturity and was recorded.

3.4.2.4. Plant height (cm)

Height of selected plants from soil surface to the tip of the stem was measured using a metre tape at the time of maturity and mean value was recorded in centimetres.

a) At 7 days after sowing

b) At 20 days after sowing

c) At harvesting stage

Plate 1. General field view

3.4.2.5. Number of pods per plant

Total number of seed-bearing pods of the selected plants in each plot was counted and mean value was recorded.

3.4.2.6. Number of seeds per pod

Number of seeds in five randomly selected pods of observational plants were counted and was averaged out.

3.4.2.7. 100 seed weight (g)

Hundred uniform seeds of the genotypes in each plot were selected and the weight was recorded in grams.

3.4.2.8. Seed yield per plant (g)

Pods collected from observational plants were dried, seeds were separated and average seed weight was recorded.

3.4.2.9. Haulm yield per plant (g)

Total weight of each plant parts other than seeds were weighed and expressed in grams.

3.4.2.10. Seed yield per plot (g per plot)

Weight of the seeds extracted from dried pods in each plot was recorded.

3.4.2.11. Haulm yield per plot (g per plot)

Total weight of plant parts other than seeds from each plot was recorded.

3.4.2.12. Harvest Index (%)

Harvest index is worked out using the given formula:

$$\text{Harvest index (HI)} = \frac{\text{Economic yield}}{\text{Biological yield}} \times 100$$

Where, economic yield included seed weight and biological yield included the seed weight and weight of total shoot biomass such as leaves, stem etc.

3.4.2.13. Leaf area (cm^2)

The area of trifoliate leaf of the selected plants was plotted on a graph paper and maximum length of leaf and maximum breadth of leaf was measured with the help of a scale. The total leaf area of the plant was calculated as per method adopted by Shinde (2012).

Total Leaf area of the plant = $L \times B \times N \times F$

Where,

L= Maximum length of leaf
B= Maximum breadth of leaf
F= Correlation factor (0.68)
N= Number of leaves

The following characters were recorded during moisture stress period:

3.4.2.14. Leaf fresh weight (g)

Leaf samples from observational plants were collected in polyethylene bags and were immediately taken to laboratory to determine the weight.

3.4.2.15. Turgid weight of leaf (g)

After noting the fresh leaf weight, the leaf samples were cut into small leaf discs and was soaked in distilled water for two hours. After blotting leaf discs with tissue paper turgid weight of leaves was recorded.

3.4.2.16. Leaf dry weight (g)

The collected leaf samples were oven dried at 80°c for 2 days to attain constant weight and then their weight was recorded.

3.4.2.17. Root length (cm)

Root length was measured from collar to tip of primary roots in centimetres.

3.4.2.18. Root dry weight (g)

Root of the selected plants were collected and oven dried at 80°c for two days and their weight was recorded in grams.

3.4.3. Physiological observation

Various parameters like fresh weight (g), turgid weight (g), dry weight (g) and leaf area during water stress and seed yield per plant recorded in 3.4.2 was used for calculating following observations.

3.4.3.1. Relative water content (%)

The relative water content of the leaves during stress was estimated by the method proposed by Barrs and Weatherly (1962).

$$\text{RWC (\%)} = \frac{\text{Leaf fresh weight} - \text{Leaf dry weight}}{\text{Leaf turgid weight} - \text{Leaf dry weight}} \times 100$$

3.4.3.2. Specific leaf area ($cm^2\ g^{-1}$)

$$\text{Specific leaf area (SLA)} = \frac{\text{Leaf area}}{\text{Leaf dry weight}}$$

3.4.3.3. Leaf area index

$$\text{Leaf area index (LAI)} = \frac{\text{Total leaf area}}{\text{Ground area}}$$

3.4.3.4. Stress tolerance index

According to Fernandez (1992),

$$\text{Stress tolerance index (STI)} = \frac{Y_{PI} \times Y_{SI}}{(Y_P)^2}$$

3.4.3.5. Geometric mean productivity

According to Fernandez (1992),

$$\text{Geometric mean productivity (GMP)} = \sqrt{}(Y_{SI})(Y_{PI})$$

3.4.3.6. Mean productivity

According to Fernandez (1992),

$$\text{Mean productivity} = \frac{(Y_{SI}+Y_{PI})}{2}$$

3.4.3.7. Yield stability index

According to Bouslama and Schapaugh (1984),

$$\text{Yield stability index} = Y_{SI}/\ Y_{PI}$$

Where,

Y_{PI} = yield of individual genotypes without stress,

Y_{SI} = yield of individual genotypes with stress and

Y_P = average yield of all genotypes of without stress.

3.4.4. Biochemical study

3.4.4.1. Estimation of Proline (µmol g^{-1})

Proline content was estimated during the moisture stress period (at post flowering stage) using the acid ninhydrin method suggested by Sadasivam and Manickam (1996).

Sample extract was prepared by homogenising 0.5 gram of fresh leaf in 10 ml of 3% aqueous sulphosalicylic acid. After filtration of homogenate, 2 ml of sample filtrate was taken in a test tube and added with 2 ml each of acetic acid and acid ninhydrin. The solution mixture was then heated at 100°c for one hour in water bath. After one hour, the reaction was terminated by placing test tubes in ice bath for 10 minutes. Then the reaction mixture was stirred well after adding 4 ml of toluene. The chromatophore containing toluene was collected, warmed to room temperature and absorbance at 520 nm was recorded with toluene as blank. A series of proline standard was prepared using L-proline powder and the standard curve was drawn. The proline content of sample was found out with the help of the standard curve.

$$\text{Proline content } (\mu\text{mol g}^{-1}) = \frac{(\mu\ \text{proline/ml} \times \text{ml toluene})}{115.5} \times \frac{5}{\text{g sample}}$$

3.4.4.2. Estimation of chlorophyll (mg g^{-1})

The chlorophyll content of leaves were estimated as per procedure reported by Arnon (1949). A 0.5 g of leaf sample taken from third fully expanded leaf was cut into tiny bits and put into test tube. The samples were then incubated overnight with 10 ml 80% acetone: DMSO mixture (1:1 v/v). The coloured solution was transferred into a measuring cylinder and made up to 25 ml with 80% acetone: DMSO mixture. The absorbance was measured at 480 nm, 510 nm, 645 nm and 663 nm against 80% acetone: DMSO mixture blank. The chlorophyll content was estimated in mg g^{-1} using following equations:

$$\text{Chlorophyll a (mg g}^{-1}) = (12.7 \times A_{663} - 2.69 \times A_{645}) \times \frac{1 \times V}{1000 \times \text{fresh weight}}$$

$$\text{Chlorophyll b (mg g}^{-1}) = (22.9 \times A_{645} - 4.68 \times A_{663}) \times \frac{1 \times V}{1000 \times \text{fresh weight}}$$

$$\text{Total chlorophyll (mg g}^{-1}) = (20.2 \times A_{645} + 8.02 \times A_{663}) \times \frac{1 \times V}{1000 \times \text{fresh weight}}$$

Where, A = absorbance at specific wavelength,
V = final volume of chlorophyll extract in 80% Acetone: DMSO mixture;
W = fresh weight of tissue extracted

3.4.5. Seed quality aspects

3.4.5.1. Estimation of crude protein content of seeds (%)

Crude protein content of seed was calculated by estimating nitrogen content of seed by Kjeldahl method (Mckenzie and Wallace,1954) and multiplying the N value with the constant 6.25.

3.4.5.2. Estimation of total phenol content in seed (mg g^{-1})

Phenol content in seed was estimated using the method suggested by Sadasivam and Manickam (1996). A 0.5 g of seed was homogenized in 5 ml of 80% ethanol. The homogenate was centrifuged at 10,000 rpm for 20 minutes and supernatant obtained was then evaporated to dryness. The residue was later dissolved in 5 ml of distilled water. A 2 ml of aliquot was pipetted out into test tubes and final volume was made up to 3 ml using distilled water. To this 0.5 ml of Folin-Ciocalteau reagent was added. After 3 minutes, 2 ml of 20% Na_2CO_3 solution was added to each tube and was thoroughly mixed. The tubes were placed in boiling water for 1 minute, cooled and absorbance reading was recorded at 650 nm against a reagent blank. From standard curve prepared with different concentrations of catechol, phenol content of sample was found out.

3.4.6. STATISTICAL ANALYSIS

3.4.6.1. ANOVA

3.4.6.1.1. Analysis of Variance of factorial CRD (laboratory study)

To estimate variance components, the mean values of various morpho-physiological observation of all treatments in laboratory experiment was subjected to FCRD (Panse and Sukhatme, 1967).

Sources of variation	d.f	Sum of squares	Mean squares	F ratio
Factor A	(a-1)	SSA	MSA = $\frac{\mathrm{SSA}}{(\mathrm{a}-1)}$	$\frac{\mathrm{MSA}}{\mathrm{MSE}}$
Factor B	(b-1)	SSB	MSB = $\frac{\mathrm{SSB}}{(\mathrm{b}-1)}$	$\frac{\mathrm{MSA}}{\mathrm{MSE}}$
A×B	(a-1) × (b-1)	SS(A×B)	MS(A×B) = $\frac{\mathrm{SS}(\mathrm{A}\times\mathrm{B})}{(\mathrm{a}-1)\times(\mathrm{b}-1)}$	$\frac{\mathrm{MS}(\mathrm{A}\times\mathrm{B})}{\mathrm{MSE}}$
Error	ab (r-1)	SSE	MSE = $\frac{\mathrm{SSE}}{\mathrm{ab}(\mathrm{r}-1)}$	
Total	(abr-1)	TSS		

Where,

a = number of levels of factor A

b = number of levels of factor B

r = number of replications

SSA = sum of squares for factor A

SSB = sum of squares for factor B	TSS = Total sum of square

SS(A×B) = sum of squares for interaction (A×B)

SSE = sum of squares for error

MSA = mean sum of squares factor A

MSB = mean sum of squares factor B

MS(A×B) = mean squares for interaction (A×B)

MSE = mean squares for error

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

Where, t_{α} = student's t table value distribution at error degree of freedom and α = level of significance (1% or 5%)

3.4.6.1.2. Analysis of Variance for field experiment (RBD)

To test the difference between the treatment means and identify the significance of differences among genotypes, ANOVA of RBD (Panse and Sukhatme, 1967) was worked out for all traits under field study.

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

Where,

r = number of replications	t = number of treatments
SSR = sum of squares for replications	MST = mean squares for treatment
SST = sum of squares for treatments	MSR= mean squares for replication
SSE = sum of squares for error	MSE = mean squares for error
TSS = total sum of squares	

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

Where, t_α = student’s t table value distribution at error d.f and α = level of significance (1% or 5).

3.4.6.2. Estimation of Genetic Parameters

3.4.6.2.1. Genetic components of variance

For each character, the phenotypic and genotypic components of the variance were estimated by utilizing the respective mean squares (MS) (Jain, 1982).

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

Environmental Variance (V_E) = MSE

Phenotypic Variance (V_P) $= V_G + V_E$

3.4.6.2.2. Coefficient of variation

Using phenotypic variance, genotypic variance and environmental variance for each trait, the respective coefficient of variations was estimated and expressed in percentage.

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

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

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

Where, $\bar{X}$ = grand mean

The GCV and PCV were sorted as low (less than 10%), moderate (10 - 20%) and high (more than 20%) as proposed by Sivasubramanian and Menon (1973).

3.4.6.3. Heritability (broad sense)

It is computed for various characters applying the formulae suggested by Burton (1952) and Johnson *et al.* (1955) and is expressed as percentage.

Heritability, $H^2 = \frac{V_G}{V_P} \times 100$

Where, V_G= genotypic variance and V_P = phenotypic variance

Classification of range of heritability by Johnson *et al.* (1955):

Low : 0 - 30%
Medium : 30 - 60%
High : 60 - 100%

3.4.6.4. Genetic Advance

Genetic advance is a measure of genetic improvement under selection which depends on genetic variability, heritability and selection intensity. Genetic advance was computed at 5 % selection intensity using the formula recommended by Johnson *et al.* (1955).

$$GA = k.H^2\sqrt{V_P}$$

Where, k = standardized selection differential (2.06 at 5% selection intensity)

Genetic advance as per cent of mean = $\frac{GA}{\bar{X}} \times 100$

Classification of range of GA as per cent of mean by Johnson *et al.* (1955):

Low : 0 - 10%
Moderate : 10 - 20%
High : 20 - 100%

3.4.6.5. Correlation Analysis

Correlation coefficient analysis measures index of relationship between two or more variables. For characters with significant variation, genotypic and phenotypic correlation coefficients were calculated using the formula suggested by Falconer (1964):

$$\text{Genotypic coefficient of correlation} = r_g = \frac{GCOV_{xy}}{\sqrt{GVx.GVy}}$$

$$\text{Phenotypic coefficient of correlation} = r_p = \frac{PCOV_{xy}}{\sqrt{PVx.PVy}}$$

Where $GCOV_{xy}$ and $PCOV_{xy}$ denotes respectively genotypic and phenotypic co-variances between the two characters x and y. GVx and GVy denotes the genotypic variance for the character x and y respectively. PVx and PVy denotes phenotypic variance for the character x and y respectively.

3.4.6.6. Path Coefficient Analysis

The direct and indirect contribution of various yield attributing characters on yield and cause of association between the characters was unravelled by path coefficient analysis as proposed by Wright (1954).

The path coefficient is found by solving simultaneous equations.

$$r_{ny} = p_{ny} + r_{n2}\,p_{2y} + r_{n3}\,p_{3y} + \ldots\ldots\ldots\ldots\ldots + r_{nx}\,p_{xy}$$

Where,

r_{ny} represents correlation coefficient between casual factor ‘n’ and yield (y).

p_{1y}, p_{2y}….p_{ny} are direct effects of character 1 to ‘n’ respectively on character y.

r_{n2}, r_{n3}………r_{nx} denote coefficient of correlation between that character and each other yield component in turn.

In the matrix form

$$\begin{bmatrix} r_{1y} \\ r_{2y} \\ \vdots \\ \vdots \\ \vdots \\ r_{ny} \end{bmatrix} = \begin{bmatrix} 1 & r_{12} & r_{13} & \cdots & \cdots & r_{1n} \\ r_{21} & 1 & r_{23} & \cdots & \cdots & r_{2n} \\ \vdots & \cdots & \cdots & \cdots & \cdots & \vdots \\ \vdots & \cdots & \cdots & \cdots & \cdots & \vdots \\ \vdots & \cdots & \cdots & \cdots & \cdots & \vdots \\ r_{n1} & r_{n2} & r_{n3} & \cdots & \cdots & 1 \end{bmatrix} \begin{bmatrix} p_{1y} \\ p_{2y} \\ \vdots \\ \vdots \\ \vdots \\ p_{ny} \end{bmatrix}$$

Matrix A Matrix B Matrix C

Where, [A] = Correlation matrix between yield and biometrical traits

[B] = Correlation matrix between different biometrical traits

[C] = Path coefficient matrix

Then value of [C] = $[B]^{-1}$ [A]

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

Where, $r^2 = p_{1y} r_{1y} + p_{2y} r_{2y} + \ldots\ldots\ldots + p_{ny} r_{ny}$

The direct and indirect effects were categorised as negligible (0.00 – 0.09), low (0.10 – 0.19), moderate (0.20 – 0.29), high (0.30 - 1.00) and very high (greater than 1.00) as mentioned by Lenka and Mishra (1973).

3.4.6.7. Genetic Divergence

The magnitude of genetic divergence was studied by technique of Mahalanobis D^2 statistics. The genotypes were arranged into different cluster constellations based on the D^2 values, following Tocher’s method (Rao, 1952).

Results

4. RESULTS

The present study entitled “Genetic diversity analysis of horse gram [*Macrotyloma uniflorum* (Lam.) Verdc.] for moisture stress tolerance in south central laterites of Kerala” was conducted at Farming Systems Research Station (FSRS), Sadanandapuram, Kottarakkara as two experiments during 2019-21. The first experiment was carried out in the laboratory to study the various morpho-physiological aspects of different horse gram genotypes to the moisture stress induced by PEG 6000 at the seedling stage. In the second experiment, these genotypes were evaluated in the field for moisture stress tolerance. The data collected were statistically analyzed and the results are presented in this chapter.

4.1. LABORATORY EXPERIMENT

Thirty different genotypes of horse gram were screened for moisture stress tolerance at two concentrations of PEG 6000 – 10% and 20% along with one control treatment and morpho-physiological observations of ten-day old seedlings were recorded.

4.1.1. Analysis of variance and mean performance of different morpho-physiological characters in the laboratory experiment

The analysis of variance (Factor A, Factor B and Factor A x B) for various morpho-physiological observations is presented in table 2.

Factor A and Factor B viz. genotypes and levels of PEG 6000 used in this study showed significant differences for the six characters - germination percentage, root length, shoot length, dry weight, vigour index 1 and vigour index 2 studied at the seedling stage. But the interaction of the two factors was significant for the characters shoot length, dry weight, vigour index 1 and vigour index 2 and not significant for germination percentage and root length.

Morpho-physiological observations and its per cent reduction of all the thirty genotypes of horse gram under different moisture stress and control conditions are presented in the table 3.

Table 2. Analysis of variance of different morpho-physiological characters of horse gram in the laboratory experiment

Characters	**Mean Sum of Square**			
	Factor A **(Genotypes)**	**Factor B** **(PEG concentrations)**	**Factor A** x **B** **(Genotypes** x **PEG concentrations)**	**Error**
Germination percentage	1374.119*	63845.000*	241.552	171.667
Root length (cm)	31.288*	953.580*	8.563	6.347
Shoot length (cm)	16.543*	3149.632*	6.141*	3.163
Seedling dry weight (g)	0.000*	0.001*	0.000*	0.000
Seedling vigour index 1	837832.300*	95612000.900*	307070.700*	123343.400
Seedling vigour index 2	0.345*	25.501*	0.099*	0.054

* Significant at 5% level

Table 3. Mean values morpho-physiological observations and its per cent reduction of thirty horse gram genotypes under moisture stress condition

Genotypes	Germination (%)					Root Length (cm)				
	10 % PEG	20% PEG	Mean	Control	% Reduction	10 % PEG	20% PEG	Mean	Control	% Reduction
IC145300	90.00	46.67	68.34	100.00	31.66	15.37	10.12	12.75	18.40	30.71
IC71841	96.67	66.67	81.67	100.00	18.33	17.72	12.10	14.91	18.60	19.84
IC139464	96.67	63.33	80.00	100.00	20.00	13.82	13.62	13.72	13.86	1.01
IC120753	96.67	33.33	65.00	100.00	35.00	16.58	11.80	14.19	19.95	28.87
IC39353	6.67	0.00	3.34	40.00	91.65	5.07	0.00	2.54	16.15	84.27
HG 34 L	56.67	26.67	41.67	90.00	53.70	12.05	7.67	9.86	12.90	23.57
IC15730	53.33	43.33	48.33	60.00	19.45	15.37	9.68	12.53	20.05	37.51
IC392329	80.00	50.00	65.00	90.00	27.78	13.00	10.00	11.50	16.00	28.13
HG 26 L	63.33	30.00	46.67	70.00	33.33	14.92	10.47	12.70	16.20	21.60
IC277671	76.67	33.33	55.00	80.00	31.25	19.02	8.85	13.94	19.80	29.60
IC406382	80.00	43.33	61.67	80.00	22.91	13.15	10.95	12.05	13.95	13.62
IC22785	83.33	56.67	70.00	90.00	22.22	15.93	10.43	13.18	16.50	20.12
IC26138	70.00	40.00	55.00	90.00	38.89	12.13	11.45	11.79	13.30	11.35
HG 31L	76.67	36.67	56.67	100.00	43.33	15.18	9.40	12.29	19.65	37.46
GDH-1	80.00	26.67	53.34	100.00	46.66	16.17	6.10	11.14	17.50	36.34
HG 27 L	83.33	33.33	58.33	90.00	35.19	16.33	8.27	12.30	21.65	43.19
IC139470	86.67	46.67	66.67	90.00	25.92	13.15	8.03	10.59	13.90	23.81
IC139435	73.33	36.67	55.00	80.00	31.25	13.75	10.23	11.99	14.60	17.88
IC139554	56.67	20.00	38.34	60.00	36.10	11.15	6.65	8.90	16.60	46.39
IC88926	70.00	36.67	53.34	80.00	33.33	15.77	8.30	12.04	16.35	26.36
IC67011	73.33	23.33	48.33	90.00	46.30	11.10	9.32	10.21	11.85	13.84
HG 18 L	50.00	10.00	30.00	60.00	50.00	8.82	7.00	7.91	18.10	56.30

Table 3. Contd

IC139453	83.33	43.33	63.33	100.00	36.67	13.28	10.28	11.78	15.35	23.26
IC22759	86.67	26.67	56.67	90.00	37.03	13.67	10.23	11.95	14.50	17.59
IC26132	70.00	36.67	53.34	80.00	33.33	13.75	9.60	11.68	14.65	20.27
IC123030	60.00	20.00	40.00	80.00	50.00	12.57	7.30	9.94	13.20	24.70
IC283202	96.67	36.67	66.67	100.00	33.33	10.35	9.05	9.70	12.85	24.51
IC22827	83.33	40.00	61.67	90.00	31.48	14.33	10.27	12.30	18.80	34.57
IC221105	76.67	46.67	61.67	100.00	38.33	14.95	8.88	11.92	15.20	21.58
HG 24 L	60.00	33.33	46.67	90.00	48.14	14.92	9.20	12.06	16.15	25.33
Mean	73.89	36.22	-	85.67	36.75	13.78	9.18	-	16.22	30.71
	S. E	C. D	-	-	-	S. E	C. D	-	-	-
Genotypes	5.349	14.977	-	-	-	1.028	2.880	-	-	-
PEG concentrations	1.381	3.867	-	-	-	0.266	0.744	-	-	-
Genotype x PEG concentrations	7.565	NS	-	-	-	1.454	NS	-	-	-

S. E: Standard Error of mean

C. D: Critical Difference

Table 3. Contd

Genotypes	Shoot Length (cm)					Seedling dry weight (g)				
	10 % PEG	20% PEG	Mean	Control	% Reduction	10 % PEG	20% PEG	Mean	Control	% Reduction
IC145300	12.25	2.63	7.44	12.95	42.55	0.0147	0.0098	0.0123	0.0152	19.08
IC71841	11.92	4.80	8.36	17.10	51.11	0.0204	0.0159	0.0182	0.0206	11.65
IC139464	10.98	2.85	6.92	12.65	45.30	0.0149	0.0137	0.0143	0.0154	7.14
IC120753	10.97	3.45	7.21	11.01	34.51	0.0144	0.0132	0.0138	0.0146	5.48
IC39353	1.77	0.00	0.89	12.60	92.94	0.0069	0.0000	0.0035	0.0113	69.03
HG 34 L	14.88	3.27	9.08	15.15	40.07	0.0169	0.0095	0.0132	0.0187	29.41
IC15730	13.60	5.17	9.39	13.40	29.93	0.0175	0.0126	0.0151	0.0186	18.82
IC392329	11.02	4.48	7.75	10.15	23.65	0.0144	0.0126	0.0135	0.0183	26.23
HG 26 L	13.57	4.95	9.26	14.40	35.69	0.0179	0.0151	0.0165	0.0193	14.51
IC277671	12.07	3.28	7.68	13.85	44.55	0.0181	0.0069	0.0125	0.0192	34.90
IC406382	11.25	5.08	8.17	14.00	41.64	0.0146	0.0136	0.0141	0.0150	6.00
IC22785	12.87	4.52	8.70	12.90	32.56	0.0150	0.0137	0.0144	0.0152	5.26
IC26138	12.92	4.40	8.66	13.40	35.37	0.0135	0.0129	0.0132	0.0141	6.38
HG 31L	14.65	4.70	9.68	14.68	34.06	0.0178	0.0114	0.0146	0.0182	19.78
GDH-1	12.62	2.90	7.76	14.70	47.21	0.0166	0.0097	0.0132	0.0211	37.44
HG 27 L	15.07	3.82	9.45	15.50	39.03	0.0173	0.0104	0.0139	0.0194	28.35
IC139470	11.97	2.88	7.43	12.95	42.63	0.0119	0.0068	0.0094	0.0127	25.98
IC139435	12.05	2.77	7.41	15.00	50.60	0.0124	0.0098	0.0111	0.0147	24.49
IC139554	12.45	1.77	7.11	11.40	37.63	0.0149	0.0078	0.0114	0.0163	30.06

Table 3. Contd

IC88926	12.72	4.35	8.54	12.80	33.28	0.0193	0.0101	0.0147	0.0201	26.87
IC67011	10.60	3.70	7.15	10.75	33.49	0.0133	0.0107	0.0120	0.0138	13.04
HG 18 L	12.02	2.87	7.45	12.10	38.43	0.0141	0.0080	0.0111	0.0156	28.85
IC139453	9.02	3.52	6.27	13.85	54.73	0.0148	0.0125	0.0137	0.0163	15.95
IC22759	11.77	4.17	7.97	12.70	37.24	0.0167	0.0114	0.0141	0.0199	29.15
IC26132	13.90	3.82	8.86	14.30	38.04	0.0167	0.0125	0.0146	0.0169	13.61
IC123030	8.85	2.38	5.62	17.25	67.42	0.0151	0.0063	0.0107	0.0168	36.31
IC283202	12.25	4.35	8.30	16.05	48.29	0.0149	0.0121	0.0135	0.0158	14.56
IC22827	14.27	4.17	9.22	15.55	40.71	0.0146	0.0122	0.0134	0.0188	28.72
IC221105	10.87	4.32	7.60	12.70	40.16	0.0138	0.0103	0.0121	0.0145	16.55
HG 24 L	15.42	4.18	9.80	15.60	37.18	0.0194	0.0094	0.0144	0.0197	26.90
Mean	12.02	3.65	-	13.71	42.33	0.0154	0.0107	-	0.0169	22.31
	S. E	C. D	-	-	-	S. E	C. D	-	-	-
Genotypes	0.726	2.033	-	-	-	0.001	0.003	-	-	-
PEG concentrations	0.187	0.525	-	-	-	0	0.001	-	-	-
Genotype x PEG concentrations	1.027	2.875	-	-	-	0.002	0.005	-	-	-

S. E: Standard Error of mean

C. D: Critical Difference

Table 3. Contd

Genotypes	Vigour index 1					Vigour index 2				
	10 % PEG	20% PEG	Mean	Control	% Reduction	10 % PEG	20% PEG	Mean	Control	% Reduction
IC145300	2485.50	612.67	1549.09	3135.00	50.59	1.326	0.460	0.893	1.520	41.25
IC71841	2865.83	1110.17	1988.00	3570.00	44.31	1.964	1.054	1.509	2.060	26.75
IC139464	2404.83	1041.67	1723.25	2385.90	27.77	1.441	0.869	1.155	1.386	16.67
IC120753	2657.33	508.67	1583.00	2786.40	43.19	1.385	0.441	0.913	1.314	30.52
IC39353	22.83	0.00	11.42	1150.00	99.01	0.047	0.000	0.015	0.452	96.68
HG 34 L	1512.50	263.33	887.92	2524.50	64.83	0.963	0.255	0.609	1.683	63.81
IC15730	1542.00	639.83	1090.92	2007.00	45.64	0.934	0.546	0.740	1.116	33.69
IC392329	1867.67	728.00	1297.84	1830.50	29.10	1.145	0.628	0.887	1.281	30.76
HG 26 L	1793.50	460.17	1126.84	2142.00	47.39	1.130	0.457	0.794	1.351	41.23
IC277671	2404.17	366.83	1385.50	2355.50	41.18	1.388	0.225	0.807	1.344	39.96
IC406382	1952.00	690.67	1321.34	2236.00	40.91	1.164	0.589	0.877	1.200	26.92
IC22785	2411.17	849.00	1630.09	2352.00	30.69	1.248	0.779	0.894	1.216	26.48
IC26138	1753.50	626.17	1189.84	2403.00	50.49	0.945	0.515	0.730	1.269	42.47
HG 31L	2267.50	520.83	1394.17	3433.00	59.39	1.357	0.498	0.928	1.820	49.01
GDH-1	2275.00	231.67	1253.34	3220.00	61.08	1.340	0.261	0.801	2.110	62.04
HG 27 L	2624.33	333.17	1478.75	3343.50	55.77	1.452	0.347	0.900	1.746	48.45
IC139470	2184.67	512.17	1348.42	2416.50	44.20	1.055	0.363	0.699	1.143	38.85
IC139435	1897.33	565.33	1231.33	2368.00	48.00	0.915	0.366	0.711	1.176	39.54
IC139554	1314.33	190.33	752.33	1680.00	55.22	0.830	0.158	0.494	0.978	49.49
IC88926	1993.83	451.33	1222.58	2040.50	40.08	1.351	0.374	0.863	1.407	38.66
IC67011	1611.33	263.50	937.42	1582.00	40.74	0.955	0.242	0.599	0.966	37.99
HG 18 L	992.00	98.67	545.34	1812.00	69.90	0.718	0.080	0.558	0.936	40.38
IC139453	2014.50	606.67	1310.59	2920.00	55.12	1.270	0.547	0.954	1.630	41.47

Table 3. Contd

IC22759	2205.83	382.33	1294.08	2448.00	47.14	1.438	0.238	0.838	1.791	53.21
IC26132	1969.50	492.50	1231.00	2026.50	39.25	1.167	0.461	0.814	1.183	31.19
IC123030	1285.00	290.50	787.75	2436.00	67.66	0.908	0.188	0.598	1.344	55.51
IC283202	2183.00	500.33	1341.67	2890.00	53.58	1.440	0.445	0.943	1.580	40.32
IC22827	2378.67	572.50	1475.59	2748.00	46.30	1.216	0.495	0.856	1.504	43.09
IC221105	1971.67	607.50	1289.59	2790.00	53.78	1.039	0.477	0.758	1.450	47.72
HG 24 L	1853.83	449.50	1151.67	2857.50	59.70	1.169	0.314	0.742	1.773	58.15
Mean	1956.51	498.87	-	2462.98	50.40	1.157	0.422	-	1.391	43.08
	S. E	C. D	-	-	-	S. E	C. D	-	-	-
Genotypes	143.378	401.465	-	-	-	0.095	0.266	-	-	-
PEG concentrations	37.020	103.658	-	-	-	0.025	0.069	-	-	-
Genotype x PEG concentrations	202.767	567.757	-	-	-	0.134	0.376	-	-	-

S. E: Standard Error of mean C. D: Critical Difference

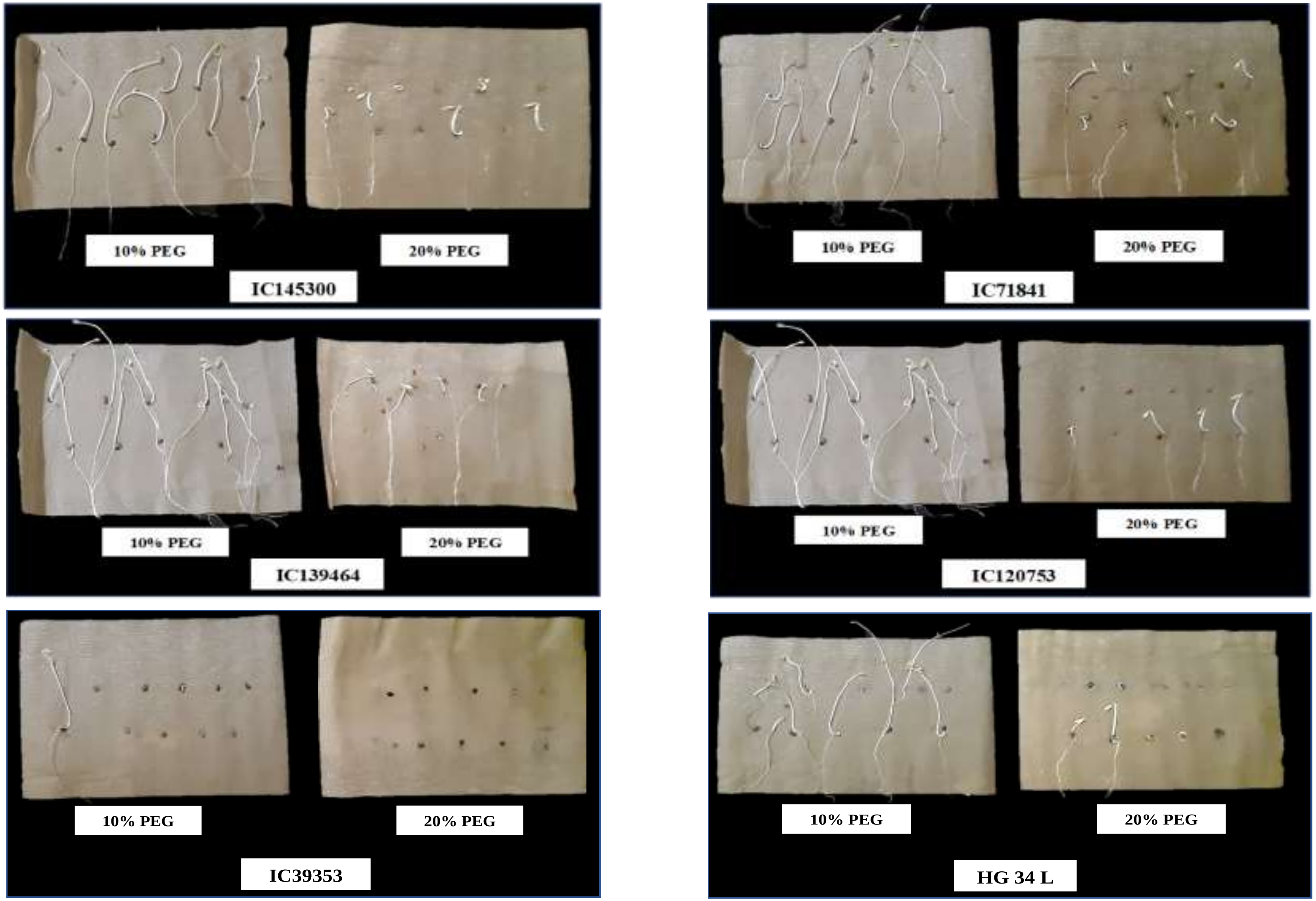


Plate 2. Performance of genotypes under 10% PEG and 20% PEG concentrations

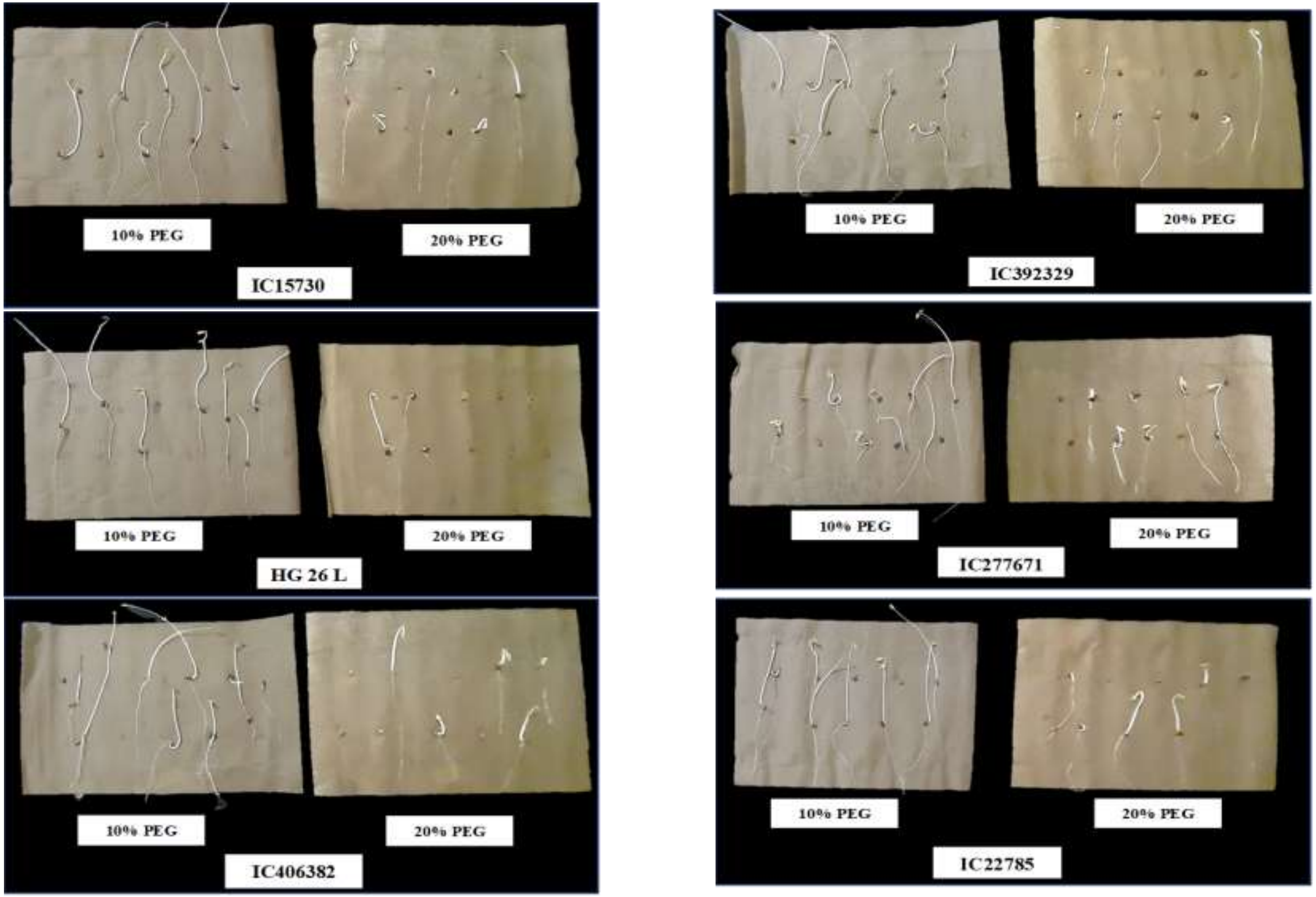


Plate 2. Performance of genotypes under 10% PEG and 20% PEG concentrations (contd.)

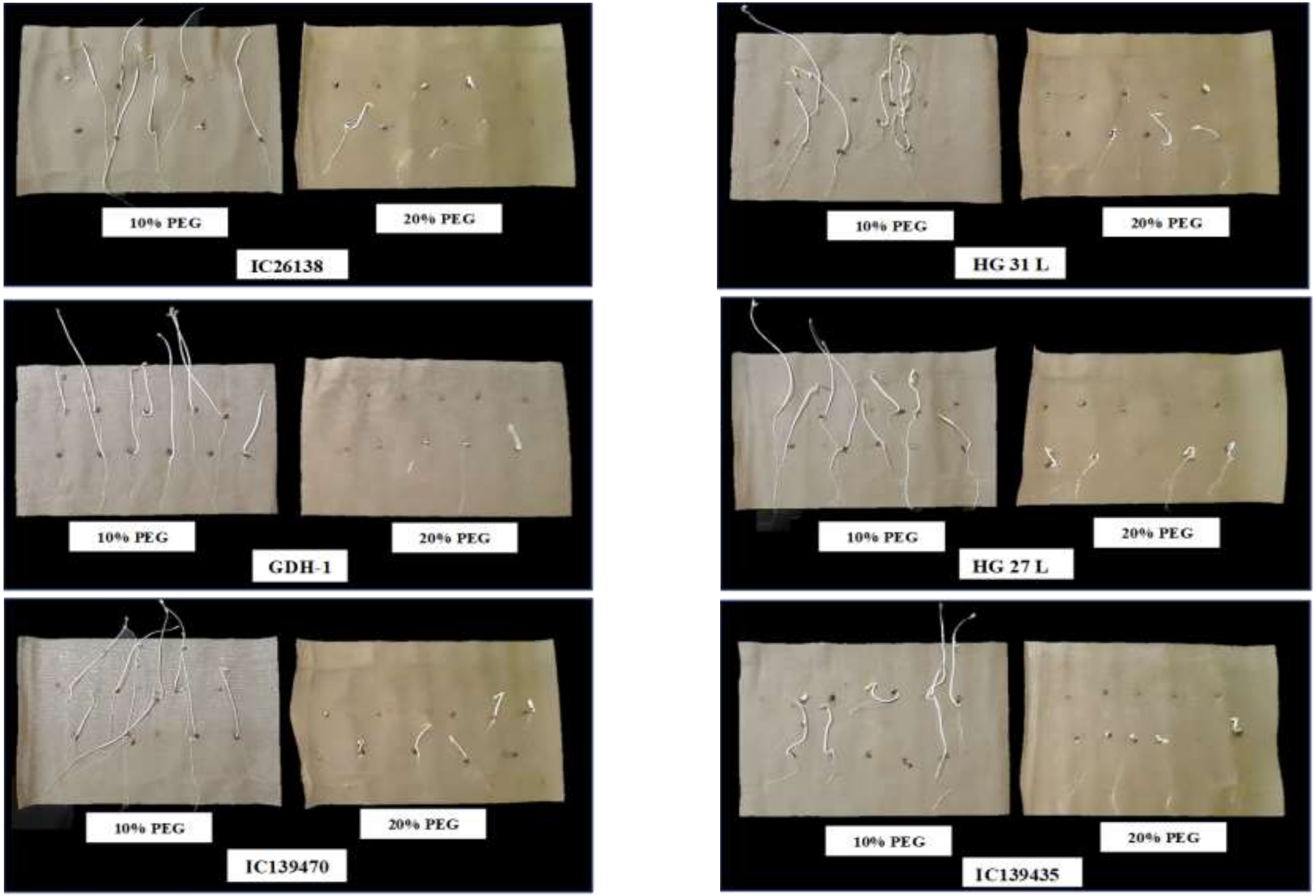


Plate 2. Performance of genotypes under 10% PEG and 20% PEG concentrations (contd.)

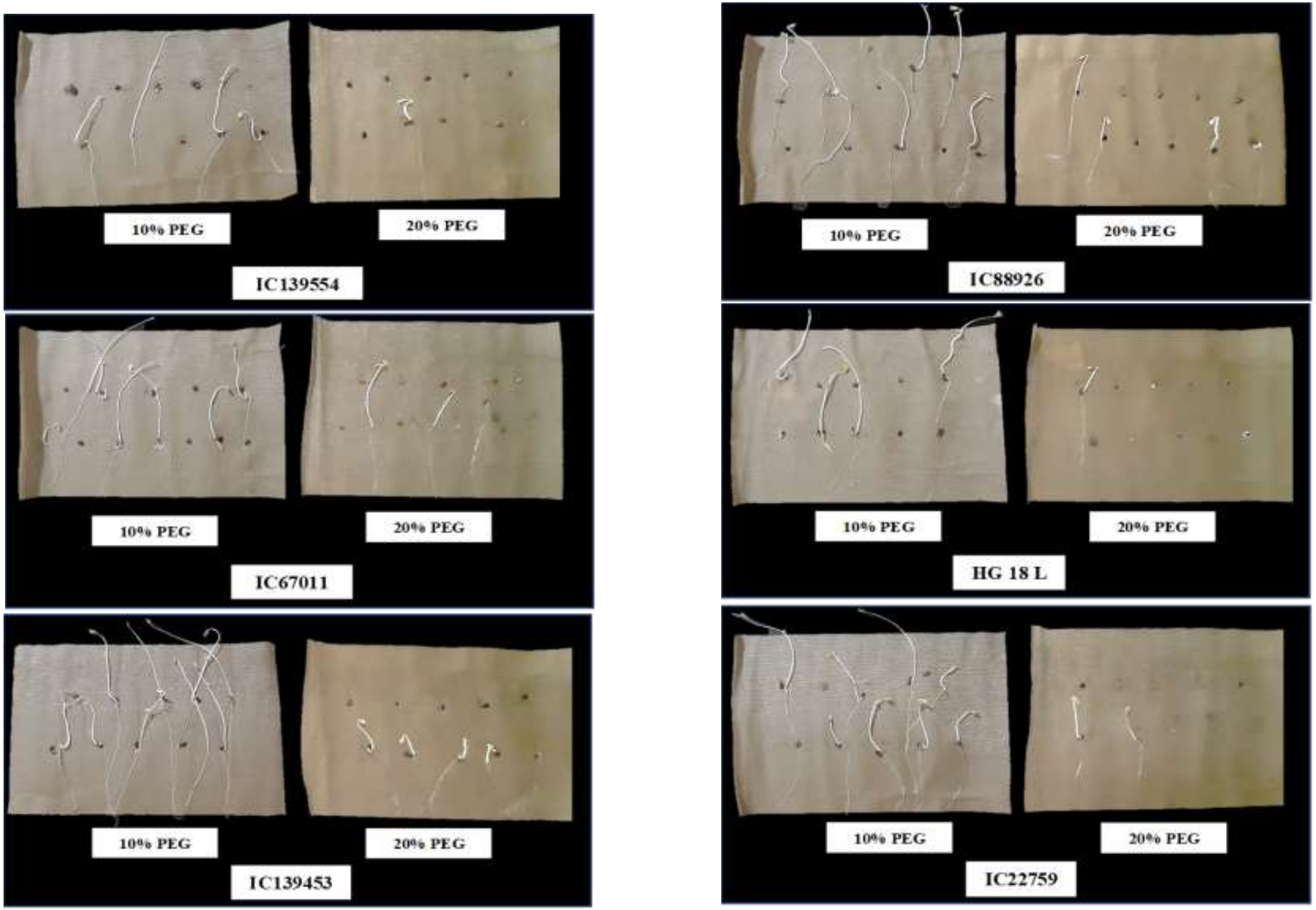


Plate 2. Performance of genotypes under 10% PEG and 20% PEG concentrations (contd.)

Plate 2. Performance of genotypes under 10% PEG and 20% PEG concentrations (contd.)

4.1.1.1. Germination percentage

A significant difference in germination percentage was noted with respect to genotypes and concentrations of PEG 6000. Among genotypes, IC71841 exhibited the highest germination percentage (81.67%), which was on par with IC139464 (80.00%), IC22785 (70.00%) and IC145300 (68.34%). IC39353 exhibited the lowest germination percentage (3.34%). All the genotypes in the control condition exhibited a higher germination percentage (82.00%) than the moisture stress treatments. In comparison to control, the lowest and highest reduction in germination percentage was recorded by IC392329 (7.14%) and IC39353 (91.65%) respectively. Germination percentage recorded was 36.22% in moisture stress induced by 20% PEG concentration and 73.89% in stress induced by 10% PEG concentration.

4.1.1.2. Root length (cm)

The genotypes and concentrations of PEG 6000 differed significantly for root length (cm). IC71841 recorded longest root length (14.91 cm), which was on par with IC120753 (14.19 cm), IC277671 (13.94 cm), IC139464 (13.72 cm), IC22785 (13.18 cm), IC145300 (12.75 cm), HG 26 L (12.70 cm), IC15730 (12.53 cm), IC22827 (12.30 cm), HG 27 L (12.30 cm), HG 31L (12.29 cm), HG 24 L (12.06 cm), IC406382 (12.05 cm) and IC88926 (12.04 cm). IC39353 recorded shortest root length (2.54 cm). Seedlings recorded lowest mean root length (9.18 cm) in 20% PEG concentration and a mean root length of 13.78 cm in 10% PEG concentration. Root length of seedlings of all the genotypes exhibited higher mean root length (16.22 cm) under control conditions. Highest and lowest reduction in root length was recorded by IC39353 (84.27%) and IC139464 (1.01%) respectively.

4.1.1.3. Shoot length (cm)

The shoot length differed significantly with respect to genotypes, concentrations of PEG 6000 and their interaction. Among genotypes, longest shoot length was recorded in HG 24 L (9.80 cm) which was statistically on par with HG 31L (9.68 cm), HG 27 L (9.45 cm), IC15730 (9.39 cm), HG 26 L (9.26 cm), IC22827 (9.22 cm), HG 34 L (9.08 cm), IC26132 (8.86 cm), IC22785 (8.70 cm), IC26138 (8.66 cm), IC88926

(8.54 cm), IC71841 (8.36 cm), IC283202 (8.30 cm), IC406382 (8.17 cm) and IC22759 (7.97 cm). IC39353 recorded the shortest shoot length (0.89 cm) among the genotypes. The highest and lowest reduction in shoot length over control was recorded by IC39353 (92.94%) and IC392329 (23.65%) respectively. The mean shoot length recorded was high in 10% PEG 6000 (12.02 cm) and low in 20% PEG 6000 concentration (3.65 cm). However, all thirty seedlings in the control condition recorded a higher mean shoot length (13.71cm) than that in the moisture stress concentrations.

4.1.1.4. Seedling dry weight (g)

Seedling dry weight differed significantly among genotypes, concentrations of PEG 6000 and their interaction. The highest seedling dry weight was noticed in IC71841 (0.0182 g), which was on par with HG 26 L (0.0165 g) and IC15730 (0.0151 g). The lowest seedling dry weight was recorded in IC39353 (0.0035 g). IC39353 (69.03%) and IC26138 (6.38%) recorded the highest and lowest reduction in seedling dry weight compared to control. A high mean seedling dry weight was noted in 10% PEG concentration (0.0154 g) while a low mean seedling dry weight was obtained in 20% PEG concentration (0.0107 g). But under controlled condition high mean seedling dry weight (0.0169 g) was recorded.

4.1.1.5. Seedling vigour index 1

Significant variation was noted in seedling vigour index 1 among genotypes, concentrations of PEG 6000 and their interaction. Among genotypes, IC71841 noted the highest mean seedling vigour index 1 (1988.000) which was on par with IC139464 (1723.251) and IC22785 (1630.090). IC39353 recorded the lowest seedling vigour index 1 (11.42). Compared to control, the lowest and highest reduction in seedling vigour index 1 was recorded by IC139464 (27.27%) and IC39353 (99.01%). The twenty per cent PEG concentration recorded a low mean seedling vigour index 1 (498.87) when compared to 10% concentration (1956.51). Mean seedling vigour index 1 was found to be higher in control condition (2462.98).

4.1.1.6. Seedling vigour index 2

A significant difference was noted in seedling vigour index 2 with respect to genotypes, concentrations of PEG 6000 and their interaction. IC71841 was found to have the highest mean seedling vigour index 2 (1.509) and IC39353 have the lowest seedling vigour index 2 (0.015). In comparison to control, the lowest and highest reduction in seedling vigour index 2 was observed in IC139464 (16.67%) and IC39353 (96.68%). Among concentrations of PEG 6000, highest (1.157) and lowest (0.422) mean seedling vigour index 2 was observed in 10% PEG concentration and 20% PEG concentration respectively. However, the mean seedling vigour index 2 was higher in control condition (1.391), than the stress concentrations.

4.2. FIELD EXPERIMENT

Biometric, physiological, biochemical and seed quality observations of 30 genotypes recorded in the field experiment were statistically analysed and presented in this chapter.

4.2.1. Soil moisture content (%)

The average soil moisture content of the treatment plot was 10.10% and 8.84% at 8'th and 15'th day respectively. While the control plot recorded an average soil moisture content of 12.52% and 12.44% at 8'th and 15'th day respectively.

4.2.2. Analysis of Variance and Mean Performance of genotypes in field

Analysis of variance was performed for the observations recorded and data on the ANOVA and mean value of genotypes are presented in the table 4 and 5 respectively.

Table 4. Analysis of variance of different characters of horse gram in the field experiment

Sl No.	**Characters**	**Mean Sum of Square**		
		Replication	**Genotype**	**Error**
1	Days to 50% flowering	23.244	1184.766*	5.727
2	Number of primary branches per plant	11.013	11.137*	1.561
3	Plant height (cm)	721.141	615.428*	107.874

Table 4. Contd.

4	No. of pods per plant	38.946	824.773[*]	42.944
5	No. of seeds per pod	0.905	1.371[*]	0.257
6	100 Seed weight (g)	0.302	0.161[*]	0.068
7	Haulm yield per plant (g)	4.025	39.845[*]	3.170
8	Haulm yield per plot (g per plot)	33142.141	18424.794[*]	1849.415
9	Harvest index (%)	10.875	629.000[*]	17.643
10	Days to maturity	89.644	681.519[*]	36.530
11	Relative water content (%)	9.624	67.653[*]	24.167
12	Leaf fresh weight (g)	0.008	0.014[*]	0.005
13	Turgid weight of leaf (g)	0.008	0.038[*]	0.010
14	Leaf dry weight (g)	0.001	0.007[*]	0.001
15	Root length (cm)	37.052	18.941[*]	9.188
16	Root dry weight (g)	0.088	0.801[*]	0.097
17	Leaf area (cm^2)	417152.89	337348.04[*]	42783.38
18	Specific leaf area (cm^2 g^{-1})	27478.825	7641.314[*]	2039.238
19	Leaf area index	0.515	0.416[*]	0.053
20	Phenol content (mg g^{-1})	1609.356	1173.250[*]	196.373
21	Crude Protein content (%)	0.579	1.253[*]	0.702
22	Total chlorophyll (mg g^{-1})	0.012	0.257[*]	0.005
23	Chlorophyll A (mg g^{-1})	0.004	0.118[*]	0.004
24	Chlorophyll B (mg g^{-1})	0.003	0.049[*]	0.001
25	Proline content (μmol g^{-1})	0.131	6.110[*]	0.186
26	Seed yield per plant (g)	1.526	15.701[*]	0.606
27	Seed yield per plot (g per plot)	6495.455	7044.996[*]	523.534
28	Stress tolerance index	0.020	0.452[*]	0.009
29	Geometric mean productivity	0.713	23.646[*]	0.326
30	Mean productivity	0.382	25.042[*]	0.152
31	Yield stability index	0.014	0.046[*]	0.005

[*] Significant at 5% level

Table 5. Mean values of 31 characters of thirty horse gram genotypes

Genotypes	1		2		3		4		5		6	
	DF	C	PB	C	HT	C	PP	C	SP	C	SW	C
IC145300	42.67	44	7.75	8.00	68.72	78.93	42.79	64.46	3.93	4.0	3.78	3.82
IC71841	41.33	43	6.57	11.25	87.43	96.20	22.15	54.43	3.53	3.8	3.30	3.38
IC139464	34.33	35	8.50	12.25	70.73	82.40	50.85	62.14	4.27	4.6	3.47	3.50
IC120753	42.33	44	5.42	7.33	50.93	66.50	63.99	72.23	3.93	4.2	3.27	3.68
IC39353	35.33	37	5.67	7.75	69.62	78.05	55.18	90.25	3.67	4.0	3.61	3.77
HG 34 L	78.00	82	10.44	10.75	99.75	111.68	14.42	24.08	2.53	3.2	3.36	3.84
IC15730	86.67	88	7.61	10.50	91.55	108.10	17.80	28.14	2.93	3.0	3.52	3.73
IC392329	87.00	91	11.00	12.75	99.17	107.63	12.78	33.07	2.80	3.2	3.36	4.00
HG 26 L	77.67	82	8.75	13.25	86.67	102.63	13.89	36.09	2.67	3.2	3.47	3.87
IC277671	36.00	37	7.83	11.00	84.80	92.84	43.59	69	4.07	4.6	3.59	3.62
IC406382	42.67	43	9.75	11.50	81.48	93.73	45.02	59.73	4.20	4.2	3.53	3.55
IC22785	36.00	37	10.25	11.25	77.86	86.85	61.72	130.82	5.07	5.2	3.84	3.86
IC26138	82.67	84	12.22	14.75	103.66	118.58	17.12	38.77	2.47	3.0	3.48	3.93
HG 31L	83.67	85	11.00	12.33	79.53	98.60	14.36	44.34	3.20	3.4	3.52	3.54
GDH-1	35.67	37	7.90	9.00	56.78	66.38	44.24	47.07	4.27	4.4	3.84	3.88
HG 27 L	79.33	81	11.00	13.00	100.65	113.65	14.40	25.42	2.53	3.6	3.57	3.60
IC139470	44.00	47	6.83	11.75	57.46	64.90	38.87	73	4.73	4.8	3.10	3.28
IC139435	34.33	35	6.42	11.00	62.83	73.23	35.08	61.77	3.53	4.2	3.61	3.64
IC139554	49.00	52	9.50	13.25	90.20	97.53	47.57	71.54	3.67	4.0	3.49	3.52

Table 5. Contd.

IC88926	45.00	46	6.86	8.75	77.86	86.85	48.17	68.46	3.80	4.2	4.14	4.19
IC67011	39.33	40	6.81	8.00	85.36	91.75	41.03	100.38	3.93	4.8	3.35	3.65
HG 18 L	83.67	84	12.50	13.25	96.58	109.23	14.47	22.79	3.07	3.8	3.48	4.34
IC139453	39.67	41	10.06	12.67	71.42	82.18	13.50	62.83	3.27	4.2	3.97	4.21
IC22759	46.33	48	7.41	9.50	85.42	98.34	51.94	87.17	4.33	4.4	3.75	3.80
IC26132	40.00	41	7.42	12.25	90.12	107.90	28.19	65.58	3.47	4.8	3.72	3.77
IC123030	43.67	46	7.25	9.25	73.63	88.93	36.68	62.67	3.80	4.2	3.46	3.50
IC283202	36.33	37	8.47	12.75	80.08	93.88	39.38	62.54	3.47	3.8	3.23	3.52
IC22827	45.33	47	8.42	11.75	94.63	107.40	38.14	48.21	3.53	3.6	3.71	3.82
IC221105	38.33	39	10.67	12.75	63.62	76.68	54.92	69.33	4.13	4.2	3.85	4.05
HG 24 L	80.33	82	11.17	13.00	94.56	113.53	14.44	28.29	2.60	3.4	3.38	3.76
Mean	52.89	54.50	8.715	11.22	81.10	93.17	34.56	58.82	3.58	4.0	3.56	3.75
S. E.	1.382	-	0.74	-	5.898	-	3.783	-	0.293	-	0.151	-
C. D. (5%)	3.911	-	2.094	-	16.6	-	10.71	-	0.829	-	0.427	-

DF	Days to 50% flowering	HT	Height of plant (cm)
PB	No. of primary branches per plant	PP	No. of pods per plant
C	Control	SP	No. of seeds per pod
		SW	100 seed weight (g)

Table 5. Contd.

Genotypes	7		8		9		10		11		12	
	HY	C	HYP^{-1}	C	HI	C	DM	C	RWC	C	LFW	C
IC145300	7.00	9.39	158.63	259.63	47.43	50.27	91.00	114.00	68.33	83.75	0.702	0.736
IC71841	7.14	15.99	133.81	549.63	28.34	31.77	95.33	119.00	67.70	88.90	0.593	1.114
IC139464	8.13	9.42	176.83	285.38	48.49	54.51	97.67	122.00	74.52	85.54	0.730	0.913
IC120753	3.32	5.56	63.34	176.63	67.68	69.54	95.67	117.00	71.75	81.48	0.738	0.871
IC39353	4.01	7.22	80.31	305.38	62.55	69.15	78.67	94.00	69.26	86.32	0.691	0.718
HG 34 L	15.17	23.75	341.96	593.75	13.91	16.66	124.33	132.00	65.85	82.23	0.837	0.844
IC15730	10.25	12.88	208.67	572.00	19.95	24.54	124.67	134.00	62.09	91.45	0.578	0.715
IC392329	14.22	17.95	302.16	448.75	13.11	25.97	121.67	138.00	61.65	79.27	0.644	0.658
HG 26 L	5.65	10.93	118.63	873.25	31.24	37.22	123.33	132.00	60.47	78.19	0.734	0.822
IC277671	13.04	21.99	279.99	724.75	35.63	40.70	103.33	114.00	68.71	79.47	0.717	1.060
IC406382	7.70	12.44	167.93	460.92	48.81	51.92	101.33	112.00	71.48	89.59	0.720	0.816
IC22785	13.80	18.40	294.87	310.00	41.14	48.73	98.67	122.00	71.89	86.60	0.656	1.227
IC26138	13.74	31.15	295.99	778.63	15.46	18.02	125.67	129.00	63.00	83.38	0.802	0.811
HG 31L	14.71	26.46	326.79	661.50	15.21	21.79	115.33	124.00	62.66	82.25	0.669	0.814
GDH-1	13.35	16.66	283.46	191.50	35.68	39.57	83.33	102.00	68.34	84.66	0.784	0.784
HG 27 L	16.14	38.60	359.61	1015.00	13.11	14.61	125.67	134.00	61.69	82.70	0.717	1.023
IC139470	4.00	11.30	79.66	282.38	51.69	52.54	105.33	122.00	62.92	81.23	0.804	1.266
IC139435	5.33	7.09	112.61	202.25	55.07	57.82	88.67	106.00	64.43	79.76	0.792	0.994
IC139554	4.57	7.84	88.31	570.88	56.38	63.64	98.67	118.00	65.66	78.02	0.731	0.741
IC88926	6.04	8.14	131.75	358.50	53.42	54.33	82.33	98.00	63.80	80.65	0.761	0.818
IC67011	3.75	9.01	82.06	300.33	64.67	65.34	102.67	112.00	71.37	82.67	0.781	0.893

Table 5. Contd.

HG 18 L	15.82	23.18	325.38	579.50	15.23	25.24	130.33	138.00	61.53	77.15	0.743	0.799
IC139453	11.85	19.00	264.62	474.88	19.19	28.33	106.33	124.00	63.69	79.62	0.683	1.072
IC22759	15.51	18.23	312.57	355.83	33.55	37.38	103.67	118.00	74.98	82.68	0.729	0.754
IC26132	14.74	22.55	264.15	563.63	21.34	26.33	84.00	96.00	61.64	78.40	0.722	0.782
IC123030	5.90	10.75	110.54	518.75	50.28	58.05	92.33	108.00	62.73	80.21	0.732	0.760
IC283202	11.73	15.45	248.59	536.25	35.00	42.92	92.67	119.00	62.84	82.98	0.582	1.177
IC22827	6.63	12.35	139.44	483.75	44.90	46.96	93.33	124.00	63.87	78.07	0.723	0.969
IC221105	14.80	17.64	317.45	340.88	36.39	43.59	103.67	118.00	78.18	87.40	0.627	0.739
HG 24 L	16.50	33.22	358.68	830.50	13.13	15.14	122.00	134.00	63.24	80.95	0.605	0.787
Mean	10.15	16.48	214.29	486.83	36.27	41.08	103.72	119.13	66.34	82.52	0.71	0.88
S. E.	1.028	-	26.12	-	0.031	-	3.489	-	2.838	-	0.042	-
C. D. (5%)	2.91	-	73.942	-	0.087	-	9.878	-	8.035	-	0.12	-

HY	Haulm yield per plant (g)	DM	Days to maturity
HY P^{-1}	Haulm yield per plot (g per plot)	RWC	Relative water Content (%)
HI	Harvest Index (%)	LFW	Leaf fresh weight (g)
C	control		

Table 5. Contd.

Genotypes	13		14		15		16		17		18	
	LTW	C	LDW	C	RL	C	RDW	C	LA	C	LAI	C
IC145300	0.9744	0.8509	0.1129	0.1444	18.80	15.45	1.23	1.03	1186.87	5733.98	1.32	6.37
IC71841	0.8172	1.2285	0.1223	0.1998	21.50	16.75	2.05	1.65	1098.83	1257.59	1.22	1.40
IC139464	0.9238	1.0375	0.1639	0.1773	20.77	15.35	2.48	2.16	1410.60	2914.07	1.57	3.24
IC120753	0.9492	1.0223	0.1972	0.2061	17.73	15.80	2.21	1.92	1087.93	6859.46	1.21	7.62
IC39353	0.9391	0.8011	0.1321	0.1909	20.60	15.65	1.59	1.22	541.66	2146.86	0.60	2.39
HG 34 L	1.2193	0.9839	0.0974	0.1978	22.15	16.85	1.37	1.23	436.90	7494.18	0.49	8.33
IC15730	0.8749	0.7711	0.0962	0.1191	19.17	15.05	1.91	1.56	1109.47	4032.38	1.23	4.48
IC392329	0.9876	0.7610	0.0985	0.2659	20.03	16.55	1.71	1.49	480.83	2241.76	0.53	2.49
HG 26 L	1.1192	1.0113	0.1474	0.1432	19.35	16.30	1.44	1.29	1168.47	6620.61	1.30	7.36
IC277671	0.9664	1.2848	0.1782	0.1904	17.95	14.85	1.53	1.45	1081.03	2419.13	1.20	2.69
IC406382	0.9561	0.8938	0.1400	0.1499	22.05	19.10	2.57	2.08	889.83	4776.03	0.99	5.31
IC22785	0.8703	1.3926	0.1080	0.1595	28.15	17.93	2.65	2.56	1576.20	3765.18	1.75	4.18
IC26138	1.1967	0.9027	0.1332	0.3488	19.80	17.70	1.40	1.28	773.83	1957.53	0.86	2.18
HG 31L	0.9890	0.9530	0.1471	0.1692	18.81	15.50	1.97	1.70	780.59	1884.96	0.87	2.09
GDH-1	1.0771	0.8549	0.1627	0.3937	25.62	19.50	2.33	2.19	1006.03	1421.48	1.12	1.58
HG 27 L	1.0960	1.2060	0.1185	0.1498	22.80	20.00	2.19	2.01	532.75	1518.97	0.59	1.69
IC139470	1.1754	1.5073	0.1789	0.2203	20.67	18.05	1.81	1.49	831.49	2255.53	0.92	2.51
IC139435	1.0512	1.1540	0.3216	0.3623	19.80	12.65	1.83	1.62	919.33	1504.37	1.02	1.67
IC139554	1.0429	0.8774	0.1419	0.2581	18.32	18.10	1.75	1.54	846.38	1999.50	0.94	2.22
IC88926	1.0673	0.9509	0.2255	0.2633	17.55	16.10	1.58	1.36	919.11	7072.16	1.02	7.86
IC67011	1.0351	1.0490	0.1578	0.1512	18.98	17.57	1.69	1.38	1457.21	3947.70	1.62	4.39

Table 5. Contd.

HG 18 L	1.1423	0.9963	0.1141	0.1324	16.60	14.13	1.17	1.10	846.38	1999.50	0.94	2.22
IC139453	1.0051	1.2914	0.1161	0.2148	19.15	15.75	1.60	1.52	881.28	2259.73	0.98	2.51
IC22759	0.9265	0.8556	0.1372	0.2694	24.87	20.35	3.46	2.86	1252.32	2512.72	1.39	2.79
IC26132	1.0907	0.9609	0.1397	0.1313	17.37	14.30	1.16	1.11	1231.75	2110.50	1.37	2.35
IC123030	1.0764	0.9013	0.1539	0.1855	20.82	10.30	1.71	1.57	643.14	3524.10	0.71	3.92
IC283202	0.8581	1.3920	0.0939	0.1262	20.62	18.40	1.52	1.36	1401.59	4156.19	1.56	4.62
IC22827	1.0517	1.1936	0.1502	0.1687	19.37	13.15	1.59	1.28	970.69	1632.17	1.08	1.81
IC221105	0.7683	0.8277	0.0962	0.1241	22.08	18.15	2.37	2.18	1528.91	8492.10	1.70	9.44
HG 24 L	0.8930	0.9360	0.0975	0.1550	17.63	13.20	1.35	1.21	1154.84	4283.98	1.28	4.76
Mean	1.00	1.03	0.14	0.20	20.30	16.28	1.84	1.61	1001.54	3493.15	1.11	3.88
S. E.	0.059	-	0.014	-	1.75	-	0.18	-	114.29	-	0.127	-
C. D. (5%)	0.167	-	0.039	-	4.954	-	0.508	-	323.538	-	0.359	-

LTW	Leaf Turgid Weight (g)
LDW	Leaf Dry Weight (g)
RL	Root Length (cm)
C	Control
RDW	Root Dry Weight (g)
LA	Leaf area (cm^2)
LAI	Leaf area index

Table 5. Contd.

Genotypes	19		20		21		22		23		24	
	SLA	C	PHE	C	CP	C	TC	C	CA	C	CB	C
IC145300	291.64	298.74	149.54	118.70	21.83	21.56	0.94	1.78	0.65	1.30	0.29	0.48
IC71841	249.14	326.33	124.14	86.40	21.76	21.43	0.74	1.61	0.57	1.19	0.17	0.43
IC139464	232.50	839.81	146.34	94.80	22.88	21.66	1.43	2.15	1.09	1.63	0.35	0.52
IC120753	284.26	285.03	141.51	112.00	23.10	22.25	1.30	1.51	0.98	1.13	0.31	0.38
IC39353	334.53	338.16	151.42	86.80	21.53	21.30	0.91	2.15	0.73	1.76	0.18	0.38
HG 34 L	298.25	309.93	84.60	71.40	22.87	22.25	0.68	1.92	0.53	1.37	0.15	0.55
IC15730	258.66	839.81	106.84	96.80	21.96	21.66	0.74	1.78	0.49	1.47	0.25	0.31
IC392329	332.90	338.75	90.15	83.40	22.10	21.81	0.74	1.06	0.55	0.84	0.19	0.23
HG 26 L	434.23	496.83	95.20	73.80	21.27	21.05	0.79	1.72	0.57	1.44	0.23	0.29
IC277671	387.72	303.70	133.14	86.50	22.60	21.66	0.98	1.17	0.68	0.85	0.31	0.32
IC406382	349.73	384.28	144.12	90.60	22.98	21.11	1.38	2.07	0.85	1.51	0.53	0.56
IC22785	250.59	359.78	121.69	86.40	22.21	22.04	1.60	1.91	1.17	1.37	0.42	0.54
IC26138	274.73	366.38	96.13	76.40	22.05	21.42	0.74	1.85	0.60	1.25	0.14	0.60
HG 31L	283.20	327.08	100.46	65.70	22.44	22.25	0.69	2.04	0.59	1.43	0.10	0.60
GDH-1	277.24	271.54	118.32	67.50	22.66	22.54	1.76	2.18	1.08	1.44	0.68	0.74
HG 27 L	254.62	322.49	101.22	84.20	21.66	21.66	0.78	1.20	0.63	0.90	0.15	0.30
IC139470	395.53	395.78	147.25	132.30	22.04	21.84	0.78	1.41	0.47	0.89	0.31	0.52
IC139435	337.40	371.24	132.73	115.70	22.02	21.82	0.89	1.30	0.67	0.96	0.22	0.34
IC139554	320.16	477.12	127.28	93.80	23.39	23.05	0.90	1.70	0.63	1.34	0.27	0.36
IC88926	291.23	309.78	137.93	102.40	23.63	22.68	1.02	2.09	0.90	1.48	0.13	0.61
IC67011	378.36	401.35	133.66	109.70	23.72	23.03	1.04	1.48	0.81	1.11	0.23	0.37

Table 5. Contd.

HG 18 L	282.16	329.78	96.40	69.70	22.47	21.93	0.69	1.56	0.49	1.13	0.21	0.43
IC139453	252.09	329.64	125.58	101.50	22.79	21.77	0.76	1.31	0.62	0.99	0.14	0.32
IC22759	221.77	410.11	136.19	126.70	21.67	21.08	1.03	1.83	0.81	1.34	0.22	0.49
IC26132	357.42	363.32	122.41	109.10	21.86	21.66	0.75	1.50	0.54	1.37	0.21	0.13
IC123030	334.26	362.10	110.18	109.60	21.90	21.81	0.93	1.05	0.63	0.73	0.30	0.32
IC283202	294.80	321.67	101.30	96.30	23.02	22.83	0.81	1.55	0.70	1.13	0.11	0.41
IC22827	336.62	388.65	100.20	97.30	22.12	22.05	0.83	1.20	0.54	0.73	0.29	0.46
IC221105	271.80	318.35	107.68	103.20	21.48	21.31	1.46	1.99	1.06	1.07	0.40	0.91
HG 24 L	302.81	341.30	120.83	86.70	22.25	21.76	0.80	2.03	0.67	1.44	0.13	0.59
Mean	305.68	384.29	120.15	94.51	22.34	21.87	0.96	1.67	0.71	1.22	0.25	0.45
S. E.	26.072	-	8.091	-	0.484	-	0.042	-	0.035	-	0.018	-
C. D. (5%)	73.806	-	22.903	-	1.369	-	0.119	-	0.099	-	0.052	-

SLA	Specific Leaf area (cm^{2} g^{-1})	TC	Total Chlorophyll (mg g^{-1})
PHE	Phenol Content (mg g^{-1})	CA	Chlorophyll A (mg g^{-1})
CP	Crude Protein (%)	CB	Chlorophyll B (mg g^{-1})
C	Control		

Table 5. Contd.

Genotypes	25		26		27		28	29	30	31
	PRO	C	SY	C	SY P^{-1}	C	STI	GMP	MP	YSI
IC145300	6.65	1.41	6.47	9.49	145.03	218.20	0.57	7.76	7.98	0.68
IC71841	6.83	1.32	2.87	7.44	54.83	186.05	0.20	4.55	5.16	0.39
IC139464	8.40	2.48	7.62	11.28	168.13	282.00	0.80	9.27	9.45	0.62
IC120753	9.66	1.92	6.94	12.69	131.49	291.89	0.82	9.38	9.81	0.55
IC39353	5.68	1.44	6.65	16.17	130.92	355.83	1.00	10.37	11.41	0.41
HG 34 L	4.52	2.14	2.42	4.75	54.45	109.20	0.11	3.39	3.59	0.51
IC15730	6.40	2.74	2.55	4.19	51.74	104.73	0.10	3.27	3.37	0.61
IC392329	4.65	1.25	2.08	6.30	44.41	157.45	0.12	3.62	4.19	0.39
HG 26 L	5.47	1.21	2.52	6.48	53.06	142.56	0.15	4.04	4.50	0.39
IC277671	6.40	2.23	7.18	15.09	153.65	301.82	1.01	10.41	11.14	0.48
IC406382	7.77	2.54	7.23	13.43	154.19	295.40	0.91	9.85	10.33	0.54
IC22785	8.88	1.64	9.62	17.49	205.32	402.16	1.57	12.97	13.55	0.55
IC26138	4.79	1.87	2.50	6.85	54.79	157.46	0.16	4.13	4.67	0.37
HG 31L	5.59	1.53	2.62	7.37	57.84	147.45	0.18	4.40	5.00	0.36
GDH-1	6.80	1.28	7.35	10.91	156.10	272.68	0.75	8.95	9.13	0.67
HG 27 L	4.45	1.75	2.42	6.61	53.67	145.31	0.15	3.99	4.51	0.37
IC139470	6.49	1.87	4.32	12.50	83.51	287.55	0.50	7.33	8.41	0.35
IC139435	6.31	2.47	6.46	9.72	138.79	223.49	0.59	7.91	8.09	0.66
IC139554	4.01	1.74	5.87	13.72	115.36	315.47	0.75	8.96	9.79	0.43
IC88926	6.26	0.94	6.86	9.68	148.91	222.69	0.62	8.15	8.27	0.71
IC67011	5.82	2.07	7.17	16.99	151.04	373.74	1.14	10.94	12.08	0.42

Table 5. Contd.

HG 18 L	5.57	2.84	2.81	7.83	58.11	195.66	0.21	4.69	5.32	0.36	5.57	2.84
IC139453	5.17	2.45	2.81	7.51	63.14	165.15	0.20	4.56	5.16	0.37	5.17	2.45
IC22759	8.20	2.37	7.77	10.88	156.83	250.30	0.79	9.18	9.33	0.65	8.20	2.37
IC26132	6.11	2.11	3.95	8.06	71.26	177.30	0.30	5.64	6.01	0.49	6.11	2.11
IC123030	5.28	2.43	5.97	14.88	118.30	327.32	0.83	9.40	10.43	0.40	5.28	2.43
IC283202	6.61	2.85	6.24	11.62	131.42	267.15	0.68	8.51	8.93	0.54	6.61	2.85
IC22827	4.07	1.63	5.27	10.93	112.67	273.30	0.54	7.59	8.10	0.48	4.07	1.63
IC221105	7.17	2.64	8.40	13.63	177.68	299.81	1.07	10.69	11.02	0.62	7.17	2.64
HG 24 L	4.43	1.87	2.49	5.93	53.93	148.18	0.14	3.84	4.21	0.42	4.43	1.87
Mean	6.15	1.97	5.18	10.34	108.35	236.58	0.57	7.26	7.76	0.49	6.15	1.97
S. E.	0.249	-	0.45	-	13.21	-	0.054	0.33	0.225	0.041	0.249	-
C. D. (5%)	0.704	-	1.273	-	37.396	-	0.154	0.933	0.636	0.117	0.704	-

PRO	Proline content (μmol g-^{1})	STI	Stress tolerance Index
SY	Seed yield per plant (g)	GMP	Geometric Mean Productivity
SY P^{-1}	Seed yield per plot (g per plot)	MP	Mean Productivity
C	Control	YSI	Yield Stability Index

4.2.3. Biometric observations

4.2.3.1. Days to 50% flowering

A significant difference was noted among genotypes for days to 50% flowering which ranged from 34.33 to 87 days, with an average of 52.89 days. Among genotypes, IC139464 and IC139435 recorded fewer days to 50% flowering (34.33 days) which was on par with IC39353 (35.33 days), GDH-1 (35.67 days), IC22785 (36.00 days), IC277671 (36.00 days) and IC283202 (36.33 days). The highest value was recorded by IC392329 (87 days). Twenty-one genotypes recorded a lower value than the average. All the thirty genotypes in the control plot recorded higher values than treatment.

4.2.3.2. Number of primary branches per plant

The number of primary branches per plant differed significantly among genotypes and ranged from 5.42 (IC120753) to 12.50 (HG 18 L) with a general mean of 8.715. The genotypes IC39353 (5.67), IC139435 (6.42), IC71841 (6.57), IC67011 (6.81), IC139470 (6.83), IC88926 (6.86), IC123030 (7.25), IC26132 (7.42) and IC22759 (7.41) were statistically on par with IC120753. Thirteen genotypes had recorded the number of primary branches per plant below the mean value. Compared to all genotypes in control plot, a reduction in the number of primary branches per plant was observed in treatment plots.

4.2.3.3. Plant height (cm)

Plant height significantly varied with respect to the genotypes and ranged from 50.93 cm (IC120753) to 103.66 cm (IC26138) with an average height of 80.10 cm. Fourteen genotypes had the plant height below the mean value. The genotypes GDH-1 (56.78 cm), IC139470 (57.46 cm), IC139435 (62.83 cm) and IC221105 (63.62 cm) were on par with IC120753. In the control condition, all the thirty genotypes were recorded to be taller than the water-stressed conditions.

In this study, IC120753, GDH-1, IC139470, IC139435 and IC139453 exhibited bushy erect growth, while remaining genotypes were semi spreading type.

4.2.3.4. Number of pods per plant

A significant difference in the number of pods per plant was observed among the genotypes. The number of pods per plant had an average of 34.56 and it ranged from 12.77 (IC392329) to 63.99 (IC120753). The genotype IC120753, was statistically on par with IC22785 (61.72), IC39353 (55.18) and IC221105 (54.92). Eighteen genotypes were recorded above the general mean value for the number of pods per plant. All the genotypes in control plot produced more pods per plant.

4.2.3.5. Number of seeds per pod

A significant variation existed among the genotypes for the number of seeds per pod. It ranged from 2.47 (IC26138) to 5.07 (IC22785). In fifteen genotypes, the number of seeds per pod was noted above the general mean (3.58) and genotypes, IC139470 (4.73), IC22759 (4.33), GDH-1 (4.27) and IC139464 (4.27) were on par with IC22785. In comparison to moisture-stressed plots, all the genotypes in the control plot recorded a greater number of seeds per pod.

A variation in seed colour was also observed among genotypes namely different shades of brown colour and black colour. IC139453, IC88926 and IC26132 were black seeded, while the remaining genotypes had different shades of brown seeds.

4.2.3.6. Hundred seed weight (g)

There was a significant difference between treatments for hundred seed weight which ranged from 3.10 g (IC139470) to 4.14 g (IC88926), with a general mean of 3.56 g. Thirteen genotypes registered a hundred seed weight above the general mean. The genotype IC88926 was statistically on par with IC139453 (3.97 g), IC221105 (3.85 g), GDH-1 (3.84 g), IC22785 (3.84 g), IC145300 (3.78 g), IC22759 (3.75 g), IC26132 (3.72 g) and IC22827 (3.71 g). All the thirty genotypes in control plot had more hundred seed weight than the treatment.

4.2.3.7. Seed yield per plant (g)

A significant difference was noticed in seed yield per plant among the genotypes and it ranged from 2.08 g (IC392329) to 9.62 g (IC22785). Seventeen genotypes

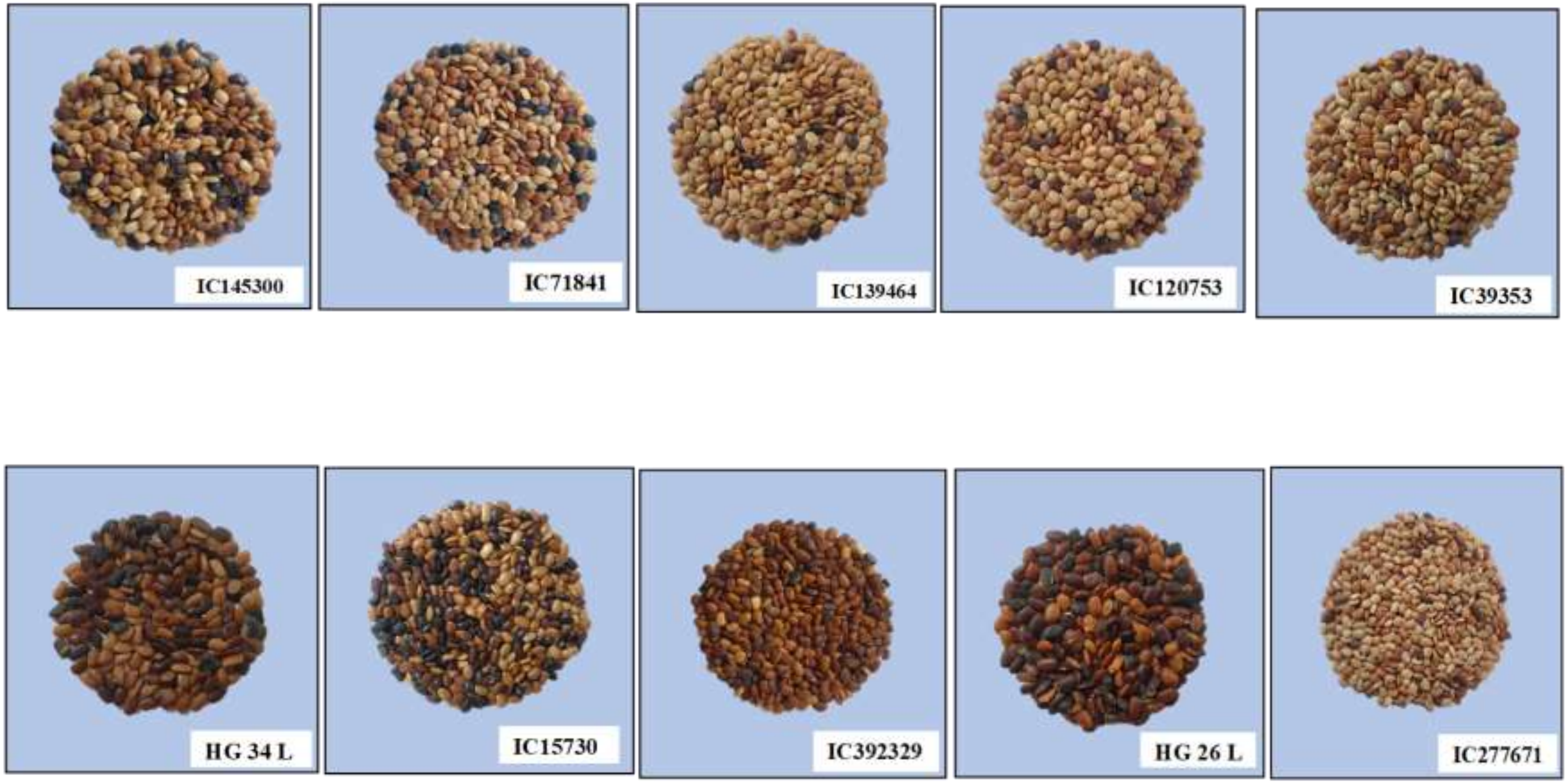
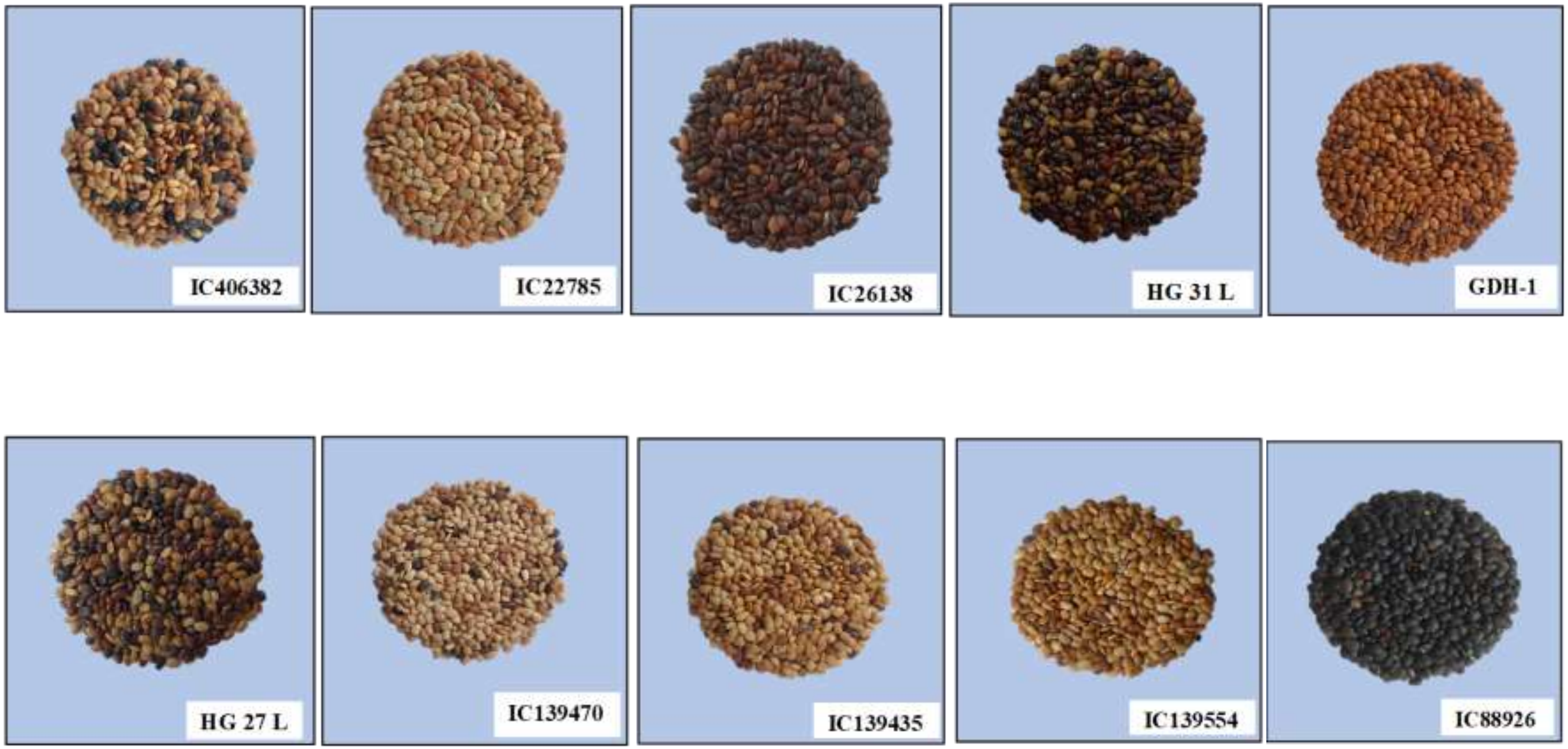


Plate 3. Variation in seeds of thirty horse gram genotypes



IC406382 IC22785 IC26138 HG 31 L GDH-1

HG 27 L IC139470 IC139435 IC139554 IC88926

Plate 3. Variation in seeds of thirty horse gram genotypes (contd.)

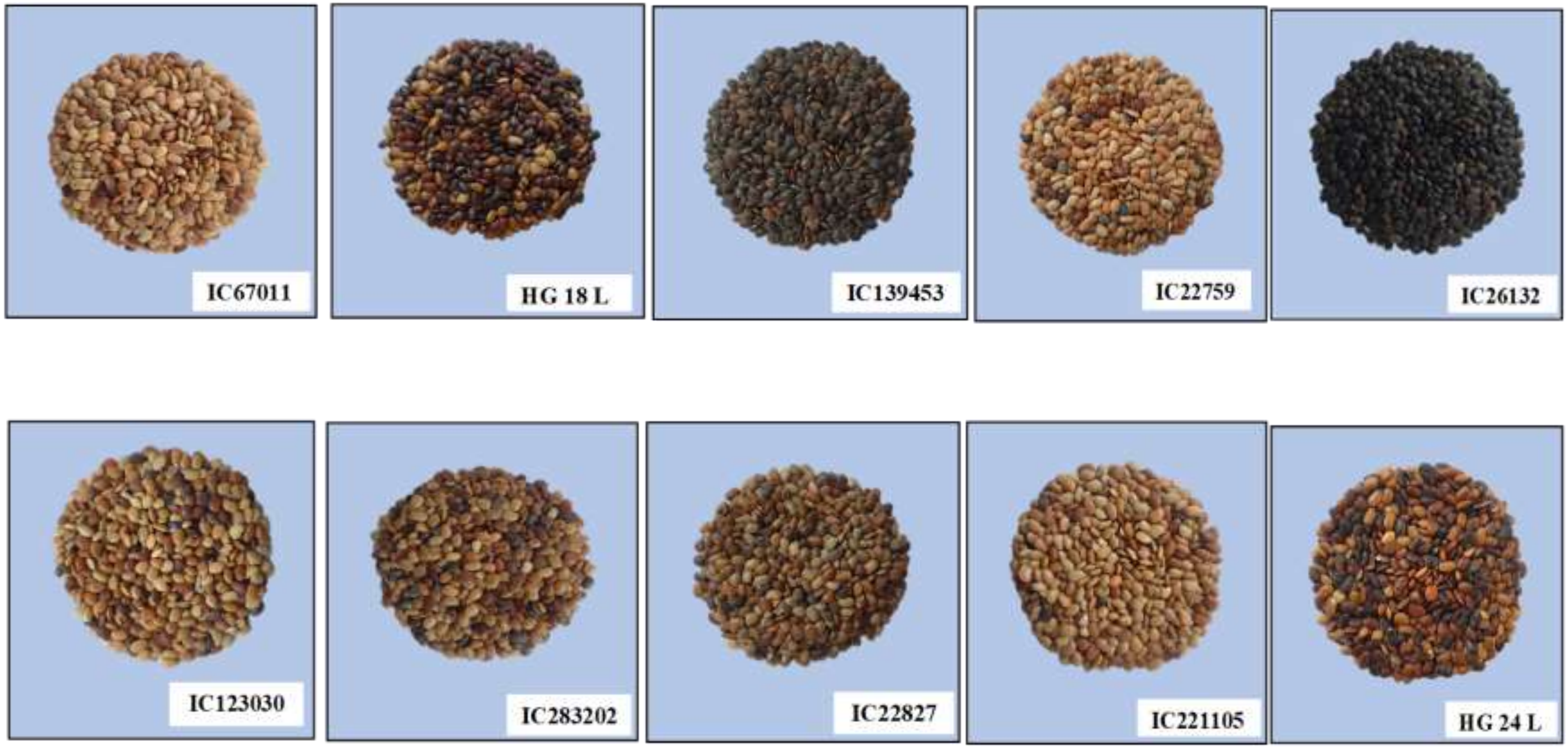

IC67011
HG 18 L
IC139453
IC22759
IC26132
IC123030
IC283202
IC22827
IC221105
HG 24 L

Plate 3. Variation in seeds of thirty horse gram genotypes (contd.)

recorded mean seed yield per plant above the general mean (5.18 g) and genotype IC22785 was statistically on par with IC221105 (8.40 g). All the thirty genotypes in control plot recorded more yield than the treatment plots.

The percentage reduction of seed yield in thirty horse gram genotypes were calculated and is presented in table 6.

Table 6. Per cent of yield reduction in thirty genotypes of horse gram

Sl. No.	Genotypes	Seed yield per plant (g) (water stress condition)	Seed yield per plant (g) (control)	Yield reduction (%)
1	IC145300	6.47	9.49	31.82
2	IC71841	2.87	7.44	61.42
3	IC139464	7.62	11.28	32.45
4	IC120753	6.94	12.69	45.31
5	IC39353	6.65	16.17	58.87
6	HG 34 L	2.42	4.75	49.05
7	IC15730	2.55	4.19	39.14
8	IC392329	2.08	6.30	66.98
9	HG 26 L	2.52	6.48	61.11
10	IC277671	7.18	15.09	52.42
11	IC406382	7.23	13.43	46.17
12	IC22785	9.62	17.49	45.00
13	IC26138	2.50	6.85	63.50
14	HG 31L	2.62	7.37	64.45
15	GDH-1	7.35	10.91	32.63
16	HG 27 L	2.42	6.61	63.39
17	IC139470	4.32	12.50	65.44
18	IC139435	6.46	9.72	33.54
19	IC139554	5.87	13.72	57.22
20	IC88926	6.86	9.68	29.13
21	IC67011	7.17	16.99	57.80
22	HG 18 L	2.81	7.83	64.11
23	IC139453	2.81	7.51	62.58
24	IC22759	7.77	10.88	28.58
25	IC26132	3.95	8.06	50.99
26	IC123030	5.97	14.88	59.88
27	IC283202	6.24	11.62	46.30
28	IC22827	5.27	10.93	51.78
29	IC221105	8.40	13.63	38.37
30	HG 24 L	2.49	5.93	58.01

4.2.3.8. Seed yield per plot (g per plot)

The seed yield per plot differed significantly between the genotypes and it varied from 44.41 g per plot (IC392329) to 205.32 g per plot (IC22785). Seventeen genotypes recorded mean seed yield per plot above the general mean (108.35 g per plot). The genotypes, IC221105 (177.68 g per plot) and IC139464 (168.13 g per plot) were on par with IC22785. The seed yield per plot was recorded higher for all the thirty genotypes in control plot.

4.2.3.9. Haulm yield per plant (g)

Among the genotypes studied, haulm yield per plant differed significantly. It ranged from 3.32 g (IC120753) to 16.50 g (HG 24 L)**.** Fourteen genotypes recorded haulm yield per plant below the general mean (10.15 g) and genotypes IC67011 (3.75 g), IC139470 (4.00 g), IC39353 (4.01 g), IC139554 (4.57 g), IC139435 (5.33 g), HG 26 L (5.65 g), IC123030 (5.90 g) and IC88926 (6.04 g) were on par with were on par with IC120753. Compared to water-stressed plots, all the thirty genotypes in the control plot recorded higher haulm yield per plant.

4.2.3.10. Haulm yield per plot (g per plot)

Haulm yield per plot varied significantly among the genotypes with a range of 63.34 g per plot (IC120753) to 359.61 g per plot (HG 27 L). Fifteen genotypes recorded haulm yield per plot above the general mean (214.29 g per plot) and genotypes IC139470 (79.66 g per plot), IC39353 (80.31 g per plot), IC67011 (82.06 g per plot), IC139554 (88.31 g per plot), IC123030 (110.54 g per plot), IC139435 (112.61 g per plot), HG 26 L (118.63 g per plot), IC88926 (131.75 g per plot) and IC71841 (133.81 g per plot) were on par with IC120753. The haulm yield per plot of all genotypes in control plot was higher than treatment plot.

4.2.3.11. Harvest Index (%)

The genotypes studied differed significantly for harvest index with a range from 13.11% (IC26138) to 67.68% (IC120753)**.** Fourteen genotypes recorded harvest index above the mean (36.27%). The genotype IC120753 was on par with IC67011 (64.67%)

and IC39353 (62.55%). The harvest index was observed to be higher for all the genotypes of control block than the treatment blocks.

4.2.3.12. Days to maturity

A significant variation was observed among genotypes for days to maturity. The days to maturity ranged from 78.67 (IC39353) to 130.33 (HG 18 L)**.** Nineteen genotypes recorded fewer days to achieve maturity than the general mean (103.72). The genotypes IC88926 (82.33 days), GDH-1 (83.33 days) and IC26132 (84.00 days) were on par with IC39353. All the thirty genotypes in the control plot recorded more days to maturity than the treatment plots.

Since no descriptors are available in this crop for categorization, descriptor available in cowpea was adopted. According to this descriptor, days to maturity can be grouped into three viz. early (upto 70 days), medium (70-80 days) and late maturing genotypes (more than 80 days). Based on this, genotypes used in this study were medium and late maturing ones. IC39353 was medium maturing genotype and all other genotypes were late maturing ones.

4.2.3.13. Leaf area (cm^2)

Results showed that the genotypes differed significantly for leaf area. The value ranged from 436.90 cm^2 (HG 34 L) to 1576.20 cm^2 (IC22785) with general mean of 1001.54 cm^2**.** Fifteen genotypes recorded above the mean and leaf areas of genotypes IC221105 (1528.91 cm^2), IC67011 (1457.21 cm^2), IC139464 (1410.60 cm^2) and IC283202 (1401.59 cm^2) were on par with IC22785. Leaf area was noticed to be higher for all the genotypes in control plot than water-stressed plots.

4.2.3.14. Leaf fresh weight (g)

A significant variation was noticed for fresh weight of leaves. It ranges from 0.578 g (IC15730) to 0.837 g (HG 34 L), with an average of 0.71 g and in nineteen genotypes fresh weight of leaves was recorded above the average and the values were on par with HG 34 L. The fresh weight of leaves was higher in the thirty genotypes of control plot than treatment plots.

4.2.3.15. Turgid weight of leaf (g)

The genotypes exhibited significant differences for the turgid weight of the leaf and it ranged from 0.76 g (IC221105) to 1.21 g (HG 34 L). The general mean was found to be 1.00 g and fifteen genotypes recorded the turgid weight of leaf below the mean. The genotypes IC71841 (0.81 g), IC283202 (0.85 g), IC22785 (0.87 g), IC15730 (0.87 g), HG 24 L (0.89 g), IC139464 (0.92 g) and IC22759 (0.92 g) recorded on par leaf turgid weight with IC221105. Turgid weight of the leaf of sixteen genotypes was lesser in control plot than in the treatment plot.

4.2.3.16. Leaf dry weight (g)

Leaf dry weight recorded significant variation among the genotypes. Leaf dry weight was varied from 0.09 g (IC283202) to 0.32 g (IC139435)**.** Twelve genotypes recorded leaf dry weight above the general mean (0.14 g). A reduction in leaf dry weight was noted for all genotypes in moisture-stressed plots than the control plot.

4.2.3.17. Root length (cm)

The genotypes differed significantly for root length. The root length ranged from 16.60 cm (HG 18 L) to 28.15 cm (IC22785). Thirteen genotypes recorded root length above the general mean (20.30 cm) and genotypes IC22759 (24.87 cm) was statistically on par with IC22785. The root length of all thirty genotypes in control plot, was shorter than treatment plots.

4.2.3.18. Root dry weight (g)

The root dry weight differed significantly with respect to the genotypes studied. It ranged from 1.16 g (IC26132) to 3.46 g (IC22759) with an average of 1.84 g. Nineteen genotypes recorded mean root dry weight above the general mean. Thirty genotypes of the control plot recorded lesser root dry weight than genotypes of water-stressed plots.

4.2.4. Physiological observations

4.2.4.1. Relative water content (%)

Relative water content (RWC) was significantly different among genotypes and it ranged from 60.47% (HG 26 L) to 78.18% (IC221105), with a mean of 66.34%. IC221105 was recorded on par with IC22759 (74.98%), IC139464 (74.52%), IC22785 (71.89%) IC120753 (71.75%), IC406382 (71.48%) and IC67011 (71.37%). Twelve genotypes exhibited RWC above the general mean and all thirty genotypes of control plot recorded higher RWC than moisture stressed plots.

4.2.4.2. Specific leaf area ($cm^2\ g^{-1}$)

Genotypes differed significantly for specific leaf areas (SLA). It varied from 232.50 $cm^2\ g^{-1}$ (IC139464) to 434.23 $cm^2\ g^{-1}$ (HG 26 L). Seventeen genotypes recorded a lower value than the general mean (305.68 $cm^2\ g^{-1}$) and these were on par with IC139464. All the thirty genotypes of control plot recorded higher SLA than water-stressed plants.

4.2.4.3. Leaf area index

Leaf area index (LAI) varied significantly among genotypes and it ranged from 0.49 (HG 34 L) to 1.75 (IC22785)**.** Fifty percentage of genotypes studied recorded leaf area index above the mean (1.11) and LAI of genotypes IC221105 (1.70), IC67011 (1.62), IC139464 (1.57) and IC283202 (1.56) were on par with IC22785. LAI of all the thirty genotypes of control block was higher than the treatment blocks.

4.2.4.4. Stress tolerance index

All genotypes exhibited significant variation in the stress tolerance index. The stress tolerance index varied from 0.10 (IC15730) to 1.57 (IC22785). Sixteen genotypes recorded a stress tolerance index above the mean (0.57).

4.2.4.5. Geometric mean productivity

Geometric mean productivity differed significantly among genotypes studied. It ranged from 3.27 (IC15730) to 12.97 (IC22785). Eighteen genotypes recorded geometric mean productivity above the general mean (7.26).

4.2.4.6. Mean productivity

All the thirty genotypes differed significantly for mean productivity and it ranged from 3.37 (IC15730) to 13.55 (IC22785). Eighteen genotypes recorded mean productivity above the general mean (7.76).

4.2.4.7. Yield stability index

Yield stability index (YSI) of different genotypes recorded significant difference and ranged between 0.39 (IC392329) and 0.71 (IC22759). Thirteen genotypes recorded higher YSI than general mean (0.49) and the IC88926 (0.71), IC145300 (0.68), IC139464 (0.62), GDH-1 (0.67), IC139435 (0.66) and IC221105 (0.62) were on par with IC22759.

4.2.5. Biochemical study

4.2.5.1. Proline content (µmol g^{-1})

Proline content showed significant variation among the genotypes and it ranged from 4.01 µmol g^{-1} (IC139554) to 9.66 µmol g^{-1} (IC120753)**.** The general mean was 6.15 µmol g^{-1} and fifteen genotypes recorded proline content above mean. All the thirty genotypes in control plots were observed to have lesser proline content than the treatment plots.

4.2.5.2. Chlorophyll content (mg g^{-1})

The genotypes differed significantly for total chlorophyll, chlorophyll A and chlorophyll B content. The total chlorophyll ranged from 0.68 mg g^{-1} (HG 34 L) to 1.76 mg g^{-1} (GDH-1)**.** In ten genotypes, total chlorophyll content was observed to be above the general mean (0.96 mg g^{-1}).

The highest value of chlorophyll A was recorded in IC22785 (1.17 mg g^{-1}), which was on par with IC139464 (1.09 mg g^{-1}) and GDH-1 (1.08 mg g^{-1}), while IC139470 (0.47 mg g^{-1}) recorded the lowest value. The average chlorophyll A content was 0.71 mg g^{-1} and ten genotypes recorded chlorophyll A content above the mean.

The genotype GDH-1 (0.68 mg g^{-1}) and HG 31L (0.10 mg g^{-1}) exhibited the highest and lowest value of chlorophyll B. Twelve genotypes recorded chlorophyll B content higher than the mean (0.25 mg g^{-1}).

All the thirty genotypes in control plot recorded higher chlorophyll content than the treatment.

4.2.6. Seed quality aspects

4.2.6.1. Crude protein content (%)

A significant difference was noted among genotypes for crude protein content. The crude protein content varied from 21.27% (HG 26 L) to 23.72% (IC88926), with an average of 22.34%. Fourteen genotypes had protein content above the general mean and these were on par with IC88926. The crude protein content of seed was noted to be lower in all the genotypes of control plot.

4.2.6.2. Total phenol content in seed (mg g^{-1})

Genotypes differed significantly for total phenol content in seed and it ranged from 84.60 mg g^{-1} (HG 34 L) to 151.42 mg g^{-1} (IC39353)**.** Thirteen genotypes recorded total phenol content in seed below the average (120.83 mg g^{-1}). The genotype HG 34 L was on par with IC392329 (90.15 mg g^{-1}), HG 26 L (95.20 mg g^{-1}), IC26138 (96.13 mg g^{-1}), HG 18 L (96.40 mg g^{-1}), IC22827 (100.20 mg g^{-1}), HG 31L (100.46 mg g^{-1}), HG 27 L (101.22 mg g^{-1}), IC283202(101.30 mg g^{-1}) and IC15730 (106.84 mg g^{-1}). In comparison to moisture-stressed plots, all the thirty genotypes in control plots recorded lesser total phenol content in seed.

4.2.7. Genetic Variability Parameters of field experiment

The phenotypic and genotypic coefficient of variation, heritability and genetic advance (5%) were computed for nineteen characters and are shown in table 7.

The PCV, GCV, heritability and GAM ranged from 4.21 to 50.42, 1.92 to 47.23, 20.70 to 98.60% and 1.80 to 92.66% respectively. High PCV and GCV were observed in days to 50% flowering, number of primary branches per plant, number of pods per plant, haulm yield per plant, harvest index, leaf area index, root dry weight, proline content, total chlorophyll content and seed yield per plant. The plant height, number of seeds per pod and specific leaf area recorded high PCV but moderate GCV. Moderate PCV and GCV were recorded in days to maturity and total phenol content in seed. Root length exhibited moderate PCV and low GCV. Low PCV and GCV were shown by hundred seed weight, crude protein content of seed and relative water content of leaves.

High heritability was recorded in days to 50% flowering, number of primary branches per plant, plant height, number of pods per plant, haulm yield per plant, harvest index, days to maturity, leaf area index, total phenol content of the seed, root dry weight, proline content, total chlorophyll content and seed yield per plant. Medium heritability was recorded in number of seeds per pod, hundred seed weight, specific leaf area and relative water content of leaves. Crude protein content of seed and root length exhibited low heritability. Days to 50% flowering recorded the highest heritability (98.60 %), while crude protein content of seed recorded the lowest (20.70 %).

Low GAM was observed in hundred seed weight, crude protein content of the seed, root length and relative water content of leaves. Days to 50% flowering, number of primary branches per plant, plant height, number of pods per plant, number of seeds per pod, haulm yield per plant, harvest index, days to maturity, specific leaf area, leaf area index, total phenol content of the seed, root dry weight, proline content, total chlorophyll content and seed yield per plant expressed a high GAM. High heritability along with high GAM was observed in days to 50% flowering, number of primary branches per plant, plant height, number of pods per plant, haulm yield per plant, harvest index, days to maturity, leaf area index, total phenol content of the seed, root dry weight, proline content, total chlorophyll content and seed yield per plant.

Plate 4: Superior genotypes identified in the study

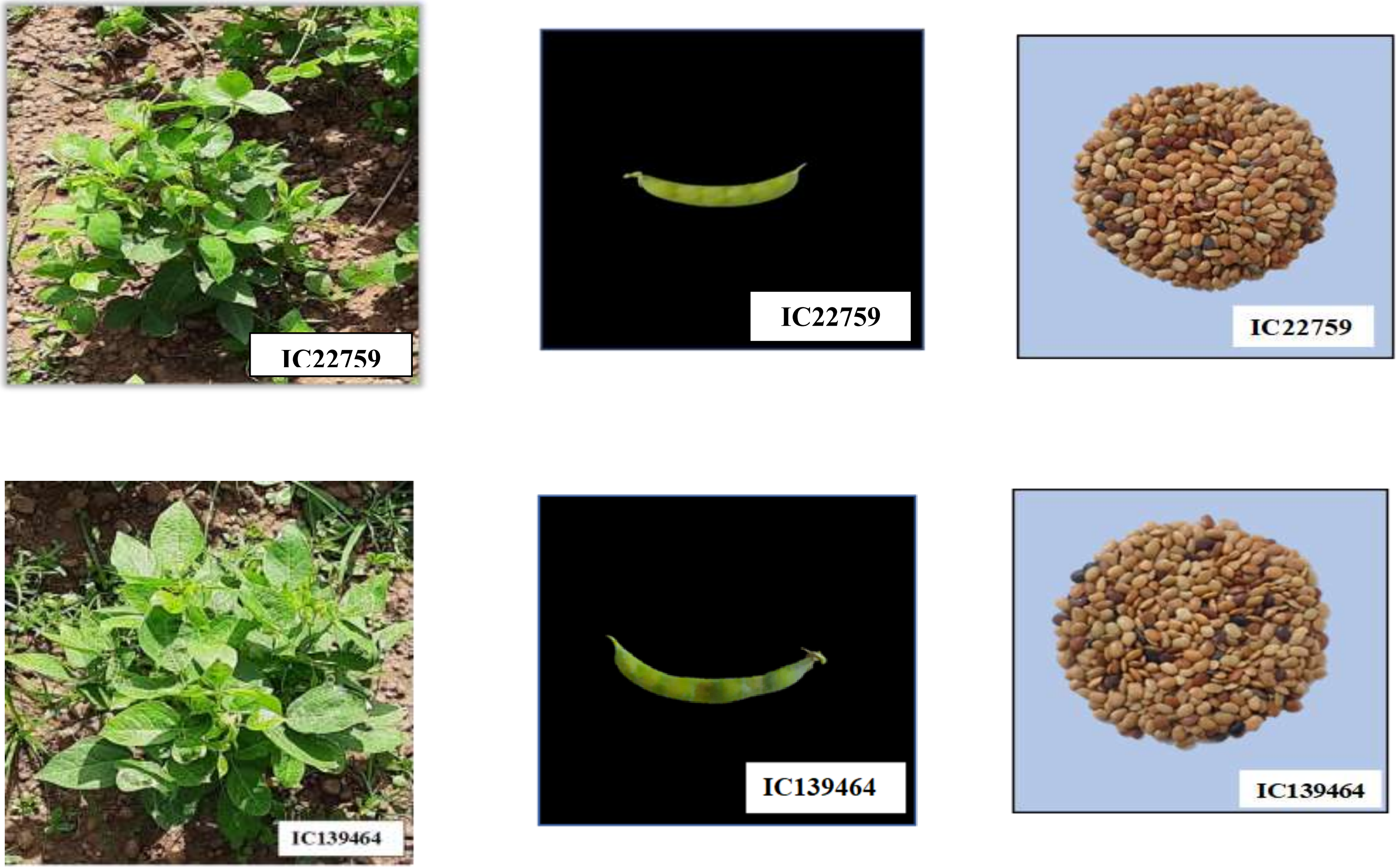


Plate 4: Superior genotypes identified in the study (contd.)

Table 7. Estimates of variability parameters of various traits in horse gram genotypes

Character	**Mean**	**PCV (%)**	**GCV (%)**	**H^2 (%)**	**GAM (5%)**
Days to 50% flowering	52.889	37.756	37.483	98.600	76.659
No. of primary branches/plant	8.735	25.409	20.755	66.700	34.925
Plant height (cm)	80.829	20.285	15.9	61.400	25.674
No. of pods per plant	34.556	50.419	46.717	85.900	89.170
No. of seeds per pod	3.580	22.142	17.022	59.100	26.956
100 seed weight (g)	3.558	8.843	4.948	31.300	5.704
Haulm yield per plant (g)	10.151	47.276	43.901	86.200	83.982
Harvest index (%)	36.267	49.581	47.225	90.700	92.660
Days to maturity	103.722	15.29	14.137	85.500	26.924
Specific leaf area (cm^2 g^{-1})	305.679	20.604	14.245	47.800	20.289
Leaf area index	1.113	34.687	28.558	67.800	48.436
Total phenol content of seed (mg g^{-1})	120.147	19.016	15.019	62.400	24.436
Crude Protein content (%)	22.342	4.212	1.918	20.700	1.799
Root length (cm)	20.303	17.315	8.852	26.100	9.322
Root dry weight (g)	1.833	31.341	26.362	70.800	45.680
Relative water content (%)	66.343	9.372	5.739	37.500	7.239
Proline content (μmol g^{-1})	6.149	23.906	22.854	91.400	45.007
Total chlorophyll content (mg g^{-1})	0.9636	30.959	30.077	94.400	60.192
Seed yield per plant (g)	5.181	45.827	43.294	89.300	84.256

4.2.8. Correlation Studies

The association between yield and various characters studied was analysed. The genotypic and phenotypic correlation coefficients are presented in the table 8 and 9 respectively.

4.2.8.1. Seed yield per plant (g)

Association studies revealed a significant positive correlation of seed yield with RWC (0.969), followed by number of pods per plant (0.966), number of seeds per pod (0.960), total chlorophyll content (0.829), harvest index (0.738), proline content (0.677), root dry weight (0.622), root length (0.596), LAI (0.585) and hundred seed weight (0.427) and a significant negative correlation with days to 50% flowering (-0.812), days to maturity (-0.712), plant height (-0.634) and number of primary branches (-0.466). SLA showed a negative but non-significant correlation with seed yield.

4.2.8.2. Days to 50% Flowering

Days to 50% flowering exhibited a significant positive correlation with days to maturity (0.906), number of primary branches (0.742) and plant height (0.727). A significant negative correlation was noted between days to 50% flowering and number of seeds per pod (-0.876), seed yield per plant (-0.812), number of pods per plant (-0.799), harvest index (-0.734), RWC (-0.712), total chlorophyll content (-0.559), proline content (-0.524) and hundred seed weight (-0.370).

4.2.8.3. Number of primary branches per plant

A positive correlation was shown by the number of primary branches per plant with days to maturity (0.865), days to 50% flowering (0.742) and plant height (0.680). A significant negative correlation was shown by number of primary branches per plant with harvest index (-0.762), number of pods per plant (-0.595), number of seeds per pod (-0.566), seed yield per plant (-0.466), proline content (-0.422), RWC (-0.366), SLA (-0.299) and root dry weight (-0.197).

4.2.8.4. Plant height (cm)

Plant height exhibited a positive significant correlation with the days to 50% flowering (0.727), days to maturity (0.711) and number of primary branches per plant (0.680). A significant negative correlation of plant height was observed with number of seeds per pod (-0.790), followed by number of pods per plant (-0.706), harvest index (-0.702), proline content (-0.674), total chlorophyll content (-0.646), seed yield per plant (-0.634), RWC (-0.574), LAI (-0.374), root dry weight (-0.366), root length (-0.341) and hundred seed weight (-0.226).

4.2.8.5. Number of pods per plant

A significant positive correlation was recorded by number of pods per plant with seed yield per plant (0.966), number of seeds per plant (0.964), RWC (0.941), harvest index (0.835), total chlorophyll (0.761), proline content (0.699), root dry weight (0.589), root length (0.484), LAI (0.483) and hundred seed weight (0.271). Days to 50% flowering (-0.799), days to maturity (-0.751), plant height (-0.706) and number of primary branches per plant (-0.595) had a significant negative correlation with number of pods per plant.

4.2.8.6. Number of seeds per pod

Number of seeds per pod recorded a positive significant correlation with number of pods per plant (0.964), seed yield per plant (0.96), RWC (0.954), total chlorophyll content (0.792), proline content (0.773), harvest index (0.739), root length (0.708), root dry weight (0.655), LAI (0.564) and hundred seed weight (0.272). However, number of seeds per pod was significantly negatively correlated with days to 50% flowering (-0.876), plant height (-0.790), days to maturity (-0.748) and number of primary branches per plant (-0.566).

4.2.8.7. Hundred seed weight (g)

A significant positive correlation was exhibited by hundred seed weight with total chlorophyll content (0.448), seed yield per plant (0.427), RWC (0.287), number of seeds per pod (0.272), number of pods per plant (0.271), root dry weight (0.207) and

LAI (0.192). Days to maturity (-0.491), SLA (-0.423), days to 50% flowering (-0.37) and plant height (-0.266) recorded a significant negative correlation with hundred seed weight.

4.2.8.8. Harvest index (%)

Harvest index showed a positive significant correlation with the number of pods per plant (0.835), number of seeds per plant (0.739), seed yield per plant (0.738), RWC (0.591), total chlorophyll content (0.468), proline content (0.431), SLA (0.420), root dry weight (0.289) and LAI (0.250). Number of primary branches per plant (-0.762), days to maturity (-0.738), days to 50% flowering (-0.734) and plant height (-0.702) were noticed to be significantly negatively correlated with the harvest index.

4.2.8.9. Days to maturity

Correlation of days to maturity with days to 50% flowering (0.906), number of primary branches (0.843) and plant height (0.711) was positively significant. The days to maturity was observed to have a significant negative correlation with number of pods per plant (-0.751), number of seeds per pod (-0.748), harvest index (-0.738), seed yield per plant (-0.712), hundred seed weight (-0.491), total chlorophyll content (-0.445), RWC (-0.427), proline content (-0.383), LAI (-0.268), root length (-0.217) and root dry weight (-0.189).

4.2.8.10. Specific leaf area (SLA) (cm^2 g^{-1})

The SLA possessed a positive significant correlation with harvest index (0.42). The root length (-0.621), root dry weight (-0.482), hundred seed weight (-0.423), RWC (-0.400), number of primary branches per plant (-0.299), proline content (-0.272), total chlorophyll content (-0.237) and LAI (-0.192) were significantly negatively correlated with SLA.

4.2.8.11. Leaf area index (LAI)

LAI was significantly positively correlated with RWC (0.731), proline content (0.644), seed yield per plant (0.585), number of seed per pod (0.564), total chlorophyll content (0.520), number of pods per plant (0.483), root dry weight (0.466), root length (0.340), harvest index (0.250) and hundred seed weight (0.192). The days to 50% flowering (-0.482), plant height (-0.374), days to maturity (-0.268) and SLA (-0.192) were significantly negatively correlated with LAI.

4.2.8.12. Root length (cm)

A significant positive correlation was recorded by root length with root dry weight (0.99), total chlorophyll content (0.855), RWC (0.763), number of seeds per pod (0.708), proline content (0.654), seed yield per plant (0.596), number of pods per plant (0.484) and LAI (0.34). Root length was significantly negatively correlated with SLA (-0.621), days to 50% flowering (-0.422), plant height (-0.341) and days to maturity (-0.217).

4.2.8.13. Root dry weight (g)

Root dry weight was positively correlated with root length (0.99), RWC (0.932), proline content (0.744), total chlorophyll content (0.695), number of seeds per pod (0.665), seed yield per plant (0.622), number of pods per plant (0.589), LAI (0.466), harvest index (0.289) and hundred seed weight (0.207). A significant negative correlation was recorded by root dry weight with SLA (-0.482), plant height (-0.366), days to 50% flowering (-0.317), number of primary branches per plant (-0.197) and days to maturity (-0.189).

4.2.8.14. Relative water content (RWC) (%)

Correlation of RWC with seed yield per plant (0.969), total chlorophyll content (0.956), number of seeds per pod (0.954), number of pods per plant (0.941), root dry weight (0.932), proline content (0.857), root length (0.763), LAI (0.731), harvest index (0.591) and hundred seed weight (0.287) were positively significant. A significant negative correlation of RWC was observed with days to 50% flowering (-0.712), plant height (-0.574), days to maturity (-0.427), SLA (-0.400) and number of primary branches per plant (-0.366).

4.2.8.15. Proline content (µmol g^{-1})

Proline content recorded a significant positive correlation with RWC (0.857), number of seeds per pod (0.773), root dry weight (0.744), number of pods per plant (0.699), total chlorophyll content (0.695), seed yield per plant (0.677), root length (0.654), LAI (0.644) and harvest index (0.431) whereas this trait was significantly negatively correlated with plant height (-0.674), days to 50% flowering (-0.524), number of primary branches per plant (-0.422), days to maturity (-0.383) and SLA (-0.272).

4.2.8.16. Total chlorophyll content (mg g^{-1})

A significant positive correlation was recorded by total chlorophyll content with RWC (0.956), root length (0.855), seed yield per plant (0.829), number of seeds per pod (0.792), root dry weight (0.695), LAI (0.520), harvest index (0.468), number of pods per plant (0.761), proline content (0.695) and hundred seed weight (0.448). The plant height (-0.646), days to 50% flowering (-0.559), days to maturity (-0.445) and SLA (-0.237) were significantly negatively correlated with total chlorophyll content.

4.2.9. Path Coefficient Analysis

Path coefficient analysis was computed to divide the genotypic association of yield and different selected characters of this study into direct and indirect effects. Seed yield was taken as a dependent variable and other component characters like days to 50% flowering, number of primary branches per plant, plant height, number of pods per plant, number of seeds per pod, harvest index, days to maturity, specific leaf area, leaf area index, root length, root dry weight, relative water content, proline content and total chlorophyll content as independent variables. The direct and indirect effects of these characters on yield are presented in the table 10. Genotypic path diagram for seed yield is depicted in Fig. 1.

4.2.9.1. Direct effect

The number of pods per plant exhibited the highest direct effect on seed yield (0.594). The moderate direct effect was recorded by plant height (0.218) with seed yield.

Table 8. Genotypic correlation of yield and various characters of horse gram

	DF	**PB**	**HT**	**PP**	**SP**	**SW**	**HI**	**DM**	**SLA**	**LAI**	**RL**	**RDW**	**RWC**	**Pro**	**TC**	**SY**
DF	1															
PB	.742**	1														
HT	.727**	.680**	1													
PP	-.799**	-.595**	-.706**	1												
SP	-.876**	-.566**	-.790**	.964*	1											
SW	-.37**	-.110	-.226*	.271*	.272*	1										
HI	-.734**	-.762**	-.702**	.835**	.739**	-.016	1									
DM	.906**	.843**	.711**	-.751**	-.748**	-.491**	-.738**	1								
SLA	-.062	-.299*	-.099	-.005	.061	-.423**	.420**	-.052	1							
LAI	-.482**	-.171	-.374**	.483**	.564**	.192*	.250*	-.268*	-.192*	1						
RL	-.422**	.041	-.341*	.484**	.708**	.148	.060	-.217*	-.621**	.340*	1					
RDW	-.317*	-.197*	-.366**	.589**	.665**	.207*	.289*	-.189*	-.482**	.466**	.990**	1				
RWC	-.712**	-.366**	-.574**	.941**	.954**	.287*	.591**	-.427**	-.400**	.731**	.763**	.932**	1			
Pro	-.524**	-.442**	-.674**	.699**	.773**	.122	.431**	-.383**	-.272*	.644**	.654**	.744**	.857**	1		
TC	-.559**	-.180	-.646**	.761**	.792**	.448**	.468**	-.445**	-.237*	.520**	.855**	.695**	.956**	.695**	1	
SY	-.812**	-.466**	-.634**	.966**	.960**	.427**	.738**	-.712**	-.051	.585**	.596**	.622**	.969**	.677**	.829**	1

DF- Days to 50% flowering
PB- Number of primary branches per plant
HT- Plant height (cm)
PP- Number of pods per plant
SP- number of seeds per pod
SW- Hundred seed weight (g)
HI- Harvest Index (%)
DM- Days to maturity
SLA- Specific leaf area (cm^2 g^{-1})
LAI- Leaf area index
RL- Root length (cm)
RDW- Root dry weight (g)
RWC- Relative water content (%)
PRO-Proline content (μmol g^{-1})
TC- Total Chlorophyll content (mg g^{-1})
SY- Seed yield per plant (g)

Table 9. Phenotypic correlation of yield and various characters of horse gram

	DF	**PB**	**HT**	**PP**	**SP**	**SW**	**HI**	**DM**	**SLA**	**LAI**	**RL**	**RDW**	**RWC**	**Pro**	**TC**	**SY**
DF	1															
PB	.600**	1														
HT	.581**	.476**	1													
PP	-.742**	-.465**	-.516**	1												
SP	-.68**	-.405**	-.523**	.676**	1											
SW	-.203*	.068	-.069	.218*	.185	1										
HI	.426**	.566**	.367**	-.373**	-.292*	.101	1									
DM	-.701**	-.63**	-.544**	.774**	.560**	.046	-.816**	1								
SLA	.827**	.62**	.484**	-.642**	-.495**	-.241*	.427**	-.643**	1							
LAI	-.026	-.135	-.049	-.057	-.061	-.207*	-.354**	.236*	-.03	1						
RL	-.401**	-.146	-.131	.406**	.413**	.134	-.019	.217*	-.232*	-.194*	1					
RDW	-.198*	-.038	-.228*	.253*	.305*	.253*	.124	.022	-.077	-.230*	.123	1				
RWC	-.266*	-.153	-.341*	.446**	.473**	.033	.060	.209*	-.153	-.227*	.232*	.494**	1			
Pro	-.426**	-.138	-.310*	.560**	.395**	.138	-.065	.344*	-.272*	-.138	0.32*	.290*	.478**	1		
TC	-.496**	-.356**	-.517**	.621**	.616**	.041	-.126	.390**	-.350*	-.132	.506**	.336*	.635**	.514**	1	
SY	-.535**	-.131	-.449**	.683**	.587**	.255*	-.063	.425**	-.411**	-.157	.431**	.453**	.56**	.534**	.641**	1

DF- Days to 50% flowering
PB- Number of primary branches per plant
HT- Plant height (cm)
PP- Number of pods per plant
SP- number of seeds per pod
SW- Hundred seed weight (g)
HI- Harvest Index (%)
DM- Days to maturity
SLA- Specific leaf area (cm^{2} g^{-1})
LAI- Leaf area index
RL- Root length (cm)
RDW- Root dry weight (g)
RWC- Relative water content (%)
PRO-Proline content (µmol g^{-1})
TC- Total Chlorophyll content (mg g^{-1})
SY- Seed yield per plant (g)

Fig 1. Genotypic path diagram for seed yield

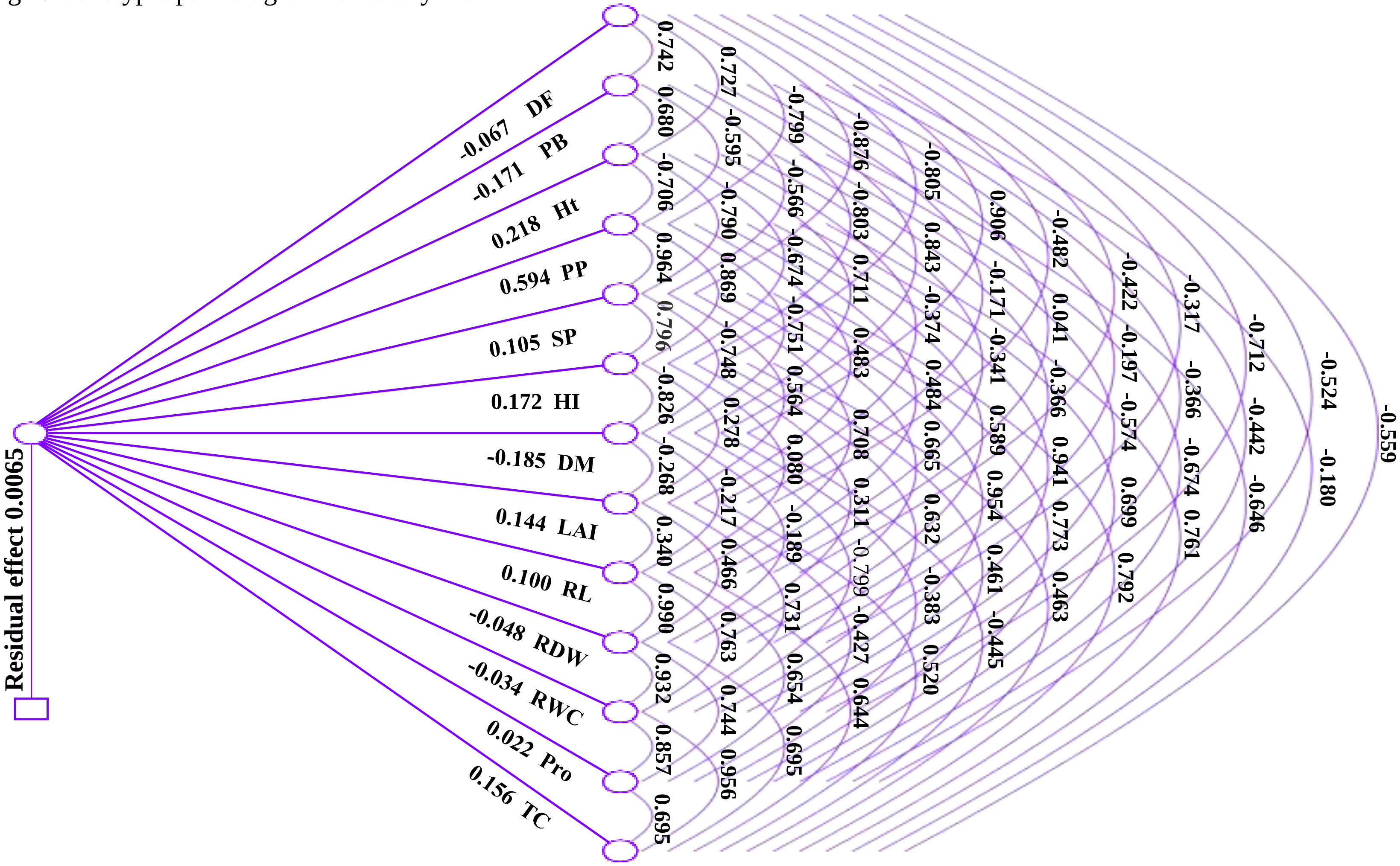


Table 10. Direct and indirect effects of different characters on yield

	DF	**PB**	**Ht**	**PP**	**SP**	**HI**	**DM**	**LAI**	**RL**	**RDW**	**RWC**	**Pro**	**TC**	**G.Cor.**
DF	**-0.067**	0.127	0.158	-0.475	-0.092	-0.126	-0.167	-0.069	-0.042	0.015	0.024	-0.011	-0.087	-0.812
PB	-0.049	**0.171**	0.148	-0.353	-0.059	-0.131	-0.156	-0.025	0.004	0.01	0.012	-0.010	-0.028	-0.466
Ht	-0.048	0.116	**0.218**	-0.419	-0.083	-0.121	-0.131	-0.054	-0.034	0.018	0.019	-0.015	-0.101	-0.634
PP	0.053	-0.102	-0.154	**0.594**	0.101	0.144	0.139	0.069	0.048	-0.028	-0.032	0.015	0.119	0.966
SP	0.058	-0.097	-0.172	0.572	**0.105**	0.127	0.138	0.081	0.071	-0.032	-0.032	0.017	0.123	0.960
HI	0.049	-0.130	-0.153	0.495	0.078	**0.172**	0.137	0.036	0.006	-0.014	-0.020	0.009	0.073	0.738
DM	-0.060	0.144	0.155	-0.446	-0.078	-0.127	**-0.185**	-0.039	-0.022	0.009	0.014	-0.008	-0.069	-0.712
LAI	0.032	-0.029	-0.081	0.287	0.059	0.043	0.050	**0.144**	0.034	-0.023	-0.025	0.014	0.081	0.585
RL	0.028	0.007	-0.074	0.287	0.074	0.010	0.040	0.049	**0.100**	-0.048	-0.026	0.014	0.133	0.596
RDW	0.021	-0.034	-0.08	0.349	0.070	0.050	0.035	0.067	0.099	**-0.048**	-0.031	0.016	0.108	0.622
RWC	0.047	-0.062	-0.125	0.558	0.100	0.102	0.079	0.105	0.076	-0.045	**-0.034**	0.019	0.149	0.969
Pro	0.035	-0.076	-0.147	0.415	0.081	0.074	0.071	0.093	0.065	-0.036	-0.029	**0.022**	0.108	0.677
TC	0.037	-0.031	-0.141	0.452	0.083	0.081	0.082	0.075	0.086	-0.034	-0.032	0.015	**0.156**	0.829

DF- Days to 50% flowering
PB- Number of primary branches per plant
HT- Plant height (cm)
PP- Number of pods per plant
SP- number of seeds per pod
HI- Harvest Index (%)
DM- Days to maturity
LAI- Leaf area index
RL- Root length (cm)
RDW- Root dry weight (g)
RWC- Relative water content (%)
PRO- Proline content (µmol g^{-1})
TC- Total Chlorophyll content (mg g^{-1})
G.Cor.- Genotypic correlation

Harvest index (0.172), number of primary branches (0.171), total chlorophyll content (0.156), LAI (0.144), number of seeds per pod (0.105) and root length (0.100) registered low direct effect. The proline content (0.022) showed a positive but negligible direct effect on seed yield. While days to maturity (-0.185) exhibited a negative direct effect on seed yield. A negative but negligible direct effect on yield was recorded by characters like days to 50% flowering (-0.067), root dry weight (-0.048) and RWC (-0.034).

4.2.9.2. Indirect effect

The highest positive indirect effect on seed yield was registered via number of pods per plant by number of seeds per pod (0.572), followed by RWC (0.558), harvest index (0.495), total chlorophyll content (0.452), proline content (0.415) and root dry weight (0.349). While root length (0.287) and LAI (0.287) recorded moderate indirect effect via number of pods per plant. But the days to 50% flowering (-0.475), days to maturity (-0.446), plant height (-0.419) and number of primary branches (-0.353) exhibited high negative indirect effect through number of pods per plant.

Characters like days to 50% flowering (0.158), days to maturity (0.155) and number of primary branches (0.148) recorded a low indirect effect on seed yield via the plant height. A negative but low indirect effect on yield was shown by the number of seeds per pod (-0.153), number of pods per plant (-0.154), harvest index (-0.153), proline content (-0.147), total chlorophyll content (-0.141) and RWC (-0.125) through plant height. The LAI (-0.081), root dry weight (-0.08) and root length (-0.074) registered a negative but negligible indirect effect on yield via plant height.

The days to maturity (0.144), days to 50% flowering (0.127) and plant height (0.116) recorded a low positive indirect effect on yield via number of primary branches per plant, while a low negative indirect effect on seed yield was shown by harvest index (-0.13) and number of pods per plant (-0.102) via number of primary branches per plant. Through number of primary branches per plant, root length (0.007) recorded a negligible but positive indirect effect, while number of seeds per pod (-0.097), proline content (-0.076), RWC (-0.062), root dry weight (-0.034), total chlorophyll content (-0.031) and LAI (-0.029) showed negative but negligible indirect effect on yield.

The number of pods per plant (0.144), number of seeds per pod (0.127) and RWC (0.102) recorded a low positive indirect effect on yield via harvest index. The total chlorophyll content (0.081), proline content (0.074), root dry weight (0.05), LAI (0.043) and root length (0.01) exhibited positive but negligible indirect effect via harvest index. A low negative indirect effect on yield through harvest index was shown by number of primary branches per plant (-0.131), days to maturity (-0.127), days to 50% flowering (-0.126) and plant height (-0.121).

A positive low indirect effect on seed yield via days to maturity was number of pods per plant (0.139), number of seeds per pod (0.138) and harvest index (0.137); while a positive but negligible indirect effect on seed yield via days to maturity was exhibited by total chlorophyll content (0.082), RWC (0.079), proline content (0.071), LAI (0.05), root length (0.04) and root dry weight (0.035). Days to 50% flowering (-0.167), number of primary branches per plant (-0.156) and plant height (-0.131) registered a negative low indirect effect on yield through days to maturity.

The number of pods per plant (0.101) and RWC (0.100) recorded a low positive indirect effect on seed yield through number of seeds per pod. While a positive but negligible indirect effect on yield through number of seeds per pod was shown by total chlorophyll content (0.083), proline content (0.081), harvest index (0.078), root length (0.074), root dry weight (0.07) and LAI (0.059). A negative but negligible indirect effect on seed yield was registered by days to 50% flowering (-0.092), plant height (-0.083), days to maturity (-0.078) and number of primary branches per plant (-0.059) through number of seeds per pod.

The number of seeds per pod (0.058), harvest index (0.049), RWC (0.047), total chlorophyll content (0.037), proline content (0.035), LAI (0.032), root length (0.028) and root dry weight (0.021) had a negligible positive indirect effect on yield through days to 50% flowering; whereas a negligible positive indirect effect on yield was exhibited by days to maturity (-0.06), number of primary branches per plant (-0.049) and plant height (-0.048) via days to 50% flowering.

A low positive indirect effect on yield via total chlorophyll content was recorded by RWC (0.149), root length (0.133), number of seeds per pod (0.123), number of pods per plant (0.119), proline content (0.108) and root dry weight (0.108). The LAI (0.081) and harvest index (0.073) had a negligible positive indirect effect on seed yield via total chlorophyll content. A negative low indirect effect on yield was shown by plant height (-0.101) through total chlorophyll content. The days to 50% flowering (-0.087), days to maturity (-0.069) and number of primary branches per plant (-0.028) via total chlorophyll content had a negative but negligible indirect effect on seed yield.

The RWC (0.105) through LAI exhibited a low positive indirect effect on seed yield. The characters like proline content (0.093), number of seeds per pod (0.081), total chlorophyll content (0.075), number of pods per plant (0.069), root dry weight (0.067), root length (0.049) and harvest index (0.036) showed a negligible positive indirect effect on seed yield through LAI; while days to 50% flowering (-0.069), plant height (-0.054), days to maturity (-0.039) and number of primary branches per plant (-0.069) recorded a negative but negligible indirect effect on seed yield via LAI.

A negligible positive indirect effect on yield via root length was registered by root dry weight (0.099), total chlorophyll content (0.086), RWC (0.076), number of seeds per pod (0.071), proline content (0.065), number of pods per plant (0.048), LAI (0.034), harvest index (0.006) and number of primary branches per plant (0.004). The days to 50% flowering (-0.042), plant height (-0.034) and days to maturity (-0.022) had a negligible negative indirect effect on seed yield via root length.

Through root dry weight, plant height (0.018), days to 50% flowering (0.015), number of primary branches per plant (0.01) and days to maturity (0.009) had a positive but negligible indirect effect on seed yield, whereas root length (-0.048), RWC (-0.045), proline content (-0.036), total chlorophyll content (-0.034), number of seeds per pod (-0.032), number of pods per plant (-0.028), LAI (-0.023) and harvest index (-0.014) had a negative but negligible indirect effect on yield.

Days to 50% flowering (0.024), plant height (0.019), days to maturity (0.014) and number of primary branches per plant (0.012) exhibited a positive but negligible indirect effect on yield via RWC, while negative but negligible indirect effect on yield through RWC was recorded by number of pods per plant (-0.032), number of seeds per pod (-0.032), total chlorophyll content (-0.032), root dry weight (-0.031), root length (-0.026), LAI (-0.025) and harvest index (-0.02).

Through proline content a positive but negligible indirect effect on seed yield was recorded by RWC (0.019), number of seeds per pod (0.017), root dry weight (0.016), number of pods per plant (0.015), LAI (0.014), root length (0.014) and harvest index (0.009), whereas plant height (-0.015), days to 50% flowering (-0.011), number of primary branches per plant (-0.01) and days to maturity (-0.008) had a negative but negligible indirect effect on yield.

The residual effect obtained was 0.0065.

4.2.10. Genetic Divergence Analysis

To know the extent of genetic diversity in the genotypes under study, Mahalanobis D^2 statistics was worked out on 19 characters viz number of primary branches per plant, days to 50% flowering, days to maturity, plant height, number of pods per plant, number of seeds per pod,100 seed weight, seed yield per plant, haulm yield per plant, harvest index, root length, root dry weight, relative water content, leaf area index, crude protein content in seed, total phenol content in seed and proline content. Using Tocher's method of clustering, thirty genotypes were clustered into four clusters (Fig. 2). The composition of genotypes into different cluster groups is presented in the table 11.

Cluster II with fourteen genotypes was the largest cluster followed by cluster I (nine genotypes) and cluster III (six genotypes). The cluster IV was solitary.

Based on D^2 values, the average inter-cluster and intra-cluster distances were computed and are presented in the table 12. The intra-cluster distance varied from 0 (cluster IV) to 10.12 (cluster II).

The inter-cluster distances extended from 14.76 to 33.57 (Fig. 3). The minimum divergence was noted between cluster IV and cluster III (14.76), while the highest inter-cluster distance was noticed between cluster I and cluster III (33.57).

Cluster I with an intra-cluster distance of 7.33, recorded the greatest inter-cluster value with cluster III (33.57) and minimum with cluster II (26.69). Cluster II had an intra- cluster distance of 10.12. This cluster recorded the greatest divergence with cluster III (18.17) and lowest with cluster IV (16.95). With an intra-cluster distance of 10.09, cluster III had 14.76 as inter-cluster distance with cluster IV.

Table 11. Distribution of horse gram genotypes into different clusters

Cluster	**No. of genotypes**	**Genotypes**
I	9	HG 34 L, HG 27 L, IC26138, HG 18 L, IC15730, HG 26 L, HG 31L, IC392329, HG 24 L
II	14	IC123030, IC22827, IC139554, IC139470, IC67011, IC88926, IC139435, IC283202, IC39353, IC26132, IC71841, IC277671, IC139453
III	6	IC22785, IC221105, IC139464, IC406382, GDH-1, IC22759
IV	1	IC120753

Table 12. Average Intra and inter-cluster D^2 values

	I	**II**	**III**	**IV**
I	7.33			
II	26.69	10.12		
III	33.57	18.17	10.09	
IV	31.77	16.95	14.76	0.00

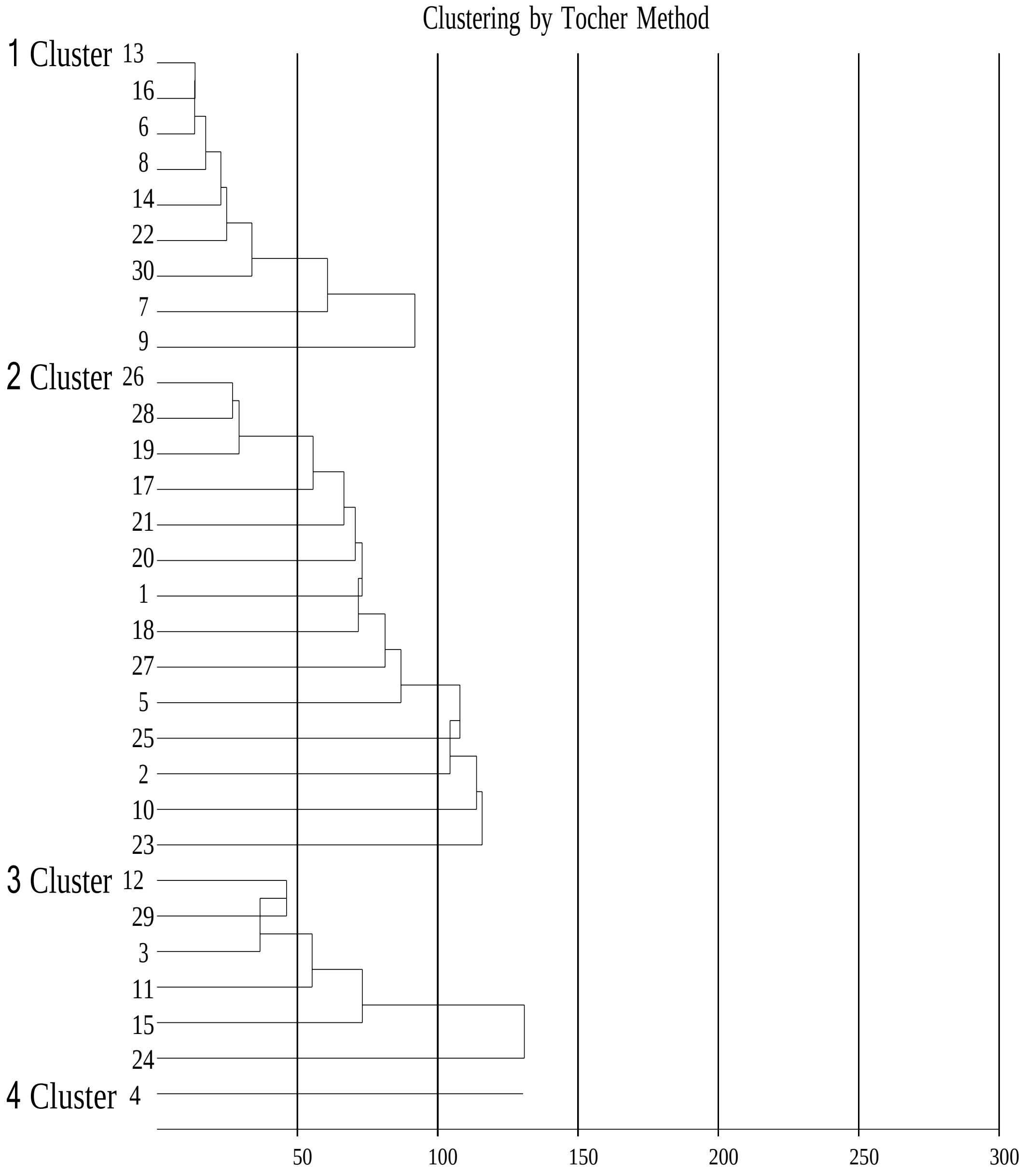


Fig 2. Dendrogram showing clustering pattern of thirty horse gram genotypes

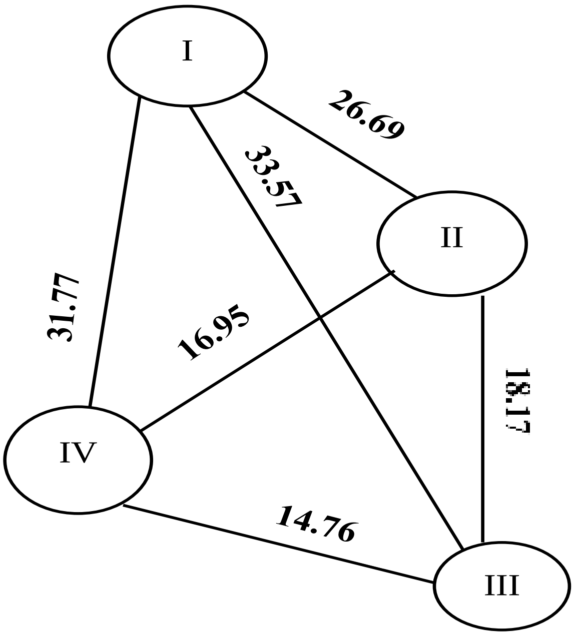


Fig 3. Cluster diagram

4.2.10.1. Cluster means

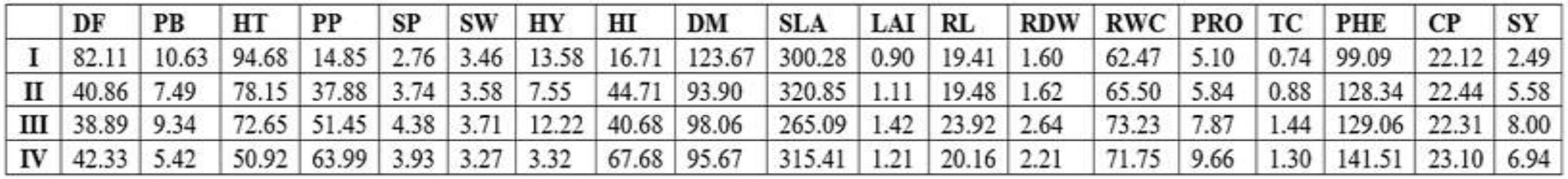
The cluster mean calculated for nineteen characters is presented in the table 13. Cluster I was observed to have the highest cluster average for days to 50% flowering (82.11), number of primary branches per plant (10.63), haulm yield per plant (13.58), plant height (94.68) and days to maturity (123.67). The number of seeds per pod (4.38), hundred seed weight (3.71), LAI (1.42), root length (23.92), root dry weight (2.64), RWC (73.23), total chlorophyll content (1.44) and seed yield per plant (8.00) had maximum cluster mean in cluster III. Cluster IV accounted to have the highest cluster mean for number of pods per plant (63.99), harvest index (67.68), proline content (9.66), phenol content (141.51) and crude protein content (23.1). The maximum cluster means for specific leaf area (320.85) was recorded in cluster II.

The lowest cluster mean for number of seeds per pod (2.76), harvest index (16.71), LAI (0.9), root length (19.41), root dry weight (1.6), RWC (62.47), proline content (4.01) total phenol content in seed (99.09), total chlorophyll content (0.74), crude protein content (22.12) and seed yield (2.49) was recorded in cluster I. The cluster means for days to maturity (93.9) was minimum in cluster II. Cluster III exhibited the lowest cluster mean for days to 50% flowering (38.89) and SLA (265.09). Cluster IV had the lowest cluster mean for number of primary branches per plant (5.42), plant height (50.92), hundred seed weight (3.27) and haulm yield per plant (3.32).

4.2.10.2. Relative contribution of characters towards divergence

The relative contribution of various characters towards divergence was calculated and is shown in the table 14. The highest contribution towards genetic diversity was made by days to 50% flowering (45.75%), followed by total chlorophyll content (15.17%), proline content (10.57%), seed yield per plant (7.82%), haulm yield per plant (5.29%), crude protein content of seed (2.99%), total phenol content in seeds (2.30%), harvest index (2.53%), LAI (2.07%), days to maturity (1.61%) and root dry weight (1.15%). While characters like number of pods per plant (0.92%), plant height (0.69%) hundred seed weight (0.46%), specific leaf area (0.46%) and number of primary branches per plant (0.23%) made a low contribution to genetic divergence.

Table 13. Cluster means of yield and various characters in horse gram



	DF	PB	HT	PP	SP	SW	HY	HI	DM	SLA	LAI	RL	RDW	RWC	PRO	TC	PHE	CP	SY
I	82.11	10.63	94.68	14.85	2.76	3.46	13.58	16.71	123.67	300.28	0.90	19.41	1.60	62.47	5.10	0.74	99.09	22.12	2.49
II	40.86	7.49	78.15	37.88	3.74	3.58	7.55	44.71	93.90	320.85	1.11	19.48	1.62	65.50	5.84	0.88	128.34	22.44	5.58
III	38.89	9.34	72.65	51.45	4.38	3.71	12.22	40.68	98.06	265.09	1.42	23.92	2.64	73.23	7.87	1.44	129.06	22.31	8.00
IV	42.33	5.42	50.92	63.99	3.93	3.27	3.32	67.68	95.67	315.41	1.21	20.16	2.21	71.75	9.66	1.30	141.51	23.10	6.94

DF - Days to 50% flowering
PB - Number of primary branches per plant
HT - Plant height (cm)
PP - Number of pods per plant
SP - Number of seeds per pod
SW - 100 seed weight (g)
HY Haulm yield per plant (g)
HI - Harvest Index (%)
DM - Days to maturity
SLA - Specific leaf area
LAI - Leaf area index
RL - Root length (cm)
RDW - Root dry weight (g)
RWC Relative water content
PRO - Proline content (µmol g^{-1})
TC - Total chlorophyll content (mg g^{-1})
PHE - Total phenol content in seed (mg g^{-1})
CP - Crude protein (%)
SY - Seed yield per plant (g)

Table 14. The relative contribution of each character to divergence

Sl. No	Source	Times Ranked 1st	Contribution (%)
1.	Days to 50% flowering	199	45.75 %
2.	Number of primary branches per plant	1	0.23 %
3.	Plant height (cm)	3	0.69 %
4.	Number of pods per plant	4	0.92 %
5.	Number of seeds per pod	0	0.00 %
6.	Hundred seed weight (g)	2	0.46 %
7.	Haulm yield per plant (g)	23	5.29 %
8.	Harvest index (%)	11	2.53 %
9.	Days to maturity	7	1.61 %
10.	Specific leaf area	2	0.46 %
11.	Leaf area index	9	2.07 %
12.	Root length (cm)	0	0.00 %
13.	Root dry weight (g)	5	1.15 %
14.	Relative water content (%)	0	0.00 %
15.	Proline content (μmol g^{-1})	46	10.57 %
16.	Total chlorophyll content (mg g^{-1})	66	15.17 %
17.	Total phenol content in seed (mg g^{-1})	10	2.30 %
18.	Crude Protein content (%)	13	2.99 %
19.	Seed yield per plant (g)	34	7.82 %

Discussion

5. DISCUSSION

Horse gram is a neglected sturdy crop. A limited scientific intervention has been made to understand the genetics of this legume. With coming to the age of declined water availability, switching to an unexplored crop like horse gram may be more rewarding than engineering the existing crops to withstand drought. The extent of tolerance exhibited by genotypes varies within a species, even to the same level of moisture stress. Recognition of the best water stress tolerant genotype from a broadly stress tolerant crop can aid in a crop improvement program.

To bring out a high heterotic effect in hybridisation, it is essential to discover and include genetically diverse parents in crossing programmes. This also helps in the development of high yielding moisture stress tolerant lines of the crop.

Considering the above facts, the present study was conducted in thirty horse gram genotypes to screen for the yield, yield components and moisture stress tolerance parameters. The performance of the genotypes to moisture stress was evaluated at both the seedling stage and reproductive stage of the crop. The results of the present investigation conducted are discussed below.

5.1. EFFECT ON PEG INDUCED MOISTURE STRESS ON MORPHO - PHYSIOLOGICAL PARAMETERS OF HORSE GRAM GENOTYPES AT SEEDLING STAGE (LABORATORY EXPERIMENT)

Water is very important for plant growth. The seed germination as well as many other metabolic activities are directly influenced by water. Polyethylene glycol (PEG) is a high molecular weight osmoticum popularly used in research to evaluate germplasm tolerance to water stress. PEG doesn’t cause any toxic effect on plants (Datta *et al.,* 2011). Due to the high viscosity of polyethylene glycol, oxygen accessibility to the root is limited and it suppresses the transportation of water through the root. By taking out water from the cell without entering the apoplast, PEG mimics the dry soil. With an increase in PEG concentration the water potential decreases.

5.1.1. Germination percentage

Germination is considered as a vital phase in the ontogeny of plants. For a successful seed establishment, seed germination and seedling growth are important. Under low water potential imposed by high PEG concentration, hydrolytic activity of various enzymes like amylase, proteases etc is affected in the seed. As a result, the conversion of starch into energy is lowered and seed germination is reduced (Kumar *et al.,* 2011).

In this study, the reduction in germination percentage under moisture stress condition increased with increased PEG concentrations. Corresponding observations were made by Kaur *et al*. (2017) in green gram and Shobanadevi *et al*. (2021) in black gram. The genotypes IC71841, IC139464, IC22785 and IC145300 exhibited a high germination percentage at stressed condition. The high germination percentage of these genotypes can be attributed to their potentiality for water stress tolerance. Under control conditions germination percentage ranged from 40-100. One of the reasons for this wide variation may be the poor quality of the seed. Percentage reduction of germination was also low in IC71841, IC139464 and IC22785.

5.1.2. Root length (cm) and shoot length (cm)

Root length is one of the parameters signaling drought tolerance. Better the root growth, better will be the drought tolerance of the genotype. In the present study, the root length decreased with an increase in PEG concentration. This was in accordance with findings of Whalley *et al.* (1998) in pea, Singh *et al.* (2013) in lentil and Roy *et al.* (2020) in lentil.

Similarly, a reduction in shoot length was noticed with the increase in PEG concentration. This was in conformity with the results of Hamayun *et al.* (2010) in soybean, Singh *et al.* (2013) in lentil and Kaur *et al.* (2017) in mungbean.

In the present study, all thirty genotypes recorded longer root and shoot length in the control condition compared to moisture stress treatment. Under stressed condition, shoot length of genotypes HG 24 L, HG 31 L, HG 27 L, IC15730, HG 26 L,

IC22827, HG 34 L, IC26132, IC22785, IC26138, IC88926, IC71841, IC283202, IC406382 and IC22759 was more. While the root length was more in IC71841 IC120753, IC277671, IC139464, IC22785, IC145300, HG 26 L, IC15730, IC22827, HG 27 L, HG 31 L, HG 24 L, IC406382 and IC88926 under stressed condition. This indicates better moisture stress tolerance of these genotypes.

In comparison to root length, shoot length was found to be small. The decrease in shoot length compared to root may be due to more allocation of carbohydrates to root under moisture stress condition (Sadr Abadi, 1989). The root develops faster to adapt to water stress condition (Kumar *et al.,* 2011).

5.1.3. Seedling dry weight (g)

Seedling dry weight reduced under moisture stressed condition compared to control in all thirty genotypes which were in confirmatory with the observations of Kaur *et al.* (2017) in mungbean and Meena (2017) in chickpea. The reduction in the dry weight of seedlings may be due to reduced shoot and root length caused by suppression of cell division and differentiation under moisture stress conditions.

In this study, genotypes with higher root and shoot lengths like IC71841, HG 26 L, IC15730, IC88926, IC26132, HG 31 L, IC22785, HG 24 L, IC139464, IC406382, IC406382 and IC22759 recorded a higher seedling dry weight in a stressed condition. A similar observation was made by Kumar *et al.* (2011) in pigeon pea.

5.1.4. Seedling vigour index 1 and seedling vigour index 2

The vigour index is also an important tool to screen drought tolerance. In the current study, the high seedling vigour index 1 and 2 was recorded by IC71841, IC139464 and IC22785. The high vigour index was due to the higher germination percentage and seedling growth exhibited by these genotypes. The difference in vigour index among genotypes can be assigned to varied responses in terms of stress tolerance.

Vigour index was reduced with the increase in PEG concentration. Similar observations were made by Kaur *et al.* (2017) in mungbean, Meena (2017) in chickpea and Shobanadevi *et al.* (2021) in black gram.

5.2. EFFECT ON MOISTURE STRESS ON BIOMETRIC, PHYSIOLOGICAL, BIOCHEMICAL AND SEED QUALITY CHARACTERS OF HORSE GRAM GENOTYPES (FIELD EXPERIMENT)

5.2.1. Days to 50% flowering and Days to maturity

Earliness in days to 50% flowering and days to maturity are important strategies to escape moisture stress condition. In the present study compared to the control plot, in all thirty genotypes a decrease in days to 50% flowering and days to maturity was observed under moisture stress condition. This may be due to the hastening of the life cycle by plants under moisture stress condition.

Among the thirty genotypes evaluated in the study under moisture stressed condition, IC139464, IC139435, IC39353, GDH-1, IC22785, IC277671 and IC283202 recorded fewer days to achieve 50% flowering. The genotypes HG 18 L, IC26138, HG 27 L, IC15730, HG 34 L, HG 26 L, HG 24 L and IC392329 recorded maximum days to achieve maturity. This was in agreement with findings of Sudha Rani (1989) in black gram, Ahirwar (2011) in chickpea and Vanaja *et al.* (2015) in pigeon pea that earliness in flowering and maturity is associated with tolerance to moisture stress condition.

5.2.2. Number of primary branches per plant

The number of primary branches per plant was found to be lower in all genotypes under moisture stress condition than control. This was in conformity with the results of Yasin *et al.* (2014) in horse gram and Mekonnen (2020) in chickpea. The decline in number of primary branches per plant may be due to lesser vegetative growth under water stress.

In the present study, HG 18 L, IC26138, HG 24 L, IC392329, HG 31 L and HG 27 L recorded the higher number of primary branches per plant under moisture stress condition. All these were late maturing genotypes with greater vegetative growth and thus had a greater number of primary branches.

5.2.3. Plant height (cm)

A reduction in plant height was recorded under moisture stress condition compared to control condition in all genotypes. This was in accordance with findings of Ranawake *et al.* (2011) in green gram, Yasin *et al.* (2014) in horse gram and Pandiyan *et al.* (2017) in black gram and green gram. This reduction in plant height may be because of a deeper root growth favoured by shortening of plant height, which helps the plant to absorb more moisture in water stress condition. Genotypes with longer shoot lengths compared to root are found sensitive to moisture stress condition.

In the present study, maximum plant height was recorded by IC26138, HG 27 L, HG 34 L, IC392329, HG 18 L, IC22827, HG 24 L, IC15730 and IC139554. These genotypes exhibited lower root length too. This indicates that IC26138, HG 27 L, HG 34 L, IC392329, HG 18 L, IC22827, HG 24 L, IC15730 and IC139554 are sensitive to water stress condition.

5.2.4. Number of pods per plant, number of seeds per pod and hundred seed weight

The number of pods per plant, number of seeds per pod and hundred seed weight are important yield contributing character. A reduction in these characters were observed in moisture stress condition in all thirty genotypes compared to the control plot. Similar observations were made by Urrea *et al.* (2009) in dry bean, Blair *et al.* (2012) in common bean and Bangar *et al.* (2019) in mung bean. The reduction in number of pods per plant, number of seeds per pod and hundred seed weight may be due to greater abscission of flower and reduced photosynthesis rate under water stress condition.

In the current study, the lower number of pods per plant and number of seeds per pod was recorded by late maturing genotypes IC392329, HG 26 L, HG 31 L, HG 27 L, HG 34 L, HG 24 L, HG 18 L, IC26138 and IC15730. This may be due to the failure of these genotypes to shift the photosynthetic assimilates from vegetative stage to reproductive stage and also due to greater flower drops under stressed condition. Higher hundred seed weight was recorded by IC139453, IC221105, GDH-1, IC22785, IC145300, IC22759, IC26132 and IC22827. This suggests the potential of these genotypes to contribute to a higher yield under stressed condition. The variation observed in seed colour of horse gram genotypes was due to the influence of differential environments during the ripening process (Nigwekar,1988).

5.2.5. Seed yield per plant (g)

Under moisture stress condition, a reduction in seed yield per plant was recorded in all genotypes, compared to control condition (Fig. 4). This was in accordance with reports of Ranawake *et al.* (2011) in mungbean, Vanaja *et al.* (2015) in red gram and Mekonnen (2020) in chickpea. The reduction in seed yield per plant under moisture stress condition may be due to a reduced rate of photosynthesis and a lesser number of pods per plant.

In the present study, IC22785, IC221105, IC22759, IC139464, GDH-1 and IC406382 recorded a higher seed yield per plant. The higher yield in these genotypes can be attributed to the presence of a better yield contributing characters like number of pods per plant and higher chlorophyll content in them.

5.2.6. Haulm yield per plant (g)

The reduction in haulm yield per plant was recorded in water deficit condition compared to the control plot in all genotypes (Fig. 5). Similar observations were made by Halilou *et al.* (2015) in cowpea and peanut and Bacharou Falke *et al.* (2019) in peanut. The reduction in haulm yield per plant may be due to lower carbohydrate synthesis caused by reduced photosynthesis under moisture stress condition.

In this study, HG 24 L, HG 27 L, HG 18 L, IC22759, HG 34 L, IC221105, IC26132, HG 31 L, IC22785 and IC26138 recorded higher haulm yield per plant. HG 24 L, HG 27 L, HG 18 L, HG 34 L, HG 31 L and IC26138 were late maturing genotypes with lesser yield. So, these genotypes are better suitable for fodder purposes. While IC22759, IC221105 and IC22785 were high-yielding genotypes. This indicates potential of these genotypes to use for both fodder and feed purpose.

Fig. 4. Seed yield per plant (g)

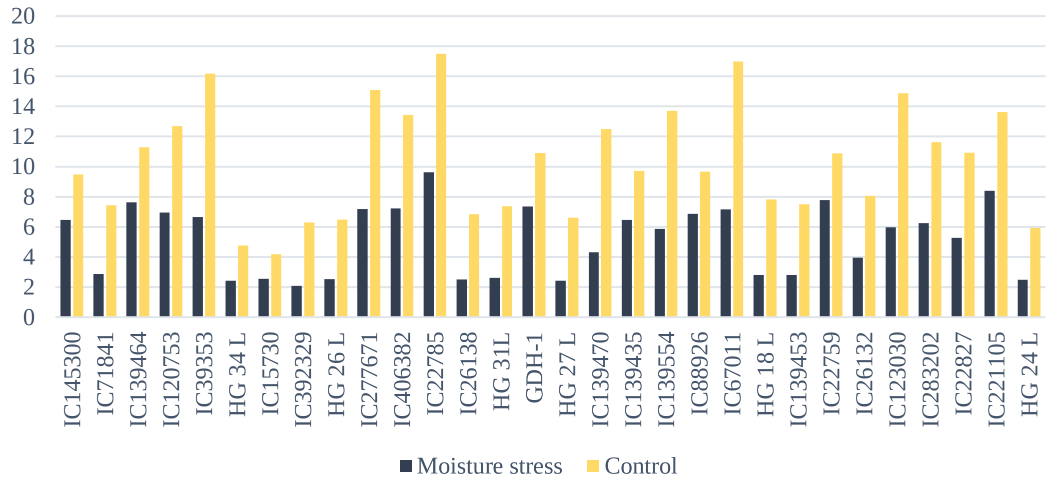
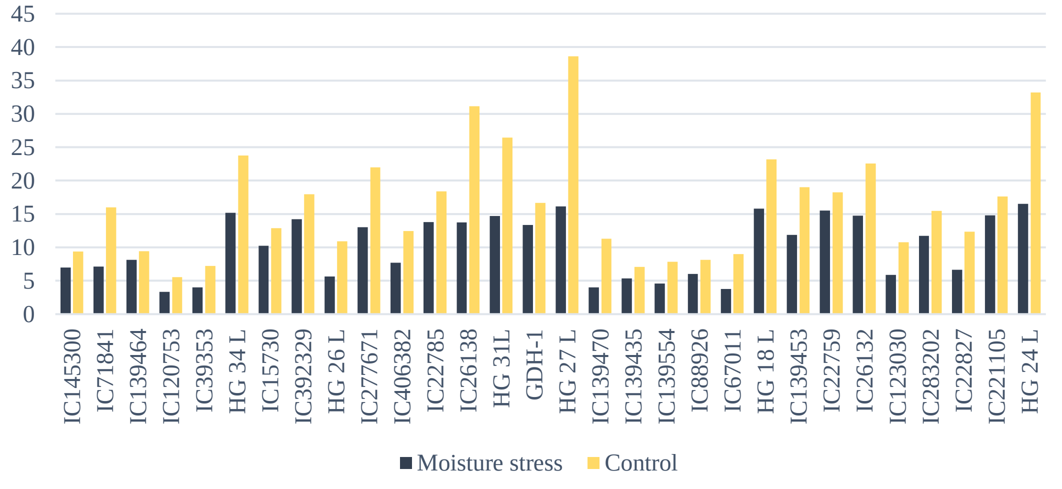


Fig. 5. Haulm yield per plant (g)



5.2.7. Harvest Index (%)

Harvest index was found to be reduced under moisture stress conditions compared to the control condition in all thirty genotypes. This was in accordance with the findings of Sadeghipour (2009) in mung bean and Mekonnen (2020) in chickpea. The decline in harvest index under moisture stress condition may be due to greater senescence of leaves under water deficit condition.

In this study, the genotypes IC120753, IC67011 and IC39353 recorded a higher harvest index. This signals the better photosynthate partitioning to seed in these genotypes.

5.2.8. Leaf area (cm^2) and Leaf area index

The leaf area is an important yield contributing character. Leaf captures light and performs photosynthesis and contributes to yield. A decline in leaf area and leaf area index was observed in water stress condition than the control plot in all genotypes. This was in confirmation with findings of Anbessa and Bejiga (2002) in chickpea and Nagajothi *et al.* (2014) in red gram. The decrease in leaf area may be due to smaller leaf size and accelerated leaf senescence under moisture stress condition.

In the present study, higher leaf area and leaf area index was recorded by IC22785, IC221105, IC67011, IC139464 and IC283202. The larger leaf area in these genotypes gave them a higher source size leading to better photosynthesis and seed yield (sink).

5.2.9. Leaf fresh weight (g), Turgid weight of leaf (g) and Leaf dry weight (g)

Leaf fresh weight, turgid weight and dry weight are parameters used for calculating the relative water content in plants. A reduction in leaf fresh weight and dry weight was recorded in all thirty genotypes than in the control condition. Similar observations were made by Abhari and Gholinezhad (2019) in chickpea and Uddin *et al.* (2021) in green gram. This reduction in leaf fresh weight and dry weight may be due to dehydration experienced by plants under water stress condition.

The turgid weight of the leaf increases with the level of water entering inside the leaf when immersed in water. If the difference between the turgid weight and fresh weight of leaf is more, it indicates the level of water inside the leaf at the field is less. In the present study, compared to the water stress condition, sixteen genotypes recorded lower turgid weight of leaf in the control condition. However, the difference between the turgid weight and fresh weight of leaf was less in all genotypes in the control condition than water stress condition, indicating more water was present in control plant leaves in the field.

In the present study, HG 34 L, IC139470, IC26138, IC139435, GDH-1, IC67011, IC88926, HG 18 L, IC120753, HG 26 L, IC123030, IC139554, IC139464, IC22759, IC22827, IC26132, IC406382, HG 27 L and IC277671 recorded a higher leaf fresh weight. While IC221105, IC71841, IC283202, IC22785, IC15730, HG 24 L, IC139464 and IC22759 recorded a lower turgid weight of leaf. The maximum dry weight of leaf was recorded in IC139435.

The genotypic variation observed in fresh weight, turgid weight and dry weight of leaf indicates their differed ability to maintain tissue water potential and turgor pressure and thus various physiological processes.

5.2.10. Root length (cm) and Root dry weight (g)

The root length and root dry weight are important drought adaptive characters. An increase in root length and root dry weight was observed in all genotypes in moisture stress condition compared to the control plot. Similar observations were made by Ramamoorthy *et al.* (2017) in chickpea, Iseki *et al.* (2018) in genus *Vigna* and Santos *et al.* (2020) in cowpea. In moisture stress conditions, a longer root length helps the plants to absorb moisture from deeper layers of soil. Increased root dry weight may be due to increased diversion of dry matter to roots and accumulation of abscisic acid, thereby improving hydraulic conductivity in plants (Blum, 1996; Maseda and Fernández, 2006).

The genotype IC22785 and IC22759 recorded a higher root length and root dry weight. IC22785 and IC22759 were high yielders also. Thus, genotypes with better root characters were capable of escaping stress condition and producing better yield.

5.2.11. Relative water content (RWC) (%)

RWC is considered a true indicator of drought stress in plants (Kramer, 1969). Compared to the control plot, a decline in water stress was recorded in water deficit condition in all thirty genotypes. This was in confirmatory with the reports of Ghanbari *et al.* (2013) in common bean and Verma *et al.* (2019) in chickpea. The reduction in RWC is due to lesser availability of water and dehydration in plants under water stress condition.

Among thirty genotypes, IC221105, IC22759, IC139464, IC22785, IC120753, IC406382 and IC67011 exhibited a higher RWC in the present study. Maintaining higher water levels by these genotypes suggests their potential for water stress tolerance.

5.2.12. Specific leaf area (SLA) (cm^2 g^{-1})

Specific Leaf Area was low in the water stress condition than the control condition in all genotypes. This was in the agreement with the findings of Berova and Zlatev (2002) in common bean and Sudhakar *et al.* (2006) in black gram and green gram. The reduction in SLA under moisture stress is associated with increased water use efficiency (Wellstein *et al.,* 2017).

In the current study, HG 26 L, IC139470, IC277671 and IC67011 recorded a higher SLA. A lower water use efficiency of these genotypes due to thinner leaves might be the reason for a higher SLA in them.

5.2.13. Drought tolerance indices - Stress tolerance index (STI), Geometric mean productivity (GMP), Mean productivity (MP) and Yield stability index (YSI)

Drought tolerance indices help to select tolerant genotypes under moisture stress condition. The drought-tolerant genotypes have greater values of drought tolerance indices like MP, YSI and STI (Fernandez *et al*., 1992; Gholinezhad *et al*., 2014; Darkwa *et al*., 2016).

In the present study, among the thirty genotypes, IC22785 and IC15730 recorded the highest and lowest STI, GMP and MP respectively. This suggests that IC22785 is a drought-tolerant genotype; while IC15730 is a sensitive one. Higher YSI was noted in IC22759, IC88926, IC145300, IC139464, GDH-1, IC139435, IC221105 and IC15730.

In the present study, STI, GMP and MP appeared to be better indices to screen tolerant genotypes than YSI as the genotype IC15730 which recorded the lowest STI, GMP and MP, registered a higher YSI. Sen *et al.* (2019) in lentils also reported STI, GMP and MP are better indices than YSI to screen tolerant genotypes.

5.2.14. Proline content (µmol g^{-1})

Proline content is a major character contributing to water stress tolerance in plants. An increase in the level of proline content of leaf was recorded in all genotypes compared to the control condition (Fig. 6). This was in agreement with the findings of Mafakheri *et al.* (2010) in chickpea, Baroowa and Gogoi (2015) in black gram and green gram and Luo *et al.* (2019) in lucerne. The increase in the level of proline content may be a mechanism adopted by the plant to lower the cellular osmotic potential and thus combat the moisture stress condition.

In the present study, a high proline content in leaves was recorded in IC120753, IC22785, IC139464, IC22759, IC406382 and IC221105. This indicates their potential for moisture stress tolerance. These genotypes also registered higher seed yield per plant. This signals that varieties with higher proline levels can endure the adverse effects of moisture stress condition and produce a higher yield. A similar observation was made by Vanaja *et al.* (2015) in pigeon pea.

5.2.15. Chlorophyll content (mg g^{-1})

Chlorophyll is the chief pigment associated with light-harvesting and aiding in photosynthesis. A reduction in chlorophyll content was observed in all genotypes under water stress treatment than in the control condition (Fig. 7). Similar observations were made by Mafakheri *et al.* (2010) in chickpea, Pandiyan *et al.* (2017) in green gram and

Fig. 6. Proline content in leaves (µmol g-^{1})

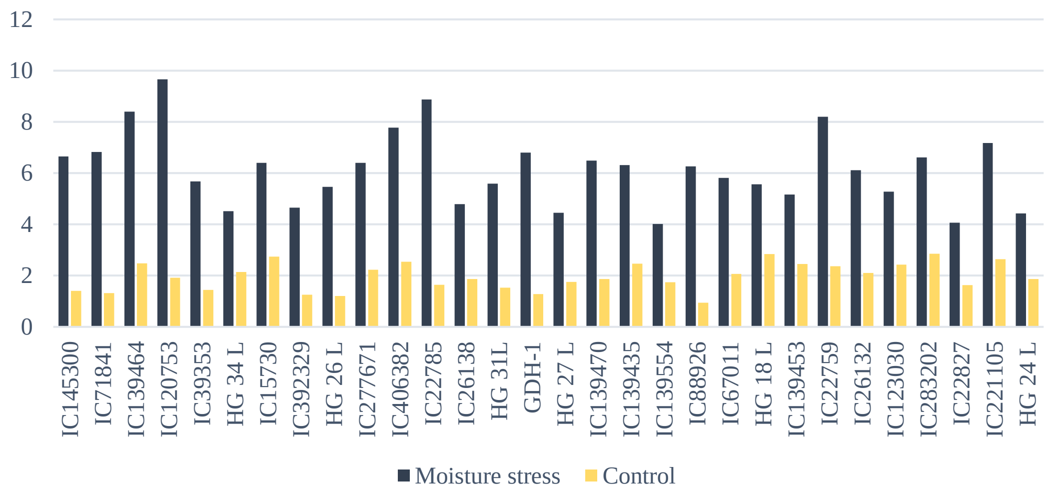


Fig. 7. Total chlorophyll content of leaves (mg g^{-1})

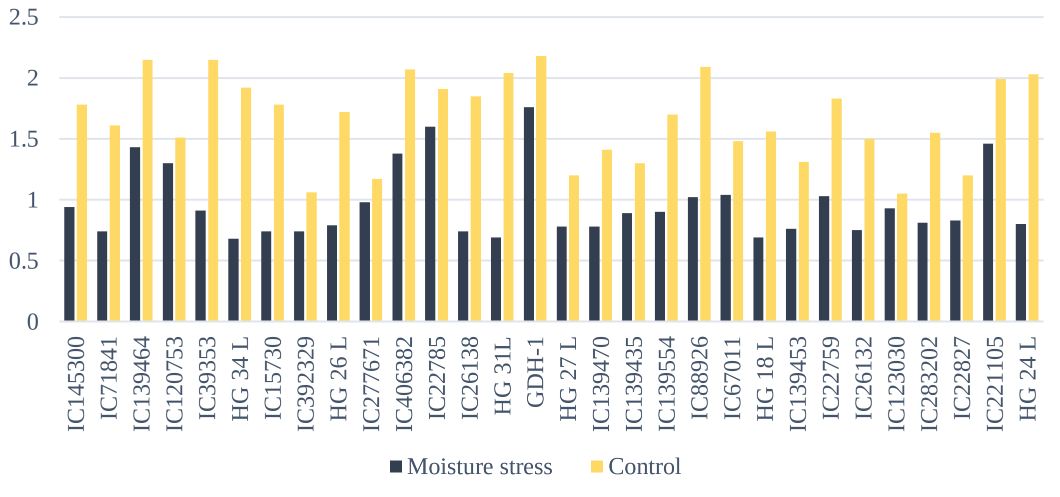


Fig. 8. Crude protein content of seed (%)

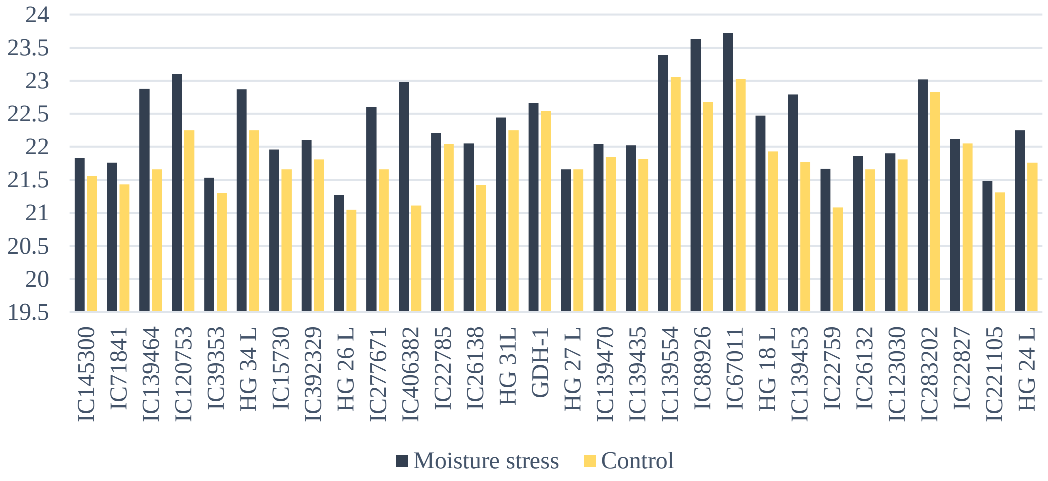
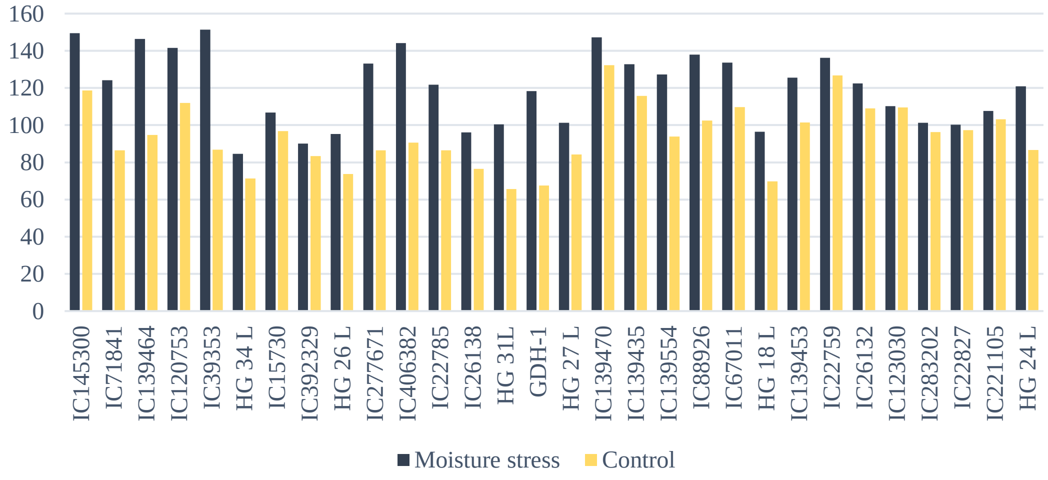


Fig. 9. Total phenol content in seed (mg g^{-1})



black gram and Jincy *et al.* (2020) in green gram. The decline in chlorophyll content under moisture stress may be due to photo-oxidation and degradation of chlorophyll (Anjum *et al.,* 2011).

In the present study, GDH-1, IC22785, IC221105, IC139464 and IC406382 recorded a higher chlorophyll content and they were high-yielding genotypes. A higher chlorophyll content in these genotypes may be indicative of their moisture stress tolerance. This was in agreement with the observation made by Jincy *et al.* (2019) in green gram.

5.2.16. Crude protein content of seed (%)

An increase in crude protein (%) content in seed was recorded in all water deficit genotypes compared to well-watered genotypes (Fig. 8). Similar results were reported by Alghamdi (2009) in Faba bean under moisture stress condition.

In the present study, IC88926 recorded the highest crude protein content in the seed which was on par with IC67011, IC139554, IC120753, IC283202, IC406382, IC139464, HG 34 L, IC139453, GDH-1, IC277671, HG 18 L and HG 31 L. The increased crude protein content in these genotypes reflects their ability to store a higher amount of nitrogen in the seeds under water stress condition. A similar observation was made by Baroowa and Gogoi (2015) in black gram and green gram.

5.2.17. Total phenol content in seed (mg g^{-1})

Total phenol content is an anti-nutritional factor in horse gram seed. Breeding programs focusing on better nutritional quality of seed with fewer anti-nutritional factors will be beneficial to the consumers. The nutritional quality of seeds is highly affected by environmental conditions. In the present study, an increase in total phenol content in seed was observed under water stress condition in all genotypes (Fig. 9). Under water stress conditions, an increase in phenol content in plants is observed (Varela *et al.,* 2016).

In the current study, HG 34 L, IC392329, HG 26 L, IC26138, HG 18 L, IC22827, HG 31 L, HG 27 L, IC283202 and IC15730 recorded the lower phenol content in seed. These genotypes are better suited for consumer consumption as they had lower phenol content even under moisture stressed condition. But, the promising genotypes of this study had recorded a higher total phenol content. Since phenol content in seed is an anti nutritional factor, its level has to be reduced in theses genotypes.

5.3 STATISTICAL ANALYSIS

5.3.1 Variability studies

The existence of sufficient genetic variability enables the breeders to create new gene combinations through hybridisation.

The analysis of variance for all morpho-physiological characters studied viz. germination percentage, root length, shoot length, seedling dry weight, vigour index 1 and vigour index 2, in laboratory experiment revealed significant differences with respect to genotypes and PEG concentrations. The interaction of genotypes and PEG concentrations differed significantly for shoot length, seedling dry weight, vigour index 1 and vigour index 2. This points to the existence of variability among genotypes and they responded to stressed condition differentially. Similar observations were made by Meena (2017) in chickpea, Jincy *et al.* (2019) in green gram and Shobanadevi *et al.* (2021) in black gram.

The analysis of variance in field experiment also showed significant difference among the genotypes for biometric characters viz. days to 50% flowering, number of primary branches per plant, plant height, number of pods per plant, number of seeds per pod, hundred seed weight, days to maturity, haulm yield per plant, harvest index, seed yield per plant, leaf area, turgid weight of leaf during stress, leaf fresh weight during stress, leaf dry weight during stress, root length and root dry weight. Similar results were observed by Poornima (2015), Priyanka *et al.* (2019) and Sivan (2019) for days to 50% flowering, number of primary branches per plant, plant height, number of pods per plant, number of seeds per pod, hundred seed weight, days to maturity, harvest index and seed yield per plant in horse gram.

Genotypes also differed significantly for physiological parameters viz. RWC, LAI, SLA, stress tolerance index, geometric mean productivity, mean productivity and yield stability index. This was in accordance with reports of Sudhakar *et al.* (2006) in black gram and green gram for SLA; Bastos *et al.* (2011) in cowpea for LAI, Ghanbari *et al.* (2013) in common bean for RWC and LAI; Yücel and Mart (2014) in chickpea, Sánchez-Reinoso *et al.* (2020) in common bean for stress tolerance index, geometric mean productivity, mean productivity and yield stability index.

Significant variation was noticed in biochemical parameters like proline content and chlorophyll content. This was in conformity with results of Mafakheri *et al.* (2010) in chickpea for proline and chlorophyll content; Bastos *et al.* (2011) in cowpea, Rambabu *et al.* (2016) in green gram for chlorophyll content; Baroowa and Gogoi (2016) in black gram for proline and Jincy *et al.* (2020) in green gram for proline and chlorophyll content.

Seed quality characters viz. crude protein content and total phenol content were also observed significantly varied. Similar observations were made by Goswami (2017) for total phenol content in horse gram; Alghamdi (2009) in faba bean, Liu *et al.* (2018) in alfalfa and Sivan (2019) in horse gram for crude protein content.

5.3.2 Genetic parameters

The genetic parameters like the genotypic and phenotypic coefficient of variation, heritability and genetic advance are commonly used for expressing the magnitude of variability present in the genotypes.

In the current investigation, PCV was higher than GCV for all selected characters (Fig. 10). A similar trend was reported by Joshi *et al.* (2007), Alle *et al.* (2016), Vijayakumar *et al.* (2016) and Sivan (2019) in horse gram. The small difference between PCV and GCV for all traits point to low environmental influence and hence, there is scope for improvement of these characters.

The PCV and GCV were highest for number of pods per plant. High GCV and PCV were registered for days to 50% flowering, number of primary branches per plant, haulm yield per plant, harvest index, leaf area index, root dry weight, proline content, total chlorophyll content and seed yield per plant. Similar findings were made by Poornima (2015) for haulm yield per plant; Alle *et al.* (2016) for seed yield per plant; Shivaji (2011), Priyanka *et al.* (2019) for number of pods per plant, number of primary branches per plant and seed yield per plant; Sivan (2019) for number of pods per plant, number of primary branches per plant, harvest index and seed yield per plant.

Moderate PCV and GCV were recorded in days to maturity and total phenol content in seed which was in accordance with results of Rishishwar (2002) for days to maturity.

Low PCV and GCV were shown by hundred seed weight, crude protein content and relative water content of leaves. This was consistent with reports of Swapna (1993), Poornima (2015) for hundred seed weight; Joshi *et al.* (2007), Shivaji (2011) and Sivan (2019) for hundred seed weight and crude protein content.

Heritability and genetic advance are two important selection indices. Heritability in broad sense is the ratio of genotypic variance to total variance. The chance for the transmission of a trait from parents to offspring is great with higher heritability. The information about the superiority of the selected individuals over the parental population can be inferred from genetic advance. Prediction about genetic gain under selection can be effectively realised using heritability along with genetic advance.

High heritability along with high GAM was observed in days to 50% flowering, number of primary branches per plant, plant height, number of pods per plant, haulm yield per plant, harvest index, days to maturity, leaf area index, total phenol content of the seed, root dry weight, proline content, total chlorophyll content and seed yield per plant (Fig. 11). The result was in consonance with the findings of Rishishwar (2002) for days to 50% flowering, days to maturity, number of pods per plant; Joshi *et al.* (2007) for plant height, number of primary branches per plant, number of pods per plant, harvest index and seed yield per plant; Poornima (2015) for days to 50% flowering and haulm yield per plant; Priyanka *et al.* (2019) for plant height, number of primary branches per plant, number of pods per plant and seed yield per plant; Sivan (2019) for days to 50% flowering, plant height, number of pods per plant and seed yield per plant; Neelima *et al.* (2021) for plant height, number of primary branches per plant and seed

Fig. 10. PCV and GCV of selected characters

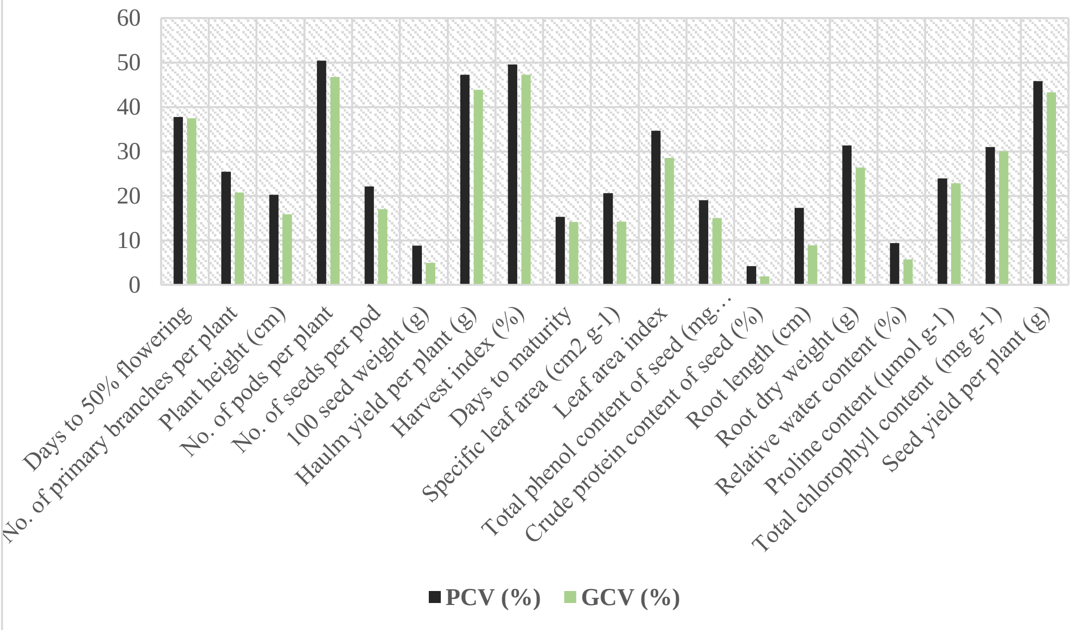
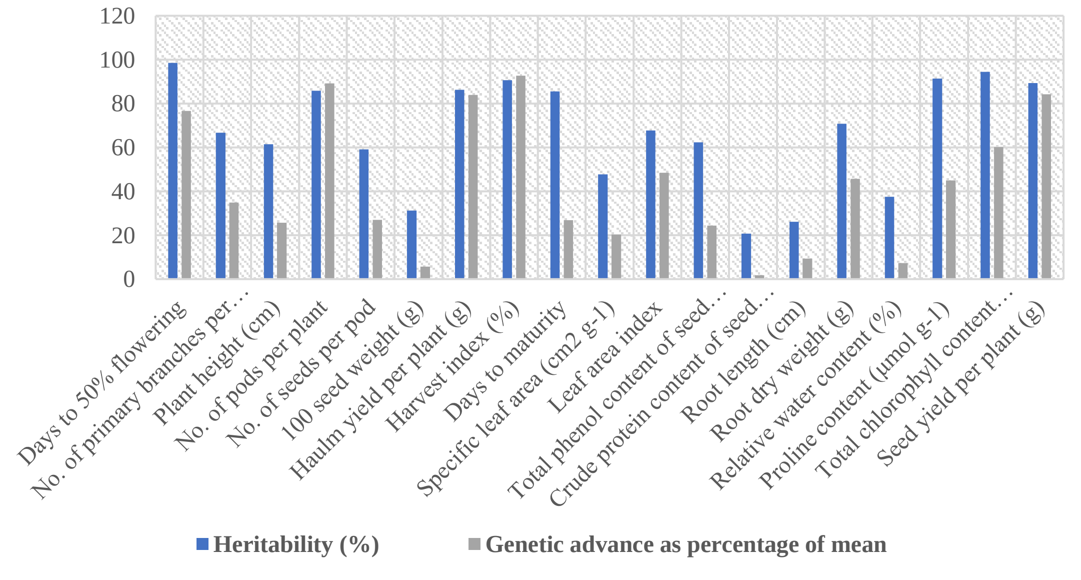


Fig. 11. Heritability and GAM of selected characters



yield per plant in horse gram. Characters with high heritability coupled with high genetic advance are governed by additive gene action and hence, selection based on the above said traits will aid in the improvement of horse gram.

5.3.3 Correlation studies

The primary objective of a plant breeder is the genetic improvement of crop yield. The seed yield is a dependent variable that is influenced by many yield contributing characters and environmental conditions. The extent and direction of the association of various characters with yield can be well understood using correlation analysis.

In the present study, genotypic correlation coefficient of different characters with yield was higher generally than phenotypic correlation coefficient. This reveals that there was a strong association between the selected characters and they were less influenced by the environmental condition. The coupling and repulsion phase of linkage between two genes are responsible for positive and negative genotypic correlation (Salini *et al.,* 2010).

In the present investigation, correlation analysis showed a significant positive association of number of pods per plant, number of seeds per pod, total chlorophyll content, harvest index, proline content, root dry weight, root length, RWC, LAI and hundred seed weight with seed yield. While, days to 50% flowering, days to maturity, plant height and number of primary branches exhibited a significant negative correlation with yield.

Likewise, under water stress condition significant positive correlation of yield was reported with number of pods per plant, number of seeds per pod, hundred seed weight and proline content by Vanaja *et al.* (2015) in red gram, RWC by Ahirwar (2011) in chickpea, Baroowa and Gogoi (2016) in black gram, number of pods per plant, number of seeds per pod, leaf area and chlorophyll content by Bordoloi *et al.* (2018) in black gram. A significant negative correlation of seed yield with days to maturity was reported by Kanouni *et al.* (2012) in chickpea, days to 50% flowering by Eswaran and Senthilkumar (2015) in green gram and Bordoloi *et al.* (2018) in black gram.

The significant positive association of traits like number of pods per plant, number of seeds per pod, total chlorophyll content, harvest index, LAI and hundred seed weight with seed yield shows that the higher the values of these characters, the higher will be the yield under water stress condition. Thus, improvement in these characters will result in higher seed yields. While, a significant negative correlation of days to 50% flowering, days to maturity, plant height and number of primary branches with yield indicates that the lower the values of these characters, the higher will be the yield under moisture stress condition.

The parameters like RWC, proline content, root dry weight and root length were significantly, positively correlated with seed yield. Hence, these traits can be used to select moisture stress tolerant genotypes in horse gram. In the present investigation, genotype IC22785 which was on par with IC221105 and IC139464, followed by IC22759 had a high yield along with high moisture stress tolerance characters.

5.3.4 Path coefficient analysis

Path analysis splits the genotypic correlation coefficient between independent characters and seed yield into direct and indirect effects. Thus, it provides a clear picture of the relative contribution of these traits on yield as well as their cause-and-effect association. Selection for a specific character will be rewarding if the association between that character and seed yield is due to its direct effect. At the same time, if the correlation is due to the indirect effect of a character through another independent trait, then indirect selection through independent trait will aid in yield improvement. If the correlation is positive but the direct effect is negative or negligible, then indirect component traits are to be regarded simultaneously for selection. However, if the correlation is negative but the direct effect is positive and high, a restricted simultaneous selection is to be adopted (Singh and Kakar, 1977).

In the present investigation, a high direct effect on seed yield was exhibited by number of pods per plant. The number of pods per plant had a significant positive correlation with yield. Hence direct selection of number of pods per plant will improve the yield in the horse gram. This was in agreement with the results of Priyanka (2019) and Sivan (2019) in horse gram.

The plant height recorded a moderate direct effect on seed yield. A similar observation was made by Shivaji (2011) in horse gram. Harvest index, number of primary branches, total chlorophyll content, LAI, number of seeds per pod and root length registered low positive direct effect. Paliwal *et al.* (2005) and Sivan (2019) also reported number of primary branches had a positive direct effect on seed yield. The proline content showed a positive but negligible direct effect on seed yield. A negative but negligible direct effect on yield was recorded by characters like days to 50% flowering, root dry weight and RWC.

A low residual effect (0.0065) was recorded in the study, which reveals that chosen traits are ideal for screening in moisture stress tolerance.

5.3.5 Genetic divergence

The study of genetic diversity among genotypes helps us to develop superior progeny by crossing diverse genotypes and exploiting heterosis. D^2 statistics aids in identifying divergent parents for hybridisation programs. The inter-cluster distance between the cluster groups is greater when genetic diversity between genotypes included in the clusters is high. The findings of Geetha *et al.* (2011), Varma *et al.* (2013) and Sivan (2019) suggest the existence of sufficient genetic diversity among horse gram genotypes.

In the present study, thirty genotypes were grouped into four different clusters. The highest genetic diversity will be produced by crossing genotypes of cluster I and cluster III as the inter-cluster distance was maximum between them. The highest intra cluster distance was recorded in cluster II, signaling those genotypes included in cluster II also considerably differ from each other. Genotype with the highest mean performance can be selected within a cluster for improving the trait of interest.

Considering the cluster means mentioned in table 13, the diverse cluster which can provide suitable parents for improving characters under moisture stress conditions are listed below:

Table 15. Suitable cluster source for different characters

Sl. No.	Characters	Source
1.	Days to 50% flowering (early)	Cluster III
2.	Number of primary branches per plant (highest)	Cluster I
3.	Plant height (shortest)	Cluster IV
4.	Number of pods per plant (highest)	Cluster IV
5.	Number of seeds per pod (highest)	Cluster III
6.	Hundred seed weight (highest)	Cluster III
7.	Haulm yield per plant (maximum)	Cluster I
8.	Harvest index (highest)	Cluster IV
9.	Days to maturity (early)	Cluster II
10.	Specific leaf area (lowest)	Cluster II
11.	Leaf area index (largest)	Cluster III
12.	Root length (longest)	Cluster III
13.	Root dry weight (highest)	Cluster III
14.	Relative water content (highest)	Cluster III
15.	Proline content (highest)	Cluster IV
16.	Total chlorophyll content (maximum)	Cluster III
17.	Total phenol content in seed (minimum)	Cluster I
18.	Crude Protein content (maximum)	Cluster IV
19.	Seed yield per plant (maximum)	Cluster III

From the study, it was inferred that among the characters, days to 50% flowering contributed the highest to genetic divergence (45.75%), followed by total chlorophyll content (15.17%), proline content (10.57%), seed yield per plant (7.82%), haulm yield per plant (5.29%), crude protein content of seed (2.99%), total phenol content in seeds (2.30%), harvest index (2.53%), LAI (2.07%), days to maturity (1.61%) and root dry weight (1.15%). While characters like number of pods per plant (0.92%), plant height (0.69%), hundred seed weight (0.46%), specific leaf area (0.46%) and number of primary branches per plant (0.23%) made a low contribution to genetic divergence. Sahoo *et al.* (2014) also reported that days to 50% flowering made a major contribution towards genetic divergence in horse gram.

Summary

6. SUMMARY

The present investigation on genetic diversity analysis of horse gram [*Macrotyloma uniflorum* (Lam.) Verdc.] for moisture stress tolerance in south central laterites of Kerala was conducted at Farming Systems Research Station, Sadanandapuram, Kottarakkara during 2019-21 with an objective to identify superior genotypes of horse gram with moisture stress tolerance having high yield and quality, suitable for south central laterites of Kerala.

The study was conducted as two experiments viz. laboratory and field experiments using thirty horse gram genotypes collected from RARS Pattambi under KAU and other SAUs. In the first experiment, thirty genotypes were evaluated at seedling stage in the laboratory using two different concentrations of PEG 6000 (10% and 20%), in a factorial completely randomized design, replicated thrice. In the field experiment, genotypes were further evaluated for water stress tolerance in randomized block design by withholding irrigation for 15 days at reproductive stage viz.flowering and podding. The soil moisture was also measured during water stress-imposed period at weekly interval by gravimetric method. The seeds were sown on raised beds of 2.25 m^2 size at a spacing of 30 cm x 30 cm and cultural operations were adopted as per the "Package of Practices Recommendations Crops 2016" of Kerala Agricultural University.

In the laboratory experiment, the genotypes were evaluated for six different morpho-physiological characters at 10 days after sowing and based on germination percentage, root length and vigour index IC71841, IC139464 and IC22785 were recognised as moisture stress tolerant genotypes. In the field experiment, genotypes were evaluated for different biometric, physiological, biochemical and seed quality characters. Genotypes recorded significant difference for all the characters under study.

In the analysis of different genetic parameters, characters like days to 50% flowering, number of primary branches per plant, number of pods per plant, haulm yield per plant, harvest index, leaf area index, root dry weight, proline content, total chlorophyll content and seed yield per plant recorded high PCV and GCV. Plant height, number of seeds per pod and specific leaf area recorded high PCV but moderate GCV. Moderate PCV and GCV were recorded in days to maturity and total phenol content in seed. Root length exhibited moderate PCV and low GCV. High heritability was recorded in days to 50% flowering, number of primary branches per plant, plant height, number of pods per plant, haulm yield per plant, harvest index, days to maturity, leaf area index, total phenol content of the seed, root dry weight, proline content, total chlorophyll content and seed yield per plant. While, crude protein content of seed and root length exhibited low heritability. The highest GCV, PCV and GAM was recorded by number of pods per plant. Days to 50% flowering exhibited the highest heritability. While the lowest GCV, PCV, heritability and GAM was recorded by crude protein content of seed.

A significant positive association of the characters viz. RWC, number of pods per plant, number of seeds per pod, total chlorophyll content, harvest index, proline content, root dry weight, root length, LAI and hundred seed weight was noted with seed yield in correlation studies. However, days to 50% flowering, days to maturity, plant height and number of primary branches showed a significant negative correlation with yield. The SLA registered a negative but non-significant correlation with seed yield. In the path coefficient analysis, number of pods per plant exhibited the highest direct effect on seed yield. While, number of seeds per pod recorded exhibited the highest indirect effect on seed yield via number of pods per plant.

In genetic divergence studies using D^2 analysis, the thirty genotypes were grouped into four cluster following Tocher's method. Cluster II with fourteen genotypes was the largest cluster followed by cluster I (nine genotypes) and cluster III (six genotypes). The cluster IV was solitary. The highest intra cluster distance was recorded in cluster II, while lowest intra cluster distance was recorded in cluster IV. The highest inter-cluster distance was noticed between cluster I and cluster III while the minimum inter-cluster distance was noticed between cluster III and cluster IV. Among the selected characters, days to 50% flowering gave highest contribution towards the genetic divergence.

In field experiment, genotypes IC22785, IC221105, IC139464 and IC22759 recorded high values for moisture stress tolerant characters viz. RWC, proline content, root length and root dry weight as well as these genotypes were identified as superior yielding ones. Thus, from both the experiments IC22785 and IC139464 were recognised as the best source of moisture stress tolerance. The superior genotypes identified can be recommended for cultivation in south central laterites of Kerala and in addition, they can be used as donor parents in future breeding programmes for varietal development by Kerala Agricultural University.

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GENETIC DIVERSITY ANALYSIS OF HORSE GRAM [*Macrotyloma uniflorum* (Lam.) Verdc.] FOR MOISTURE STRESS TOLERANCE IN SOUTH CENTRAL LATERITES OF KERALA

by

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(2019-11-111)

Abstract of the thesis
Submitted in partial fulfilment of the
requirement for the degree of

MASTER OF SCIENCE IN AGRICULTURE

Faculty of Agriculture
Kerala Agricultural University

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2021

ABSTRACT

The study entitled "Genetic diversity analysis of horse gram [*Macrotyloma uniflorum* (Lam.) Verdc.] for moisture stress tolerance in south central laterites of Kerala" was carried out at Farming Systems Research station, Sadanandapuram during October, 2020 – March, 2021 with the objective to identify superior genotypes of horse gram with moisture stress tolerance having high yield and quality, suitable for south central laterites of Kerala.

The 30 horse gram genotypes collected from RARS Pattambi under KAU and other SAUs were evaluated for moisture stress tolerance at seedling stage in laboratory using two different concentrations of PEG 6000 (10% and 20%), in factorial completely randomized design replicated thrice. These 30 genotypes were further evaluated for water stress tolerance in field by withholding irrigation for 15 days at reproductive stage, in randomized block design replicated thrice. The seeds were sown on raised beds of 2.25 m^2 size at a spacing of 30 cm x 30 cm and cultural operations were adopted as per the "Package of Practices Recommendations Crops 2016" of Kerala Agricultural University. The soil moisture was also measured during water stress-imposed period at weekly interval by following gravimetric method.

In laboratory experiment, genotypes were evaluated for six different morpho-physiological characters and in field experiment, genotypes were evaluated for 31 characters which included biometric, physiological, biochemical and seed quality characters. The genotypes showed significant differences for all the characters studied. Genetic parameter analysis was performed for nineteen characters and for all the characters PCV values were higher than GCV values indicating the influence of environment. High heritability coupled with high GAM was observed in days to 50% flowering, number of primary branches per plant, plant height, number of pods per plant, haulm yield per plant, harvest index, days to maturity, leaf area index, total phenol content of the seed, root dry weight, proline content, total chlorophyll content and seed yield per plant.

The correlation studies revealed significant positive correlation of the characters RWC, number of pods per plant, number of seeds per pod, total chlorophyll content, harvest index, proline content, root dry weight, root length, LAI and hundred seed weight with seed yield. However, days to 50% flowering, days to maturity, plant height and number of primary branches showed a significant negative correlation with yield. Path analysis of the thirteen characters showing significant correlation with seed yield revealed high positive direct effect of the number of pods per plant on seed yield. High indirect effect on yield was observed for number of seeds per pod through number of pods per plant.

Genetic divergence analysis using Mahanalobis D^2 statistic following Tocher's method grouped the 30 genotypes into four clusters. Cluster II with 14 genotypes was the largest followed by cluster I (9 genotypes), cluster III (6 genotypes) and clusters IV was solitary cluster. Highest intra cluster distance was recorded among the genotypes of cluster II and lowest in cluster IV whereas highest inter cluster distance was observed between the genotypes of the clusters I and III, while lowest inter cluster distance was between the genotypes of the clusters III and IV.

The present study revealed that the genotypes IC71841, IC139464 and IC22785 as water stress tolerant ones in laboratory experiment and in field experiment, genotypes IC22785, IC221105, IC22759 and IC139464 were identified as high yielding and moisture stress tolerant ones. The superior genotypes identified in the study can be recommended for cultivation and future breeding programs.

സംഗ്രഹം

“കേരളത്തിലെ ദക്ഷിണ - മദ്ധ്യ വെട്ടുകൽ പ്രദേശത്തിന് അനുയോജ്യമായ വരൾച്ചയെ പ്രതിരോധിക്കാൻ കഴിവുള്ള മുതിരയിനങ്ങൾക്കായുള്ള ജനിതക വൈവിധ്യപഠനം” എന്ന ഗവേഷണ പദ്ധതി സദാനന്ദനപുരം കൃഷി സമ്പ്രദായ ഗവേഷണ കേന്ദ്രത്തിൽ 2020-21 കാലയളവിൽ നടത്തുകയുണ്ടായി. ഉയർന്ന വിളവ്, ഗുണനിലവാരം, വരൾച്ചയെ ചെറുക്കുവാനുള്ള കഴിവ് എന്നീ ഗുണങ്ങളുള്ള മുതിരയുടെ ജനിതകയിനങ്ങൾ കണ്ടെത്തുകയെന്നതായിരുന്നു പഠനലക്ഷ്യം.

കേരള കാർഷിക സർവ്വകലാശാലയ്ക്ക് കീഴിലുള്ള പട്ടാമ്പി പ്രാദേശിക ഗവേഷണ കേന്ദ്രത്തിൽ നിന്നും, മറ്റു സംസ്ഥാന കാർഷിക സർവ്വകലാശാലകളിൽ നിന്നും ശേഖരിച്ച 30 ജനിതകയിനങ്ങളാണ് പഠനത്തിനായി ഉപയോഗിച്ചത്. പരീക്ഷണശാലയിലും കൃഷി സ്ഥലത്തിലുമായി രണ്ട് ഘട്ടങ്ങളിലായാണ് പഠനം നടത്തിയത്. പരീക്ഷണശാലയിൽ നടത്തിയ പഠനത്തിൽ കൃത്രിമമായി വരൾച്ച നല്കുന്നതിനായി പോളി എത്തിലീൻ ഗ്ലൈക്കോൾ - 6000 എന്ന രാസവസ്തു 10%, 20% എന്നീ രണ്ട് വ്യത്യസ്ത ഗാഢതയിൽ ഉപയോഗിച്ചു. രണ്ടാം ഘട്ട പരീക്ഷണം ഗവേഷണ കേന്ദ്രത്തിന്റെ ഫാമിലാണ് നടത്തിയത്. 2.25 ചതുരശ്രമീറ്റർ വിസ്തീർണമുള്ള തടങ്ങളിൽ 30 × 30 സെ. മീ. അകലത്തിൽ വിത്തുകൾ പാകി, വളർച്ചയുടെ പ്രത്യുല്പാദനഘട്ടത്തിൽ ജലസേചനം 15 ദിവസത്തേക്ക് നിർത്തിവച്ചു, കൃത്രിമമായി വരൾച്ച സൃഷ്ടിച്ചു. കേരള കാർഷിക സർവ്വകലാശാല ശുപാർശ ചെയ്ത വിള പരിപാലന മുറകൾ അനുസരിച്ചാണ് കൃഷി ചെയ്തത്.

പരീക്ഷണശാലയിൽ മുളപ്പു മുതൽ 10 ദിവസം പ്രായമാകുന്നതുവരെയുള്ള സമയത്ത് തൈകളുടെ ആറ് വ്യത്യസ്ത ഗുണ സ്വഭാവങ്ങളും, കൃഷിയിടങ്ങളിൽ 31 സ്വഭാവഗുണങ്ങളും വിലയിരുത്തി. വിവിധയിനങ്ങൾ തമ്മിൽ പ്രത്യക്ഷമായ വ്യത്യാസങ്ങൾ രേഖപ്പെടുത്തി. പ്രധാനപ്പെട്ട പത്തൊമ്പത് ജനിതക സ്വഭാവങ്ങൾ വിശകലനം ചെയ്തപ്പോൾ ഉയർന്ന പരിസ്ഥിതി സ്വാധീനവും പൈതൃകക്ഷമതയും കണ്ടെത്തി. 50% ചെടികൾ പൂവിടാനെടുക്കുന്ന സമയം, പ്രാഥമിക ശാഖകളുടെ എണ്ണം, ചെടിയുടെ ഉയരം, കായ്കളുടെ എണ്ണം, വൈക്കോലിന്റെ അളവ്, വിളവെടുപ്പ് സൂചിക, വിള ദൈർഘ്യം, ഇലയുടെ വിസ്തീർണ്ണ സൂചിക, വിത്തിലെ ഫീനോളിന്റെ അളവ്, വേര് ഉണക്കിയ ശേഷമുള്ള ഭാരം, പ്രോലീനിന്റെ അളവ്, ഹരിതകത്തിന്റെ അളവ്, വിളവ് തുടങ്ങിയവയും ഉയർന്ന പൈതൃകക്ഷമതയും ജനിതക മുന്നേറ്റവും രേഖപ്പെടുത്തി.

വിവിധ സ്വഭാവങ്ങളുടെ പരസ്പര ബന്ധം വിശകലനം ചെയ്തപ്പോൾ ആപേക്ഷിക ജലത്തിന്റെ തോത്, കായ്കളുടെ എണ്ണം, കായിലെ വിത്തുകളുടെ എണ്ണം, വിളവെടുപ്പ് സൂചിക, ഹരിതകത്തിന്റെ അളവ്, പ്രോലീനിന്റെ അളവ്, ഉണക്കിയ ശേഷമുള്ള വേരിന്റെ ഭാരം, വേരിന്റെ നീളം, നൂറു വിത്തിന്റെ ഭാരം, ഇലയുടെ വിസ്തീർണ്ണ സൂചിക എന്നിവ കൂടുന്നതിനനുസരിച്ച് വിളവും കൂടുന്നതായി കണ്ടെത്തി. ഈ പ്രതീകങ്ങൾ വിളവിനെ എങ്ങനെയാണ് ബാധിക്കുന്നതെന്ന് വിശകലനം ചെയ്തപ്പോൾ കായ്കളുടെ എണ്ണം വിളവിനെ നേരിട്ട് സ്വാധീനിക്കുന്നതായി മനസ്സിലാക്കാൻ സാധിച്ചു.

ജനിതക അകലം കണ്ടെത്തി വിവിധയിനങ്ങളെ ക്ലസ്റ്ററാക്കി മാറ്റുന്ന രീതി അവലംബിക്കുകയുണ്ടായി. ടോർച്ചർ രീതി ഉപയോഗിച്ചുള്ള ക്ലസ്റ്റർ വിശകലനത്തിലൂടെ 30 മുതിരപ്പയറിനങ്ങളെ നാല് ക്ലസ്റ്ററുകളാക്കി തരം തിരിച്ചു. 14 ജനിതകയിനങ്ങൾ അടങ്ങിയ ക്ലസ്റ്റർ II ഏറ്റവും വലിയ ക്ലസ്റ്റർ ആയിരുന്നു. ക്ലസ്റ്റർ I ൽ ഒൻപതും, ക്ലസ്റ്റർ III ൽ ആറും, ക്ലസ്റ്റർ IV ൽ ഒന്നും ഇനങ്ങൾ ഉൾപ്പെടുന്നു. ക്ലസ്റ്ററിനുള്ളിൽ ജനിതകയിനങ്ങൾ തമ്മിലുള്ള ഏറ്റവും കൂടതൽ ക്ലസ്റ്റർ II ലെ ഇനങ്ങൾ തമ്മിലും, കുറവ് ക്ലസ്റ്റർ IV ലെ ഇനങ്ങൾ തമ്മിലും രേഖപ്പെടുത്തി. ക്ലസ്റ്ററുകൾ തമ്മിലുള്ള അകലം താരതമ്യപ്പെടുത്തിയപ്പോൾ ക്ലസ്റ്ററുകൾ ഒന്നും മൂന്നും തമ്മിൽ ഏറ്റവും കൂടുതൽ അകലവും, മൂന്നും നാലും തമ്മിൽ ഏറ്റവും കുറഞ്ഞ അകലവും കണ്ടെത്തി.

പരീക്ഷണശാലയിൽ നടത്തിയ പഠനത്തിൽ നിന്നും IC71841, IC139464, IC22785 എന്നീ ഇനങ്ങൾക്ക് വരൾച്ചയെ ചെറുക്കുന്നതിലുള്ള കഴിവ് കൂടുതലുള്ളതായും, IC22785, IC221105, IC22759, IC139464 എന്നീ ഇനങ്ങൾക്ക് കൃഷിയിടത്തിൽ കൂടുതൽ വിളവ് രേഖപ്പെടുത്തുന്നതിനു പുറമെ വരൾച്ചയെ ചെറുക്കുന്നതിനുള്ള കഴിവും പ്രകടിപ്പിച്ചു. ഈ പഠനത്തിൽ നിന്നും കണ്ടെത്തിയ മികച്ച ഇനങ്ങളെ കർഷകർക്ക് കൃഷി ചെയ്യുവാനും, പുതിയ ഇനങ്ങൾ വികസിപ്പിക്കുവാനുമുള്ള ഗവേഷണങ്ങളിൽ ഉൾപ്പെടുത്താനുമാവുന്നതാണ്.