"DORMANCY STUDIES IN *IN-SITU* GERMINATION IN MUNGBEAN *(Vigna radiata* L.)"

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M. Sc. (Agriculture)

DOCTOR OF PHILOSOPHY

IN

AGRICULTURAL BOTANY

(SEED TECHNOLOGY)

DEPARTMENT OF AGRICULTURAL BOTANY

COLLEGE OF AGRICULTURE, PARBHANI

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PARBHANI - 431 402 (M.S.) INDIA

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BY

KADAM SANDEEP RAOSAHEB

M. Sc. (Agriculture)

A thesis submitted to

Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani

In partial fulfilment of the requirement for the degree of

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IN

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2022

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I hereby declare that the thesis entitled, **"DORMANCY STUDIES IN *IN-SITU* GERMINATION IN MUNGBEAN (*Vigna radiata* L.)"** submitted by me is based on the actual work carried out by me under the guidance and supervision of **Dr. J. E. Jahagirdar**. The extent of information derived from the existing literature have been duly cited and referenced. The existing research work or its any part is not submitted anywhere else for the award of any degree or diploma.

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Research Guide & Chairman

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(Kadam S. R.)

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ABBREVIATIONS

%	:	Per cent
µg	:	Micro gram
/	:	Per
µl	:	Microliter
Agric.	:	Agriculture
Aust.	:	Australian
Bot.	:	Botany
Biol.	:	Biology
>	:	Greater than
<	:	Less than
C.D.	:	Critical differences
cm	:	Centimeter
CV	:	Co-variance
D.F.	:	Degree of freedom
α-amylase	:	Alpha amylase
EC	:	Electric Conductivity
et al.,	:	And others
Etc.	:	Etcetera (and so on)
e.g.	:	Exempli gratia (for example)
q	:	Quintal
Fig.	:	Figure
ha	:	Hectare
g	:	Gram
ha^{-1}	:	Per hectare

TPF	:	Triphenyl Formazan
i.e.	:	Id est (that is)
Inter.	:	International
TCC	:	Triphenyle Tetrazolium Chloride
J.	:	Journal
kg/ha	:	Kilogram per hectare
MC	:	Moisture Content
mg	:	Milli gram
MT	:	Metric tonnes
MMT	:	Million metric tonnes
MSS	:	Mean sum of square
Pak.	:	Pakistan
Res.	:	Research
RBD	:	Randomized Block Design
SD	:	Standard deviation
SE±	:	Standard error
NS	:	Non-significant
Sci.	:	Science
Sr. No./ SN	:	Serial number
Univ.	:	University
USA	:	United States of America
Viz.,	:	Such as (Namely)
&	:	And

THESIS ABSTRACT

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1	Title of the thesis	:	"Dormancy studies in *in-situ* germination in Mungbean (*Vigna radiata* L.)."
2	Name of Student	:	Sandeep Raosaheb Kadam
3	Reg. No.	:	2019A/10P
4	Research Guide	:	Dr. J. E. Jahagirdar
5	Designation	:	Associate Dean, Vilasrao Deshmukh College of Biotechnology, Latur,VNMKV, Parbhani
6	Department	:	Agricultural Botany (Seed Technology)
7	College	:	College of Agriculture, VNMKV, Parbhani
8	Degree to be awarded	:	Ph. D.

ABSTRACT

The present investigation was undertaken to assess the Dormancy in Mungbean having entitled "**Dormancy studies in *in-situ* Germination in Mungbean (*Vigna radiata* L.)"** at Department of Agricultural Botany, VNMKV, Parbhani during *kharif* 2020 and *kharif* 2021. The experiment arranged in Randomized Block Design with two replications and every treatment has four rows of 4.5 meter long with 45 cm distance in between rows. The package of practices was carried out as per recommendation for raising the good crop. The experimental materials included in the present study were 34 entries containing 25 genotypes and 9 standard checks which were collected from the Agriculture Research Station, Badnapur, VNMKV, Parbhani and Pulses Research Unit, Dr. PDKV, Akola.

The observations were recorded on twenty three traits of yield contributing and seed quality characters. The yield contributing characters were days to 50 % flowering, days to maturity, days to shattering, plant height(cm), number of primary branches, number of cluster per plant, length of pods (cm), number of seed per pod, 100 seed wt. (g), seed yield per plant (g), biological yield per plant (g) and harvest index % whereas, seed quality parameters were recorded on germination (%), hard seed (%), time to opening pod (hrs), seedling length (cm), vigour index I, vigour index II, seedling dry wt. (g), seed hardness(Kg/cm^2), α-amylase (mg/g) and

dehydrogenase(µg/g).The observations on field level were taken of five randomly plants of all the yield contributing characters except days to 50% flowering, days to maturity and days to shattering. Laboratory work has completed in the laboratory of Seed Technology, Department of Agricultural Botany, VNMKV, Parbhani and laboratory of Soil Science and Agriculture Chemistry, College of Agriculture, VNMKV, Parbhani. The statistical analysis of data was carried out as per the standard method by Panse and Sukhatme.

The genotypes BM-2019-1, AKM-1609, Phule M 818-8, AKM-1606 and check PKV Green Gold showed earliness and genotype TBM-6 showed late for day to 50 % flowering in *kharif* 2020 whereas in *kharif* 2021 and in pooled mean a genotype AKM-1609 recorded early and TBM-6 late in this trait. In days to plant maturity character earliness of maturity showed in the genotypes AKM-12-14, AKM-1609, AKM-1602 and Phule M 818-8 while genotype Phule M 817-13 observed late in *kharif* 2020. In second season i.e. in *kharif* 2021 and in pooled mean of both seasons genotype Phule M 818-8 showed early and TBM-4 for late maturity whereas genotype AKM-12-14 observed earliness while Vaibhav Ch. found late.

The observations responsible for yield showed in the trait of plant height in cm, on the basis of pooled mean data, genotype Phule M 402-2-1 recorded tallest plant height, followed by check varieties PKVM-4 and Utkarsh whereas genotype Phule M 707-5 recorded dwarf plant height. In number of primary branches per plant which is directly contribute to yield and showed the range values of from 2.5 to 7.0. The next one number of pods per cluster is also an important factor which has effect on seed yield showed the range from 2.9 to 5.5. The number of pods per plant and length of pod also the important factors, which are also yield contributing traits and showed the positive correlation with seed yield. Among the genotypes Phule M 816-10 recorded highest and AKM-1606 lowest number of seeds per pod and range values were found from 9.4 to 15.1 in this trait. In the observation of 100 seed weight (test wt.) data revealed the genotypes TBM-4 recorded highest and AKM-1608 lowest test wt.

The traits of seed yield per plant (g) and biological yield were observed range values from 5.4 to 11.7 g of seed yield per plant and 14.4 to 31.6 g of biological yield per plant in both seasons. These two traits showed significant relation to harvest

index % and genotype Phule M 818-8 recorded high harvest index % followed by PKVM-8802, Phule M 817-13 and PKV-Green Gold while PKVM-4 exhibited low harvest index percentage.

The main important seed quality parameter is germination percentage which has direct influence on seed yield by maintaining plant population in field. The germination percentage of different genotypes in this study measured the range from 72.8 to 93.8 %. Among the genotypes germination percentage values were recorded more than the Minimum Seed Certification Standard (MSCS) excepting only one genotype *i.e.* TBM-6. MSCS for mungbean is 75 % minimum.

The seedling dry weight (g) showed a direct relation to the seedling length. Analyzed data showed highly positive significant relationship between seedling length (cm) and seedling dry weight (g).

Seed vigour is a complex physiological trait that is necessary to ensure the rapid and uniform emergence of plants in the field. In this study vigour index I and vigour index II recorded positive significant with germination percentage. The genotypes Phule M 818-8, AKM-1605, Phule M 817-13 and Phule M 504-20-2 showed significant in germination %, vigour index I and II.

The Fresh Seed Dormancy (FSD) of mungbean has assessed in this study by observing the time of opening of pods (hrs) in *in-situ* germination. The range values were observed from 0.8 to 80.8 hrs. Analyzed data revealed the result regarding different genotypes and checks, six were showed less, 18 were moderate and remaining ten were categorized in high fresh seed dormancy (FSD).

The enzymatic activity of the enzymes α-amylase and dehydrogenase showed highly positive correlation with the character germination percentage, vigour index I and II in mungbean. It means increase in enzyme activity of α-amylase and dehydrogenase with increased germination percentage, vigour index I, vigour index II and *vice-versa*. However, it noticed negligible range of correlation with α-amylase and negligible non-significant negative correlation with time to opening of pods.

(Key words: α-amylase, dormancy, dehydrogenase, germination percentage, vigour index)

CHAPTER -I

INTRODUCTION

CHAPTER – I

INTRODUCTION

Most people refer to pulses as "poor man's meat." It serves as the primary source of dietary protein for a sizable portion of the world's vegetarian population. Average protein content in pulses ranges from 20 to 30%, which is around 2.5 to 3.0 times the amount typically found in cereals. Pulses are crucial for fixing biological nitrogen and so improving soil fertility. Through atmospheric nitrogen fixation, it enhances the nutrient status of the soil, adds humus to the soil, is appropriate for dry land farming and is mostly utilized as an intercrop with other crops. Additionally, it works well as concentrates and feed (Favero *et al*., 2021).

The world's food supply is 71 million tonnes and 79 million hectares of pulses (Anonymous, 2021). The global area of mungbean is approximately 7.3 million ha and the global production is approximately 5.3 million tonnes. The mungbean is a well-known crop in Asian countries and India is the world's largest producer and consumer of pulses, accounting for 30% of global production (Ram Nair, 2019).

It is the third crucial pulse crop after red and bengal gram which is a significant grain legume, notably in Asia. The most crucial crop in the pulse family in terms of cost-effectiveness is the mungbean (*Vigna radiata* L.). The mungbean is also referred to as the moong, green gram and golden gram. Mungbean, a member of the subgenus *Ceratotropis*, is a significant pulse crop in India (Kirti Rani, 2012).

The presence of mungbean at archaeological sites across the continent is said to be proof that they have Indian origins. It is indigenous to Asia's north-eastern areas of India and Myanmar (Anonymous, 2013). The majority of it is grown in South China, Formosa, Bangladesh, India, Pakistan, Sri Lanka, Thailand, Laos, Cambodia, and Vietnam. It is presumably recent in Africa and the USA. It is a warm-season crop that may be grown in the dry and semi-arid tropics and during hot, humid seasons (Sumera Akram, 2020).

Traditional indeterminate mungbean types require repeated harvests due to their lengthy (90 to 110 day) lifecycles. Mungbean is an economically

significant short-duration pulse crop that are notable for being more pleasant, nutritious, affordable, and non-flatulent than other pulses (Kamleshwar *et al*., 2014).

Since it is essential for providing the body with easily digestible protein, mungbean have long value for their dietary or nutritional worth. It is ingested not only as divided pulse but also as entire pulse, which is a crucial dietary addition for cereals. The major dishes that are made with it include dhal, curries, soup, desserts and snacks. The aged, ill and babies are advised to eat the moong dhal-khichdi because it is a complete meal and is easily digested. Due to the complementary nature of the essential amino acids, when wheat or rice is combined with mungbean, the biological value increases significantly and recognized as a high-quality pulse (Sue, *et al.,* 2015).

When compared to asparagus or mushrooms, sprouted seeds are more nutrient-dense. Thiamine, niacin, and ascorbic acid concentrations rise during sprouting (Dahiya, *et al.*, 2015). Food benefits of mungbean include Protein - 24-25%, Calcium - 124 mg/100 g, Fat - 1.3%, Phosphorus - 326 mg/100 g, Minerals - 3.5%, Iron - 7.3 mg/100 g, Fiber - 4.1%, Calorific value - 334 Kcal/100 g, Carbohydrate - 56% and Moisture - 10% (Anonymous, 2013).

The main obstacles to increasing yield are the varieties' naturally low yielding potential due to a lack of genetic diversity, the lack of ideotypes suitable for various cropping systems, the low harvest index and the susceptibility to abiotic and biotic stresses, such as drought, calcareous or saline soil, diseases and insects (Nair *et al*., 2019 and Yadav, *et al.*, 2020).

It is best to avoid planting mungbean right after mungbean or cabbage since the subsequent mungbean crop may be negatively impacted by harmful pathogenic microorganisms from the prior mungbean or cabbage crops. It has diploid nature *i.e.* 2n=22 (Mehandi *et al*., 2019).

Mung bean is a perennial plant with occasionally twining tops. The twining growth predominates over the erect habit. The mungbean is an erect or sub-erect, 0.3 to 1.4 m tall plant with deep roots, long petioles, and numerous branches. The leaves are trifoliate, alternating, ovate, dark or light green, and range in size from 2 to 10 cm long and 5 to 12 cm wide. The leaflets of heterozygous genomes are

intermediately lobed (Itefa Degefa, 2016). Mungbean petals are spirally coiled with a horn-like shape and the flowers are described as being bright yellow. Pods are 6 to 12 cm long, short and hairy. The color of the pod, which is covered in fine hair, might be buff, grey or dark brown (Lee *et al*., 2021).

The unripe pod color is known to be influenced by the genes responsible for blossom color. The majority of seeds are green, although they can also be black, speckled, yellow or reddish brown (Monjurul *et al*., 2011). Green seed coat and speckled seed coat colors are controlled by identified dominant genes. The grain is mainly globose in form and weight between 15 and 85 mg (Earl *et al.*, 1977).

Mungbean has reported that photoperiod insensitivity predominates over flowering time sensitivity and that seed breaking at maturation is due to one dominant gene. The *Vigna sublobata* and *Vigna glabra* are its wild ancestor of mungbean (Ezagi *et al*., 2018).

Since the commencement of yield 2.5 million tonnes over an area of around 4.5 million acres, India comes in third. In Maharashtra, the most significant pulse crops is the mungbean (*Vigna radiata* L. Wilczek). Maharashtra produced mungbean 2.79 lakh tonnes from 4.81 lakh ha in 2018–19, with a productivity of 424 kg/ha. Given that this is less than half of the national productivity (625 kg/ha), there is room to increase productivity. Maharashtra contributed 16.19% of the country's total area and 13.46% of the last ten years' average production in pulses mainly Mungbean (Anonymous, 2021).

The term "vivipary" describes the germination of seeds while the pods are still attached to the mother plant. It displays a continuous progression of growth from embryo to germination without a maturation interval characterized by occurrences like desiccation, storing of reserves, quiescence or dormancy. Due to seeds sprouting in pods while the crop is in the field, pre-harvest mungbean germination results in significant losses. Pre-harvest sprouting (PHS) would entail the germination of mature, fully formed seeds before their harvest. The process of physiologically ripe grains sprouting in the ear, panicle, or pod, typically under moist conditions, just before harvest, is known as pre-harvest sprouting (PHS). The PHS takes place in mungbean because it hasn’t fresh seed dormancy (PHS). The dormancy

can be defined as it is the state or condition in which seeds are unable to germinate even in environments that are favorable for germination, such as those with the right temperature, water, light, gas, seed coats and other mechanical constraints. Dormancy is very useful for protection of Vivipary germination.

Excessive moisture conditions, such as prolonged and frequent intermittent rains, heavy dew, high humidity and even low temperatures, lead to this condition. Many different crops, including wheat, barley, maize, rice and grain legumes including soybean, chickpea, black gram and green gram, undergo pre-harvest sprouting (PHS). PHS results in considerable economic losses since it not only reduces grain yield but also decreases grain quality and seed viability. In regard to standing crops, PHS also causes harm to the harvested piles in farms and crushing yards (Singh and Ahlawat, 2005).

Despite being covered by their outer pods, mungbean seeds are sensitive to pre-harvest sprouting (PHS) after rain because they lack fresh seed dormancy (FSD), which lowers the quality of the grain or seed that is developed. Mungbean seed quality can be significantly reduced by *in-situ* germination in uncontrollable rainfed situations. Farmers are unable to sell their goods for a fair price because of the loss of seed quality. This problem can be solved by making seeds dormant dormant. Hence, it has become crucial to create mungbean cultivars with short (10–15 day) fresh seed dormancy (FSD) periods in order to reduce the losses brought on by pre-harvest sprouting (PHS).

Due to a late start to the rain followed by a protracted dry spell, seeding was not completed within the anticipated time frame, which significantly lowered the yield over the past few years. Due to the late seeding, *in-situ* germination occurs since the maturity coincides with strong rains in August-September.

Endosperm formation in cereals and its physiological functions are well known. The embryo scutellum initially produces and secretes gibberellin, a hormone that aids in germination, into the aleurone layer of the endosperm. Ultimately, it improves the aleurone layer's ability to produce hydrolytic enzymes. Protease, amylase and acid phosphatases are examples of hydrolytic enzymes that hasten the establishment of seedlings and the germination of seeds. However, the

activities of these enzymes in seeds are decreased by the presence of heavy metals of hydrolytic enzymes.

During seed germination, the alpha amylase enzyme actively participates in the breakdown of starch. It specifically breaks the starch's α-glycosidic bond. Through the provision of solute sugar throughout the seed germination period, it may also be responsible for maintaining the necessary water potential and energy (Awatif and Alaaeldi, 2017 and Sumera *et al*., 2021).

Dehydrogenase played a role in the catalysis of stored products during the anaerobic phase seed germination. It means dehydrogenase provide energy to embryo during germination in anaerobic phase. This caused the energy utilized during the early stages of seed growth in the germination of seeds to be released. The activity of the dehydrogenase enzymes curves infer that the start of seed germination and seedling vegetative growth in seeds is preceded by an early burst of dehydrogenase activity.

When seeds mature at high temperatures, their moisture content is rapidly lost or they dry out quickly. Additionally, because of this situation's inhibition of the enzyme necessary for seed germination, the efficiency of the seed mitochondria's equilibrium is affected, leading to a decrease in the enzyme responsible for respiration. One of the key biochemical components in seeds is the dehydrogenase enzyme, which is found in mitochondria and required for the respiratory process (Burke *et al*., 1982 and Kim *et al*., 2012). The concentration of the dehydrogenase enzyme is typically thought to indicate the seed's viability.

Taking into consideration of above points, the experiment entitled, “Dormancy Studies in *in-situ* Germination in Mungbean (*Vigna raidata* L.)” was planned and conducted on following objectives:

1. To assess the dormancy by *in-situ* germination in mungbean.
2. To study the enzyme α-amylase responsible for germination and dormancy in mungbean.

3. To study the dehydrogenase activity in Mung bean regarding seed germination and vigour.

4. Correlation studies of enzymes α-amylase and dehydrogenase with seed quality.

5. To evaluate yield and its associated traits.

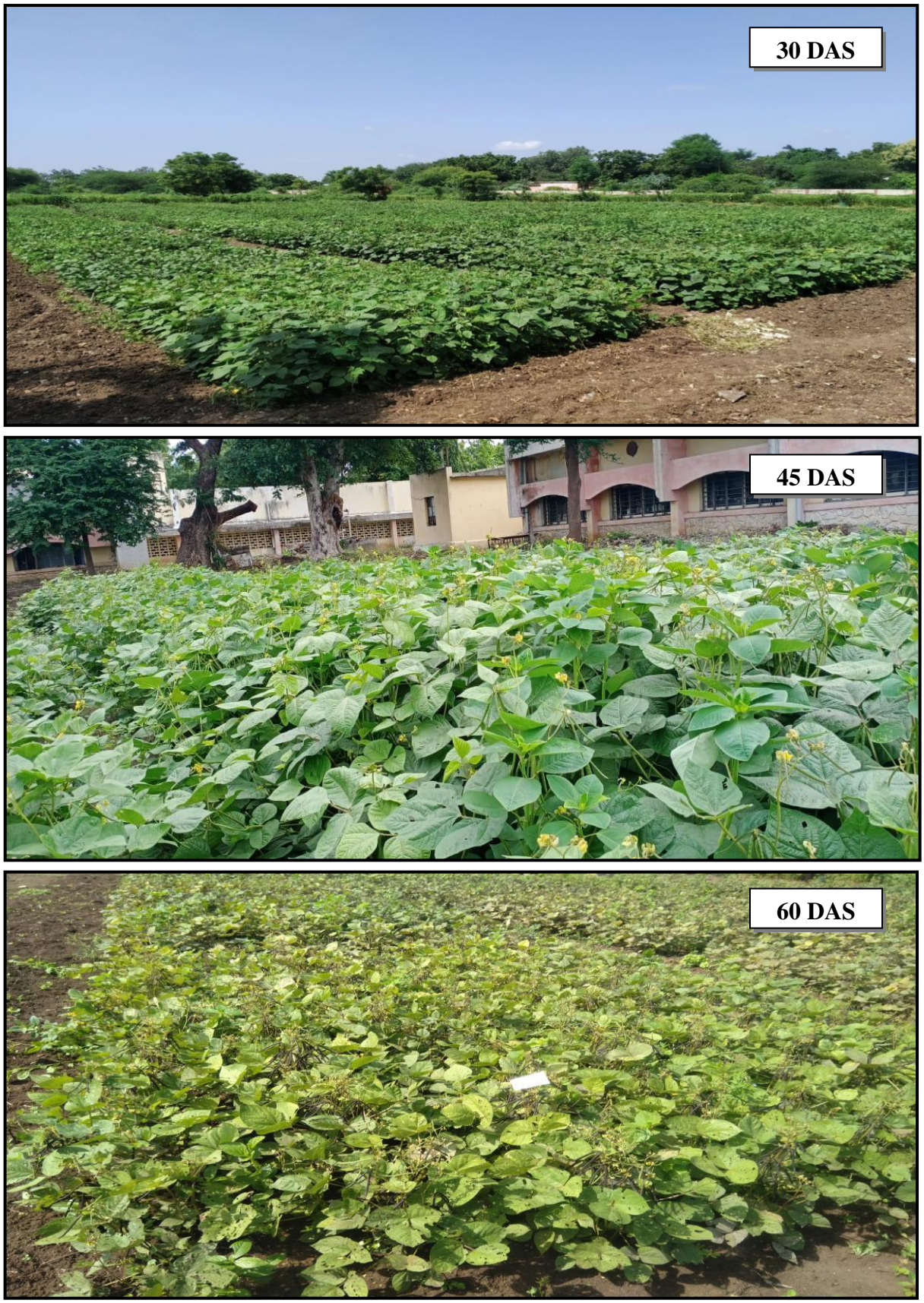

Plate 1: General view of experimental plot of mungbean

CHAPTER -II

REVIEW OF LITERATURE

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REVIEW OF LITERATURE

The literature relevant to present investigation entitled "Dormancy Studies in i*n-situ* Germination in Mungbean (*Vigna raidata* L.)" was planned and conducted with objectives to assess the dormancy by *in-situ* germination in mungbean, study the enzyme α-amylase responsible for germination and dormancy, study the dehydrogenase activity in mungbean regarding seed germination and vigour, correlation studies of enzymes α-amylase and dehydrogenase with seed quality and evaluate yield and its associated traits.

Literature on the above aspects has been reviewed and given here under with following subheadings.

2.1 Pre Harvest Sprouting (PHS): Dormancy assessment

Dormancy is the seed characteristics, the degree of which defines what conditions should be met make the seed germination. It provides a strategy for seeds to spread germination in time in order to reduce the risk of plant death and possible species extinction in an unfavorable environment. A problem in distinguishing dormancy-relieving factors from factors stimulating germination is that the actual state of dormancy cannot be measured directly (Thomson and Ooi, 2013). Koorneef *et al*. (1989) defined dormancy as a state of a whole plant or plant organ that is generally characterized by a temporary arrest in growth and development. In the crop of mungbean it is of much importance as seed exhibit germination when it is not necessary. Hence it is helps in reducing harvest losses of seeds.

Mungbean is an important rainy season pulse crop of India. The average productivity of this crop is low and uncertain due to neglected

management and poor adoption of the production technology due to the risk of pre harvest sprouting.

Pre harvest sprouting (PHS) is the premature germination of mungbean grains or in other words starting of embryo growth while still attached to the mother plant in the field. Mungbean is prone to pre-harvest sprouting. Once mungbean grain reaches at harvest maturity, it begins to germinate if it is exposed to adequate moisture and suitable temperature. Therefore, pre harvest sprouting depends on duration and severity of moist condition prior to harvest. During such wet weather, growth stage of ripening grain and the inherent dormancy level attributable to a variety's genetics.

Durga and Kumar, (1997) elaborated that the mungbean genes interact with environment to predispose a variety to pre harvest sprouting. Therefore depending on the environment and weather conditions to which the plants are exposed. Sometimes losses due to pre harvest sprouting will be as high as 60-70%. Pre harvest sprouting negatively affects the grain quality by losing the grain weight, viability and seedling vigor. High yielding varieties developed or identified in recent years, despite their high yield potential, could not increase or stabilize the yields of this crop due to lack of resistance to pre harvest sprouting. Therefore it is essential to develop resistant tolerant varieties to pre harvest sprouting by understanding the mechanism and genetics of resistance. Information on the genetics of pre harvest sprouting and the traits responsible for pre harvest sprouting are not available.

Cheralu *et al*., (1999) indicated and stated that the genetic analysis of predominance of additive gene action for pod beak length, pod wall thickness and pod wall epicuticular wax, while hard grain percent and pre harvest sprouting were under the control of non-additive gene action. Both additive and non-additive gene actions were found to operate for moisture absorption rate through the pod wall.

Issa *et al*., (2010) studied inheritance of fresh seed dormancy in Spanish Spanish crosses with two sets of segregating populations, an F2 population derived from true F, hybrids identified with peanut microsatellites markers and other populations (F2, BCPs and BCPs) from randomly selected F, individuals. They resulted that in the population, the chi square test was not significant for the

deviation from the expected 3:1 (dormant: non-dormant) ratio. They again found that the bimodal frequency distribution curve with the F2 population gave more evidence that fresh seed dormancy is controlled by a single dominant gene.

Suryawanshi *et al*., (2013) revealed the quality of the seeds and preharvest sprouting in mung bean, the effects of foliar spraying CCC [chlormequat] (500 ppm) and maleic hydrazide (100 ppm) at 45, 50, 55, and 60 days after sowing (DAS) were investigated. Plant growth regulators used topically greatly improved seed quality, yield, and growth. In general, the augmentation of vegetative and generative growth was better achieved by foliar spraying growth regulators at the early growth stages, but the enhancement of seed quality parameters was better achieved by applying plant growth regulators at the advanced growth stages. Raw seeds contained more protein, carbohydrates, and total sugar than sprouted seeds did.

Ahmad *et al*., (2014) designed an experiment to evaluate 112 diverse genotypes of mungbean for their pre-harvest sprouting tolerance. They used seed germination % in pods, as a measure of pre-harvest sprouting tolerance and found that it is ranged from 2.09 in *Vigna radiata* var. *sublobata* to 100.0 in the cultivar MH 318. A diverse set of 105 Urdbean genotypes comprising of released cultivars, advance breeding lines of inter-varietal and inter-specific origin, local germplasm collections, the wild progenitor of cultivated Urdbean (*Vigna mungo* var. *silvestris*) and five checks were evaluated by Singh *et al*. (2012) for their pre-harvest sprouting tolerance and other important agronomic traits. Seed germination % in pods, which was a measure of pre-harvest sprouting, ranged from 8.8 in *Vigna mungo* var. *silvestris* to 99.4 in PCPGR 8057, a cultivated variety.

Lamichaney *et al*. (2017) investigated variations in pre harvest sprouting, fresh seed germination and activity of c-amylase enzyme in 163 mungbean genotypes. They found 14 genotypes which were tolerant (< 20 %) to pre harvest sprouting. Seed germination in a pod, varied from 7.14% in germplasm accession Chamu 4 to 82.52% in cultivated variety IPM 2-3. They concluded that, there is increase in c-amylase activity in genotypes showing high fresh seed germination and pre harvest sprouting, especially at 48 and 72 hrs after germination as compared with pre harvest sprouting tolerant genotypes.

Priyanka *et al*., (2017) observed that pre-harvest sprouting is the germination of physiologically developed grains in the pod, commonly under moist conditions right before harvest. They assessed the dormancy in mungbean to prevent losses during the rainy season (PHS). In most parts of the world, field crops like cereals and pulses grow before harvest. When growing mungbean in the summer their non-dormant nature is unfavorable because showers are almost always experienced at the crop's harvest stage, which results in significant yield losses due to the sprouting of pods in the field. In areas of soil with significant soil moisture retention capacity, it is more difficult. In situ germination has been reported to cause a 50–70% decrease in mungbean yield. It is more important to look into unconventional ways to make mungbean become dormant in order to preserve the crop and the seed quality against field sprouting. Field sprouting also reduces the supply of seeds.

Singh *et al*., (2017) observed the twenty diverse genotypes of mungbean for their pre harvest sprouting tolerance (PHS) seed germination % in pods was used as a measure of PHS tolerance and it ranged from 2.078 in *Vigna radiata* var. *sublobata* (wild progenitor of mung bean) to 99.9 in the cultivar PDM139. The low seed germination % (5.6%) in *V. radiata* var. *sublobata* showed that presence of seed dormancy would be there. They observed that cultivated genotype Pusa Vishal (13.50%) exhibited lowest seed germination % followed by Kopergaon and TARAM-18 with 21.00% and 22.01% seed germination %, respectively and concluded that these genotypes too exhibited lower seed germination % which may be due to presence of higher amount of hard seeds.

Biradar *et al.,* (2022) studied on dormancy in mungbean and reported that to reduce production losses from viviparous germination, pre-harvest sprouting (PHS) tolerant cultivars must be developed. To produce desired diversity, F2 seeds from the DGGV-2 x Pant Moong-1 crosses were exposed to 60 kR gamma rays. Segregants with a narrow beak and angle, a thick wall, hard seededness, and increased epicuticular wax and lignin content were separated in the F2M2 generation. From 206 progenies made up of 4812 plants, desirable mutants granting PHS tolerance were chosen. The desired plants with less than ve percent PHS were rigorously identified by morphological and biochemical markers during the succeeding successive generations. Genotypes that are naturally resistant to seed breaking pods have the

potential to reduce yield losses brought on by viviparous germination. Introduction Poor seed quality owing to fungal infestation and the sprouting of seeds within pods is frequently the outcome of an extended wet spell during maturation.

2.2 Correlation coefficient in yield and yield attributing characters:

The extent and nature of association between yield and its component traits help breeders to ascertain the real components of yield and effective basis of phenotypic selection. Estimates of correlation coefficient are the measures of association between characters and provide the basic information in identifying characters that have little or no importance in the selection programme. Correlation studies measure only mutual association between two traits and it does not imply the cause and effect of relationship. Selection procedure is more difficult in a trait, where heritability is low or is not precisely measurable. Indirect selection in such a situation is more effective and study of correlation among different economic traits are therefore, essential for an effective selection programme because selection for one or more trait results in correlated response for several other traits (Scarle, 1965) and sequence of variation will also be influenced (Waddington and Robertson, 1966).

Hence, the knowledge of genotypic and phenotypic correlation between yield and its contributing characters is very essential. The path coefficient analysis elucidates the intrinsic nature of observed association between yield and its attributes. Path analysis provides estimates for direct and indirect causes of yield (Wright, 1921).

Dewey and Lu (1959) made the first time in plants, correlation coefficient for route analysis. Breeders can determine the true components of yield and an effective phenotypic selection foundation by looking at the degree and kind of correlation between yield and its component traits. Direct and indirect causes of association have both been found to benefit from path coefficient analysis, which also assesses the relative importance of each causative element and enables a detailed investigation of the specific forces acting to form a given connection.

The plant breeder uses correlation to determine the actual relationships between different plant characteristics and to set selection criteria for grain yield in parental lines and segregating populations. The type, nature, and strength of any link

between any two characters are revealed by the correlation coefficient. The link between two traits that can be seen directly and are affected by environmental changes is known as phenotypic correlation.

Singh and Singh (1973) mentioned there is a positive association between the number of pods and clusters per plant and the seed output. The primary contributing element to yield was the number of pods per plant, whereas the number of clusters per plant had an impact on the production through the number of pods per plant.

Giriraj and Vijaykumar (1974) elaborated in their studies that the the number of pods per plant, the number of seeds per pod, and the days to 50% flowering plant height were all positively connected with seed yield. Pod length and the character 100-seed weight were significantly positively connected, whereas seed yield, days to 50% flowering, and plant height were adversely correlated. They also discovered a strong positive association between the number of pods per plant and the number of days till blossoming.

Singh *et al*., (1977) recorded positive significant association of seed yield with number of primary branches per plant, number of clusters per plant, number of pods per cluster and number of pods per plant.

Rathnaswamy *et al*. (1978) reported a significant positive link between seed yield and number of pods per plant was found by At the genotypic level, the number of seeds per pod was positively linked with seed yield. We found a negative association between seed output and weight of 100 seeds. Pod length and 100-seed weight had a negative correlation with the number of pods produced per plant.

Saraswathy *et al*. (1979) according to research by them , the number of clusters had the most direct positive impact on seed yield. The number of pods per plant has a direct detrimental impact on seed production.

Upadhyaya *et al*. (1980) reported on their studies the character association in 115 varieties of green gram of different maturity groups from the main yield components in the early maturity group were the number of pods per plant, plant height, and number of seeds per pod, whereas in the late maturity group the

main yield components were the number of pods per plant, 100-seed weight, and number of branches per plant.

Gupta *et al*. (1982) observed higher magnitude genotypic correlation coefficients than phenotypic correlation coefficients. The number of clusters per plant, number of pods per plant, number of seeds per pod, and days to maturity were all positively and significantly linked with the amount of seeds produced per plant.

Deore (1983) found that plant height and days to 50% flowering had a negative link, whereas the number of pods per plant, pod length, 100-seed weight, and harvest index showed a substantial positive association with seed yield.

Thandapani and Rao (1984) found that clusters per plant had the greatest direct impact on seed yield, although pod length and seed weight were also directly related to it. This statement gieby them on the basis of study on 15 different genotypes of green gram which were evaluated for yield parameters and their relevance in connection to seed yield.

Satyan *et al*. (1986) noted plant height, pod length, and the number of pods per plant all had less direct effects on seed yield than the 100-seed weight.

Malik *et al*. (1987) founded there is an inverse relationship between seed yield and days until maturity, pod length, and grain weight. Additionally, they looked at the mungbean plant's maximum relative selection efficiency for branches per plant.

Patil and Narkhede (1987) stated that there is a positive link between plant height, days to maturity, the number of pods per plant, the number of seeds per pod, and the weight of 100 seeds.

Ramana and Singh (1987) discovered that in their study of character associations in 37 promising green gram varieties and two controls grown in the spring and rainy season, in both seasons, there were significant correlations between seed yield per plant and plant height, pods per plant, clusters per plant, and seeds per pod. In both seasons, phenotypic correlations were less significant than genotypic correlations.

Natarajan *et al*. (1988) discovered a strong and positive correlation between seed yield and plant height, clusters per plant, pods per plant, and seeds per pod in examining the genetic relationships among 45 genotypes of green gram,

Raut *et al*. (1988) reported the genotypic correlation coefficients were found to be greater than the phenotypic correlation coefficients. They also noted a positive genotypic association between seed yield and the quantity of seeds per pod, branches per plant, clusters per plant, and pods per plant. Negative and insignificant correlation was seen between the number of pods per plant and seed output. The number of clusters per plant, 100-seed weight, and seeds per pod all showed a significant positive contribution to the total amount of seeds produced by each plant.

Falconer, (1989) stated that about non-additive gene action, it measures environmental variances. Genetic correlation, also known as additive and (additive x additive) gene effects, is the correlation of breeding values. Improvement of yield for which direct selection is ineffective requires knowledge of the relationships between yield components and yields.

Lakshmaiah *et al*. (1989) and Satyan et al. (1989) demonstrated that the number of clusters per plant, plant height, number of pods per plant, days to blooming, and days to maturity all significantly positively correlated with seed yield per plant. They came to the conclusion that during selection, attention should be paid to clusters per plant and pods per plant in order to increase the yield of green gram. Similar conclusions were reported by Pokle and Nomulwar (1978).

Borah and Hazarika (1995) found the selection for these traits will aid in the identification of high yielding varieties of green gram. They found that seed yield per plant was substantially related with practically all yield attributing variables.

Khattak *et al*. (1995) studied on ten mungbean genotypes, were examined in RCBD with three replications and given their findings, there was a positive and substantial link between seed yield per plant and seed weight per hundred seeds. The number of branches per plant showed a weak but substantial negative connection with seed output. Clusters per plant, however, showed no correlation with seed output.

(Kuo, 1998) listed the key elements of mungbean yield include the number of harvested plants per unit area, the number of pods per plant, the weight of the grain, and the number of grains per pod. Numerous research projects have been conducted to examine the relationships between these key characteristics and in mungbean seed yield. Such types of report were also given by Ghafoor *et al*., 1990; Khattak *et al*., 2001; Malhotra *et al*., 1974; Yucel, 2004.

Ghafoor *et al*. (2000) discovered cluster analysis for nine quantitative features in mungbean. They found a substantial negative link between days to maturity and all the features, with the exception of branches per plant, and indicated that cultivars of mung beans with short to medium maturities should be chosen for their high yield. In search of the best mung bean cultivars, they identified 44 pure lines based on significant agronomic qualities that were suggested for testing under a variety of agro-ecological conditions.

Khan *et al*. (2001) assessed 15 different genotypes and revealed a positive and significant correlation between seed yield and plant biomass, number of branches, and pods per plant. Days to 50% flowering, days to maturity, and pod length all showed a weakly positive correlation with seed output. The mungbean yield components that performed best were found to be number of branches, number of pods, and total dry biomass. Significant positive correlations between seed yield and pods per plant, biological yield, harvest index, and 100-seed weight were found by Dixit *et al*. (2002).

Venkateshwarlu (2001b) noted there is a strong and favorable correlation between seed yield and the number of pods per plant, days to maturity, plant height, 100-seed weight, seeds per pod and pod length.

Haritha and Reddy Sekhar (2002) found in their study of 50 mungbean genotypes, a strong significant positive association between grain production and harvest index, biological yield per plant, pods per plant, and pods per cluster. Pods per plant, clusters per plant, and pods per cluster were highly positively and significantly correlated with harvest index and biological yield per plant. Additionally, they discovered a phenotypic and genotypic correlation between grain yield and harvest index, followed by biological yield per plant and pods per plant.

Saifullah and Mahmood's (2002) evaluated the number of seeds per pod, number of pods per plant, harvest index, and biological yield were all positively and significantly connected with seed production. The quantity of branches and biological yield were positively and significantly correlated with plant height. The number of days until flowering was strongly and positively linked with biological yield. The biological yield per plant and the harvest index were significantly positively correlated with the number of pods per plant. In two distinct investigations, a favorable correlation between the number of pods per plant and the number of grains per pod and the grain production in mungbean genotypes of various provenance was found.

Madrap *et al*. (2003) studied on the number of days till maturity, the quantity of secondary branches per plant, the quantity of pods per plant, and the weight of 100 seeds were all positively and substantially connected with seed yield.

Reddy *et al*. (2003) evaluated both at the genotypic and phenotypic levels, the amount of seeds produced per plant was strongly and favorably linked with both plant height and the quantity of clusters produced per plant.

Kumar *et al*. (2004) tested 21 other mungbean genotypes on at both phenotypic and genotypic levels, they reported a strong and positive correlation between seed yield per plant and days to maturity, plant height, primary and secondary branches per plant, pods per cluster, pods per plant, and harvest index.

Gupta *et al*. (2005) reported seed yield had a positive and highly significant relationship with pods per plant, biological yield per plant, and harvest index, with the highest direct contribution coming from pods per plant, biological yield, and harvest index.

Maddewad (2005) observed the number of seeds per pod, the length of the pod, and the weight of 100 seeds all significantly positively correlate with seed yield.

Avcicek and Yildirim, (2006) reported the selection for high yield genotypes can be accomplished through yield components by studying the direct and indirect effects of yield components, which can serve as the foundation for a breeding

program's success. Accordingly, the problem of yield increase can be more successfully addressed on the basis of the performance of yield components and selection for closely related characters. A good indicator of the relationship between characters is provided by correlation analysis, which also makes it easier to identify crucial characteristics for selection that will increase yield.

Rao *et al*. (2006) investigated 60 genotypes of mungbean. Genetic correlation showed a favorable and extremely significant relationship between seed output and harvest index as well as pods per plant and biological yield per plant.

Iqbal *et al*. (2007) used 43 different mungbean genotypes in their experiment to examine the relationship between seed yield per plant, pod bearing branches per plant, pod clusters per plant, and pod clusters on branches. They found that these relationships were positively and significantly related to seed yield.

Kaveri *et al*. (2007) examined 116 mungbean germplasm lines in RBD using two replications and showed that the number of clusters per plant, the number of pods per cluster, the length of the pod, the number of seeds per pod, and the weight of 100 seeds were all significantly and positively connected with grain yield. Significantly negative connection between days to 50% flowering and seed yield was observed.

Pandey *et al*. (2007) evaluated the phenotypic and genotypic levels of 20 mungbean genotypes in RBD, found that harvest index had the highest significant connection with seed output. In addition to harvest index, the genotypic variables pod number, seed weight per pod, and pod length significantly positively correlated with seed yield. Significant and favourable correlations between plant height, seed number, pod length, and seed were found at the phenotypic level.

Parameshwarappa and Salimath's (2007) studied and stated, the number of branches per plant, plant height, and pods per plant were all significantly and favorably correlated with seed yield per plant.

Saeed *et al*. (2007) evaluated the number of pod-bearing branches and pod clusters per plant were positively and significantly correlated with the amount of

seeds produced per plant in mungbean. They came to the conclusion that more pod clusters per plant might be employed as a more effective selection criterion.

Wani *et al*. (2007) investigated 20 genotypes which were analyzed by the relationship between qualitative and quantitative features. They discovered a substantial and positive association between seed yield and plant height, cluster size, and pod length.

Gul *et al*. (2008) developed correlations between plant height, days to 50% flowering, days to maturity, seed yield per plant, weight of 100 seeds, harvest index, and seed output per hectare. They noticed that there was no statistically significant correlation between the seed production per plot and the weight of 100 seeds. The connection between the harvest index and the plant-level seed yield was highly positive. Additionally, they discovered a favourable correlation between seed production per plant, seed yield per hectare, and harvest index.

Hakim (2008) used 350 mungbean genotypes and examined with three replications in RBD. According to his findings, seed yield was significantly and positively connected with plant height, days till flowering, days until maturity, and the number of pods per plant. In contrast, there was a strong and inverse relationship between seed yield and seed size.

Rozina *et al*. (2008) studied 26 different mungbean genotypes found a strong and positive correlation between seed yield and the number of pods per plant and harvest index. Plant height was inversely connected with 100-seed weight and harvest index, but significantly and positively correlated with days to maturity, seeds per pod, and dry weight per plot. Days to 50% flowering were inversely related to days to maturity, number of pods per plant, plant height, and dry weight, whereas they were favorably related to days to maturity, number of pods per plant, number of pods, and dry weight.

Arshad *et al*. (2009) reported on both at the phenotypic and genotypic levels, plant height among the characters showed a positive and significant correlation with seed yield per plant. Additionally, a positive and substantial association between plant height and the number of secondary branches per plant and the number of days till flowering was found.

Dadepeer and others (2009) stated that both the phenotypic and genotypic levels, a significant and positive association between seed output and 50% blooming, harvest index, and pods per plant was found.

Singh *et al*. (2009) conducted an experiment to calculate the correlation coefficients between 12 quantitative features. Using 80 mungbean germplasm lines in three conditions, additionally, a positive phenotypic and genotypic correlation between pods per cluster and seeds per pod as well as between pods per plant and harvest index was observed.

Tejbir *et al*. (2009) studied on 40 mungbean genotypes were the subject of a correlation study by which included three replications across four different settings. They stated that at the phenotypic level in all settings, the seed yield showed a positive and substantial correlation with the number of seeds per pod, 100 seed weight, biological yield, and harvest index. In two of the four conditions, there was a substantial and positive association between the number of days until 50% flowering and plant height and biological yield. Contrary to number

Huda *et al*. (2010) noted a substantial positive correlation between seed yield and pod number and seed size. Good seed size appeared to be major contributors to the mungbean seed output, however it was discovered that seed size continued to have a negative correlation with seed number.

Kumar *et al*. (2010) discovered a very significant association between seed yield character relationship in 23 mungbean genotypes and harvest index at both the genotypic and phenotypic levels.

Rahim *et al*. (2010) investigated 26 genotypes of mungbean. The number of days to 50% flowering and the number of days to 80% maturity were found to be positively correlated. Plant height and the number of seeds per pod were positively correlated with days to 50% flowering, while 100-seed weight was inversely correlated. There was a positive association between days to 80% maturity and pod length. With regard to pod length, seeds per pod and grain yield, the number of pods per plant had a positive correlation.

Vinay *et al.*(2010) found pods per plant and harvest index at both phenotypic and genotypic levels were have highly significant correlations with seed production per plant in the study of character association in 23 mungbean genotypes for various quantitative characters. On the other hand, at both the phenotypic and genotypic levels, days to maturity and plant height were negatively linked with seed output per plant.

Khajudparn and Tantasawat (2011) analyzed 14 characteristics and 56 mungbean accessions. They demonstrated that seed yield was inversely connected with biomass and positively correlated with pods per plant, clusters per plant, seeds per pod, seeds per plant, and branches per plant.

Khanpara *et al*. (2012) investigated by using 58 genotypes of green gram with correlation coefficients among 12 yield-contributing characteristics. The number of pods per plant, number of pods per cluster, and number of clusters per plant all significantly and positively correlated with the amount of seeds produced per plant, both at the genotypic and phenotypic levels.

Mondal *et al*., (2012) identified limiting growth characters for the effective application of physiology breeding for higher yields, growth parameters including leaf area (LA), total dry mass (TDM) production, crop growth rate (CGR), relative growth rate (RGR), and net assimilation rate (NAR) were compared in six varieties of mungbean under subtropical conditions (248 N 900 E). The results showed that the majority of TDM was produced after anthesis, with a relatively smaller amount produced before flower initiation. Due to maximum leaf area (LA) development at this stage, the highest CGR was seen in all types at the pod filling stage. The greater TDM production was attributed to two plant features, LA and CGR. Results showed that higher LA, higher TDM production capacity, superior CGR at all growth stages, and higher relative growth rate and net assimilation rate at the vegetative state should be present in high yielding mungbean varieties. These traits would produce superior yield components.

Srivastava and Singh (2012) analyzed the number of pods per plant, the weight of the 100 seeds, the number of days till maturity, and the number of pods per cluster all had a positive and significant link with seed yield.

Zaid *et al*. (2012) assessed the correlation between 20 mungbean genotypes for variables that contribute to yield, including plant height, pods per plant, pod length, seeds per pod, biological yield, and grain production. Characters like plant height, pods per plant, and pod length were shown to have a phenotypic impact on seed yield by genotypic correlation analysis. They came to the conclusion that the optimal breeding programme criteria for enhancing yield in mungbean genotypes may be grain yield and seeds per pod.

Gadakh *et al.* (2013) calculated the correlation coefficient, analyzed 50 different mungbean genotypes for 15 quantitative features. Character relationship revealed a substantial positive correlation between seed yield and the harvest index and 100-seed weight.

Kumar *et al*. (2013) evaluated in their study that there is a strong positive direct relationship between the number of secondary branches per plant, bunches per plant, pods per plant, grains per pod, pod length, and 100-seed weight, as well as a positive and significant correlation between these variables and grain yield.

Nand and Anuradha (2013) reported in their study that the factors like days to 50% flowering, number of branches per plant, number of pods per plant, days to maturity, and 100-need weight all have a positive and substantial link with seed yield.

Narasimhulu *et al.* (2013) elaborated the number of pods per plant, clusters per plant, pods per cluster, and biological yield per plant were all positively and significantly correlated with seed output. There is no correlation between seed output and weight of 100 seeds. The number of clusters per plant was significantly and favorably correlated with the number of branches, pods, and clusters per plant. Clusters per plant and the weight of one hundred seeds were shown to be negatively correlated. The relationship between pods per plant and 100 seed weight was shown to be significantly unfavorable.

Ahmad *et al.,* (2014) reported in 14 genotypes of mungbean, the genetic variation, heritability, and genetic advance expressed as a percentage of mean for variables that contribute to yield were examined (*Vigna radiata* L.). The number of pods per plant and the number of days to maturity had large genotypic and

phenotypic variations. Heritability was highest for seed output per plant and lowest for seed weight per 100 seeds. The additive gene effect for these features was demonstrated by strong heritability and high genetic progress as a percentage of mean for the number of pods per plant. The results of the analysis of variance for parameters revealed considerable variances for each and every variable taken into account. Variation already present may be useful for future breeding programme involving hybridization and selection.

Canci and Toker (2014) assessed the mungbean yield components. They discovered a significant correlation between grain weight and pod length and width. Pods per plant and branches per plant had a substantial and favourable relationship. The biological and straw yields were strongly correlated with the seed yield.

Lavanya *et al.* (2014) stated in a study of correlation in several mungbean genotypes for quantitative attributes. The relationship between yield and the factors that contributed to yield showed that the quantity of seeds produced per plant was positively correlated with days to maturity, plant height, and the number of pods per plant.

Singh and Kumar (2014) examined 12 attributes across 58 different genotypes. They discovered that the number of pods per plant, pods per cluster, clusters per plant, and the number of seeds per pod all exhibited highly significant and positive associations with seed yield per plant at both the genotypic and phenotypic levels. Days to maturity and days to 50% blooming only exhibited genotypically significant negative correlations with the amount of seeds produced per plant, respectively. Other variables, such as the number of branches per plant, the number of pods per cluster, and the weight of 100 seeds per plant, showed a positive and significant related to protein content but the seed production per plant did not.

Das and Barua (2015) examined 23 genotypes of green gram. The results demonstrated substantial positive associations between seed yield per plant at both the phenotypic and genotypic levels for seeds per pod, 100-seed weight, pods per plant, pod filling percentage, and pod length.

Naeem *et al*. (2015) examined ten mungbean genotypes for seed yield and characteristics associated to yield. The direct and indirect effects of several physical and economic features were calculated, as well as their correlation. They demonstrated a favourable correlation between seed yield per plant at the genotypic and phenotypic levels for traits such primary branches per plant, pods per plant, and days to 50% flowering. Additionally, they noticed that, at the phenotypic and genotypic levels, respectively, plant height and the number of seeds in each pod positively correlated with plant seed yield.

Dhoot *et al*. (2017) investigated in F2 populations of mungbean, correlations among quantitative features and their direct and indirect effects on seed yield. According to correlation analysis, seed yield was significantly and positively correlated with clusters per plant, primary branches per plant, clusters per plant, pods per plant, straw yield per plant, and harvest index in the F2 population of Mcha x Pusa Vishal and with plant height, primary branches per plant, clusters per plant, pods per plant, and harvest index in the F2 population of Mcha x GM-4.

Ghimire *et al*. (2017) demonstrated an experiment on seven mungbean genotypes were the subject for correlation and path research. The findings demonstrated a positive and significant correlation between seed yield and grain weight, biological yield, principal branches, and secondary branches. The factors that directly and most positively influenced seed yield were biological yield, pod length, days to 50% flowering, and number of grains per pod.

Ghosh *at el*. (2017) evaluated that the increased production of TDM was influenced by two plant characteristics, LA and CGR. According to the findings, high yielding mungbean varieties should have a larger LA, greater TDM production capacity, superior CGR at all growth stages, and high relative growth rate and net assimilation rate at vegetative stage, which would result in superior yield components. According to the association study, the traits that most contributed to yield were branches plant-1, pods plant-1, and pod length. For future mung bean yield improvement programs, selection based on the traits branches plant-1, pods plant-1, and pod length would be beneficial.

Hossain *et al*. (2017) observed the Crop Physiology and Ecology Research Field of Hajee Mohammad Danesh Science and Technology University, Dinajpur, an experiment was run to assess the leaf features and yield performances of mungbean (*Vigna radiata* L.) under various light levels. Leaf area was increased due to reduced light levels in all mugbean varieties but the increment was significant in only at 75% light intensity at 40 days after sowing. Due to reduced light levels, leaf dry weight was affected more in BINA Mung-5 and BU Mung-4 than BARI Mung-6 and BINA Mung-8. The leaf thickness was reduced under shade in all the mungbean varieties, except in BU Mug-4 at 75% light intensity, and the reduction in leaf thickness was mainly due to the reduction in thickness of spongy layer. The palisade layer thickness was influenced insignificantly but spongy layer thickness was increased in BINA Mung-5 at 100% light intensity. The grain yields (T/ha) of BARI Mung-6 and BINA Mung-8 remained stable under partial shade condition but the grain yield of BINA Mung-5 and BU Mug-4 was reduced drastically under partial shade condition. Higher leaf dry weight, number of pods / plant, seeds / pod and heavier grains in BARI Mung-6 and BINA Mung-8 contributed to the higher grain yield / plant under normal condition.

Kritika and Yadav (2017) investigated in ML-776 and MH 2-15 were used to create the 70 mungbean RILS (F. generation) that They discovered a substantial positive association between seed yield and plant height, number of branches per plant, number of pods per plant, number of seeds per pod, and weight of 100 seeds.

Rekha Sai (2017) found a correlation analysis was done using 31 mungbean genotypes for several physiological and contributing yield variables. Days to 50% flowering, days to maturity, plant height, number of clusters, number of pods, number of seeds per pod, 100 seed weight, harvest index, SPAD chlorophyll metre reading, relative water injury, relative injury percentage, chlorophyll content, specific leaf area, and seed yield plant-1 traits were all correlated. The breeder's ultimate interest in seed yield, which is thought to be a very complex feature, is revealed through correlation, which provides information on the size of the association of various component characters with seed yield. In this investigation, the magnitude of the phenotypic coefficient of variation was marginally greater than that of the

genotypic coefficient of variation. At both the phenotypic and genotypic levels, a highly significant positive correlation between seed yield and harvest index was found, followed by the traits SCMR, 100 seed weight, RWC, number of clusters plant-1, and number of pods plant-1, indicating that increasing these traits would directly increase the seed yield. In contrast, plant height, number of pods cluster-1, chlorophyll content, and specific leaf area showed a significant negative correlation with grain yield. Therefore, choosing high yielding mungbean genotypes under summer conditions would benefit greatly from selection based on these positively relevant features.

Divya Ramakrishnan *et al*. (2018) evaluated in 374 different genotypes of mungbean, 20 yield and yield-related factors. Following number of pods per plant, number of clusters per plant, and shelling %, association analysis revealed a substantial positive link between seed yield per plant and pod yield per plant.

Padol *et al*. (2021) estmated the genetic variability, heritability, genetic advance, correlation coefficient, and path coefficient analysis for yield and its component traits, twenty one genotypes of mungbean (*Vigna radiata* L. Wilczek) were studied. All of the genotypes for the studied characters showed a sizable level of genetic variation. Number of major branches per plant, 100 seed weight, and number of clusters per plant were all ranked higher than GCV and PCV. 100 seed weight, followed by the number of clusters per plant, plant height, and number of major branches per plant, were found to have high genetic progress and high heritability. The correlation coefficient and path analysis's combined findings showed that the number of primary branches per plant, 100 seed weight, biological yield, and harvest index are significant.

Parihar *et al*. (2018) investigated in 80 genotypes of mungbean and studied the relationships between several quantitative features. They discovered a strong positive association between days to 50% flowering, days to maturity, plant height, and pods per plant. The number of pods per plant correlates positively and significantly with plant height, the number of secondary branches per plant, and days to maturity. Days to maturity and the number of secondary branches per plant positively and significantly correlate with plant height.

Parsania *et al*. (2022) reported that after following chickpea and pigeon pea in importance is mungbean. They studied 19 mungbean genotypes that make up the experimental materials represent various geographic origins. To evaluate the genetic diversity, heritability, and genetic advancement in mungbean, the experiment was set up using a Randomized Block Design (RBD) with three replications for different variables. All eleven of the characters had a highly significant difference, according to the analysis of variance. In terms of seed yield per plant, branches per plant, and pods per cluster, higher heritability together with strong genetic progress as a percentage mean are seen. This demonstrates increased additive gene action, which suggests that direct intervention could result in improvement.

2.3 Role of enzyme *α*-amylase in seed quality of mungbean:

Bain and Mercer (1966) evaluated the cotyledons of germination-stage seeds and seedlings in pea, -amylase and soluble sugar are responsible for the embryo growth that led to seedling growth.

Abdul-Baki and Anderson (1972) reported the seed viability and enzymes were found to be correlated. Seed viability decreases due to enzyme activity as a result of physiological and biochemical degradation. Additionally, they reported that this enzyme activity causes the embryo to die.

Wadhawa *et al*. (1988) studied and reported that encapsulating groundnut seeds in either nitrocellulose (NC) or ethylene cellulose (EC) had a substantial impact on the mobilisation of reserve material during seed germination. Following seed encapsulation, the activity of the enzymes lipase, α-amylase, and invertase increases while the activity of the enzyme protease decreases, resulting in modest levels of protein breakdown during the early stages of germination (0-9 days after sowing). When using NC-encapsulation, hydrolysis is transmitted to the growth axis more quickly while EC-encapsulation increases isocitratelyase activity.

Shigeshi *et al*. (1991) evaluated the fluctuations in α-amylase activity in rice (*Oryza sativa* L.) seed over the course of the grain's 18 days of germination in a dark environment. In vitro testing was done to determine the effect of α-amylase activity. After germination, rice's α-amylase activity was initially noted on the fourth day, and it significantly increased on the 12th and 16th days.

Desai (2004) reported starch is the main form of stored carbohydrate present in the majority of seeds. Starch, which is frequently present as amylose and amylopectin, is hydrolytically broken down by α-amylases and β-amylases.

Rahman *et al*. (2009) investigated the enzyme activity and seed storage degradation in a number of chickpea seed variations at varied germination times. Hydrolytic enzymes such amylase, invertase, protease, and lipase are activated during germination in order to use the substance employed to store the seeds for seedling growth. These enzyme activities were found to be related to growth, vigour index, and germination percentage.

Mohankumar and Manonnmani (2011) showed the increased α-amylase activity in primed sunflower seeds may be due to proper hydration during imbibitions, which encourages faster germination, improved germination uniformity, and higher seedling dry weight.

Ghavidel and Mehdi (2011) evaluated the phytase, α-amylase, and protease activity in untreated, soaked, and germinated (for 24, 48, and 72 hours) legume seeds were studied, according to With the exception of chickpea phytase activity, which did not significantly change after pre-germination soaking, enzyme activities increased. The enzymatic activity of all legumes rose markedly and peaked for up to 72 hours during germination. Mungbean protease activity, however, peaked 48 hours after germination and subsequently started to decline. All bean seeds had higher levels of enzyme activity after the biotechnological germination process.

Chandrika *et al*. (2013) stated that enzyme activity is necessary for each stage of plant development, starting with the initial responses to seed germination. The enzyme's overall antioxidant activity peaked in partially purified germinated seed at 304 µg/ml. The seeds that have germinated exhibit the highest levels of enzymatic activity and can be employed in a range of industrial processes.

Deshmukh (2013) looked at the seed quality and biochemical indicators of freshly harvested soybean seeds from the JS-335 and MAUS-71 kinds during storage for up to 120 days. The showed that at 0, 60, and 120 days of storage, the soybean variety JS-335 had higher seed amylase activity than variety MAUS-71, and that amylase activity declines with longer storage intervals up to 120 days.

Awatif and Allaeldin (2017) reported that the productivity of plants can be predicted in part by the seed germination stage of plant development. The rate of seedling survival and vegetative growth, which in turn affect yield and quality, are significantly correlated with physiological and biochemical changes that occur during germination. The goal of this study is to concentrate on how the most important metabolic processes—reserve mobilisation, phytohormonal regulation, glyoxylate cycle, and respiration—proceed under stressful and non-stressful conditions in order to make suggestions for and carry out the more effective experimental advancements. When a seed is ingested, many metabolic processes are activated, including the creation of hydrolytic enzymes that cause the hydrolysis of reserve food into a simple form that the embryo can absorb. Abiotic stresses may have an impact on seed germination and seedling establishment through a variety of mechanisms, including decreased water availability, modifications in the mobilisation of reserve energy, changes in the hormonal balance, and modifications to the protein structure.

Wei Yu *et al*. (2020) evaluated the protein concentration in mungbean sprouts was lower than that in the seeds (37.59 mg/mL), which may be because the storage proteins were continuously hydrolyzed by the activated mungbean proteases to provide the nutrition required for seed germination and seedling growth.

Padilhal *et al.,* (2021) revealed their studies abiotic stress circumstances, seeds with high vigour exhibit a stronger potential for hydrolysis and mobilisation of stored reserves, which leads to the development of vigorous seedlings. In order to determine the relationship between this enzyme and the vigour of the seed lot under these circumstances, this study proposes to analyse the association of the enzyme alpha-amylase in lots of common-bean seeds with differing vigour. All the investigated characteristics were found to be negatively impacted by the stress situation, but the cultivars classed as having greater vigour demonstrated improved physiological performance under stress, according to the results. Alpha-amylase activity during germination is decreased by salt stress in common-bean seeds, whereas high-vigor seed lots showed increased enzyme activity in the absence of stress.

Matheus Santin Padilha *et al.* (2021) investigated characteristics were negatively impacted by the stress situation, as demonstrated by ; however, cultivars with higher vigour demonstrated improved physiological performance under stress. Common bean seeds that have been exposed to salt stress perform worse and have less -amylase activity during germination. High vigour seed batches showed more enzyme activity in the absence of stress.

Sumera *et al*., (2021) evaluated the hydrolysis of proteins and starches both helps to effectively mobilise seed stores and start seed germination. We investigated the hydrolytic enzyme activities in mung bean (*Vigna radiata*) seeds that were germinating after being exposed to cadmium stress at 0, 25, 50, 75, and 100 mg. L-1. In comparison to controls, exposure to Cd stress reduced the rate of seed germination and early seedling growth parameters such root and shoot length and plant fresh and dry biomass. In comparison to root length, the negative effects of Cd were more obvious in shoot length. With increasing Cd exposure, seedling -amylase and protease activity significantly decreased. Additionally, we observed a decrease in total soluble proteins and carbohydrates due to Cd, although there was an increase in the content of free amino acids. The reduction of seedling germination and early growth features was mostly caused by a decrease in the hydrolysis process of reserve carbohydrates, proteins, and reduced reserve translocation.

2.4 Role of enzyme dehydrogenase in seed quality of mungbean:

Burke *et al.* (1982) developed a method was to partially purify succinate dehydrogenase from the cotyledons of soybean (*Glycine max* [L] Merr. v. Ransom) and mung bean (*Vigna radiata* L.) plants. Triton X-100 extraction and ammonium sulphate precipitation were used in the technique. The final fraction contained a b-type cytochrome, two polypeptides with molecular weights of roughly 67,000 and 30,000 daltons each, a pH optimal range of 7.0 to 7.5, and the ferredoxin-type and high potential iron-sulfur protein-type electron paramagnetic resonance signals that have been associated with the iron-sulfur centres of mammalian succinate dehydrogenase. Oxaloacetate and malonate had inhibition values of 1.15 and 24.6 micromolar, respectively.

Moore (1988) recorded in the work, a non-dissociating gradient polyacrylamide-gel-electrophoresis approach that was recently developed [Kuonen, Roberts, and Cottingham (1986) Anal. Biochem. 153, 221-226] is used to analyse plant mitochondrial NADH dehydrogenases. On 3-22% (w/v) gradient polyacrylamide gels with 0.1% Triton X-100, solubilized submitochondrial particles from the mung bean (*Phaseolus aureus*) were examined and labelled for various NADH dehydrogenase activity. On the basis of co-migration with the pure mammalian enzyme, a rotenone-sensitive NADH dehydrogenase (Complex I) was discovered.

Sugimoto and Morohashi (1989) studied and reported in mung bean and cucumber cotyledons, the emergence of mitochondrial NAD+-malate dehydrogenase (EC 1.1.1.37) was observed. utilising the antibodies produced in opposition to it, both during and after germination. Between the two, the developmental patterns were very dissimilar. 3–4 days after the start of imbibition, the amount of mitochondrial malate dehydrogenase in cucumber continued to rise. This was caused, at least in part, by the enzyme protein being actively synthesised, and the synthesis appeared to be controlled by the availability of the enzyme's translatable mRNA.

Dacha, *et al.* (1999) According to some, yellow soybean seeds are of a higher calibre than green soybean seeds. Because dehydrogenase enzymes are responsive to the decrease of seed moisture, the formazzan extraction approach can be used to assess seed viability and demonstrate the presence of dehydrogenase enzymes in soybean seeds. There was a strong positive association between seed viability and the quantity of dehydrogenase enzymes already present. As a result, picking the ideal planting date is essential for the development of soybean seeds. Extremely hot conditions should also be avoided during harvesting since they hasten drying and impede enzyme activity during germination.

Verma *et al*. (2003) evaluated *Brassica campestris* seeds of two promising cultivars, Sangam and TH 68, were kept for 4 years in ambient circumstances. According to these two kinds, each with four seed lots, were examined for several aspects of seed quality. Results showed that in seeds that were 1 and 2 years old, the germination percentage of both of these types remained over

the allowed Minimum Seed Certification Standard (85.00%) level. Seed yield (q/ha), seed viability (%), dehydrogenase activity test, respiration rate (µlO2/seedling/h), oil content (%), pH of the seed leachates, total protein (mg/g), and peroxidase enzymes (unit g 1 Fr. wt.min1) significantly decreased as the seed yield increased.

Aniszewski (2010) reported in *Phaseolus lunatus* seed testa enzyme assays demonstrate succinate dehydrogenase (SDH) and acid phosphatase (ACP) activity. Testa strata may be actively involved in imbibitions and the early nutritional stage of germination based on the strong enzyme activity in the meso and endotesta and the mobilisation of vesicles in the mesotesta.

Aurellia Tatipata (2010) demonstrated that the quality of soybean seeds rapidly deteriorated, making long-term storage difficult. It uses three elements: storage period, moisture content (8, 10 and 12 percent), and packing materials (polythene, wheat, and aluminium foil) (0, 1, 2, 3, 4, 5 and 6 months). Additionally, it was demonstrated that raising the initial seed moisture level above 8% can result in a decrease in the specific gravity of succinate dehydrogenase. Soybean seeds stored in aluminium foil bags showed better viability, succinate dehydrogenase and cytochrome oxidase specific activities, and coefficient of velocity of germination than seeds stored in polythene or wheat bags. In order to prevent seed degeneration, seeds were also kept at low moisture content.

Bozena and Jan (2010) reported that the Polyethylene glycol (PEG) decreased α-amylase activity after 14 hours of incubation. The overall dehydrogenase activity increased after 20 hours of incubation under a water deficit, whereas the α-amylase activity decreased after 14 to 20 hours. After 20 hours of incubation, the α-amylase activities of the treatments were identical. Gibbrelic acid (GA3) and ethephon had no effect on the activities of α-amylase or dehydrogenase.

Reddy *et al*. (2010) according to research on the effects of ageing on seed quality parameters and biochemical components of two wheat genotypes, it was discovered that biochemical parameters such as total soluble protein, total soluble sugar, total lipids, total micronutrients, and enzymes like total dehydrogenase and α-amylase activities were also found decreased during the ageing of wheat seed.

Biswas *et al*. (2011) evaluated pre-storage dry seed invigoration treatment with powdered pharmaceutical formulation, including aspirin @ 50 mg/kg of seed, bleaching powder @ 2 g/kg of seed, red chilli powder @ 1 g/kg of seed, neem/leaf powder, and spinach powder @ 29 /kg of seed, as well as mid-storage wet seed treatment, were reported to significantly reduce the loss of vigour and viability of high-vigor onion seeds during storage under ambient The medication decreased the levels of sugar and electrolytes while increasing the dehydrogenase enzyme activity in comparison to the untreated control group.

Deshmukh (2013) to examined newly harvested soybean seeds from the JS-335 and MAUS-71 types were used in a study by seed quality and biochemical indicators after storage for up to 120 days. The study found that the soybean variety JS-335 had higher seed dehydrogenase activity than variety MAUS-71 at 0, 60, and 120 days of storage, and that dehydrogenase activity declined as storage time rose up to 120 days.

Salimath *et al.* (2016) reported the stored of seeds in polylined gunny bags and discovered that HDPE had the highest dehydrogenase enzyme activity (0.467 OD value) (0.448 OD value). For seeds stored in cotton bags, dehydrogenase enzyme activity absorbance was found to be lower (0.435 OD value).

Singhal *et al*. (2017) investigated the three seed lots were used in the experiment, including newly harvested seed (Lot-1), seed that had been stored for a year (Lot-2), and seed that had been stored for two years, according to the impact of natural storage on seed deterioration, all the seed lots were examined for various seed quality criteria, including the Tetrazolium test (viability%), pH exudate test (%), Dehydrogenase activity test (OD g-1 ml-1) and Electrical conductivity test (S cm-1 seed-1). Except for electrical conductivity, which showed a considerable rise as seed age increased due to loss of membrane integrity, the results showed that the value of other seed quality metrics decreased significantly as seed age increased.

Kittiwan Klarod *et al.* (2021) reported in tomato seed lots that the low quality seeds coated with all concentrations of PNF had significantly increased Total Dehydrogenase activity at 48 hrs after seed imbibitions, and low quality seeds coated with PF1 and PF4 had significantly increased.

CHAPTER -III

MATERIAL AND METHODS

CHAPTER-III

MATERIALS AND METHODS

The present investigation entitled "**Dormancy Studies in *in-situ* Germination in Mungbean (*Vigna radiata* L.)**" has been undertaken during *kharif* 2020 and *kharif* 2021at experimental field of Department of Agricultural Botany, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani. The material and methods for this experiment is described as under.

3.1 Experimental layout

This experiment has completed in both seasons in black soil of the experimental field of the Department of Agricultural Botany, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani during *kharif* 2020 and *kharif* 2021. The sowing dates of this experiment were 29/06/2020 in *kharif* 2020 and 24/06/2021 in *kharif* 2021. The experiment arranged in randomized block design (RBD) with two replications and every treatment has four rows of 4.5 meter long with 45 cm distance in between rows. The package of practices was carried out as per recommendation for raising the good crop condition.

3.2 Experimental material

The experimental material included in the present study comprised of 34 genotypes including checks were collected from the Agriculture Research Station, Badnapur, VNMKV, Parbhani and Pulses Research Unit, Dr. PDKV, Akola. Genotypes and checks involved in the present investigation are presented in Table 3.1.

3.3 Sampling

From each plot of each replication, observations on field level were taken of five randomly plants of all the quantitative characters except days to 50% flowering, days to maturity and days to shattering. The laboratory work has completed at the laboratories of Seed Technology, Department of Agricultural Botany

and Soil Science and Agricultural Chemistry, College of Agriculture, VNMKV, Parbhani.

3.4 Experimental details

1.	Experiment design	:	Randomized Block Design
2.	No. of replications	:	Two
3.	No. of genotypes	:	34
4.	Spacing (cm)	:	45 X 10
5.	No of rows per plot	:	04
6.	Plot size	:	0.90 X 4.5 m^2
7.	Fertilizer dose	:	25: 50: 00 Kg N: P: K kg/ha

3.5 Observations recorded:

Five random competitive plants excluding border ones were selected from each plot in each replication to record observations. The twenty three characters were recorded in the field and laboratory and the mean values were subjected for statistical analysis. The data following on yield, yield components and seed quality characters were recorded.

3.5.1 Morphological characters:

3.5.1.1 Days to 50 % flowering

The number of days taken from sowing to the opening of flowers in 50 percent of plant in each plot was recorded. The lines were classified into three categories as early (< 35.00 days), medium (35.00 to 40.00 days) and late (> 41.00 days).

3.5.1.2 Days to maturity

The total number of days taken from date of sowing to complete maturity was taken as days to maturity. The lines were classified into three categories as early (< 62.00 days), medium (63.00 to 74.00 days) and late (> 75.00 days)

Table 3.1: Experimental material (genotypes and checks) used in the study

Sr. No.	Genotypes & checks	Source
1	Phule M 707-5	MPKV, Rahuri
2	AKM-12-14	Dr. PDKV, Akola
3	Phule M 602-9	MPKV, Rahuri
4	AKM-12-24	Dr. PDKV, Akola
5	BM-2019-1	VNMKV, Parbhani
6	Phule M 702-1	MPKV, Rahuri
7	AKM-1609	Dr. PDKV, Akola
8	AKM-1603	Dr. PDKV, Akola
9	AKM-1602	Dr. PDKV, Akola
10	Phule M 816-10	MPKV, Rahuri
11	Phule M 817-13	MPKV, Rahuri
12	TBM-4	BARC, Trombay
13	TBM-6	BARC, Trombay
14	AKM-12-28	Dr. PDKV, Akola
15	TBM-10	BARC, Trombay
16	TBM-127	BARC, Trombay
17	Phule M 809-12	MPKV, Rahuri
18	AKM-12-23	Dr. PDKV, Akola
19	Phule M 818-8	MPKV, Rahuri
20	Phule M 809-10	MPKV, Rahuri
21	Phule M 402-2-1	MPKV, Rahuri
22	Phule M 504-20-27	MPKV, Rahuri
23	AKM-1606	Dr. PDKV, Akola
24	AKM-1605	Dr. PDKV, Akola
25	AKM-1608	Dr. PDKV, Akola
26	BM-4 (Ch)	VNMKV, Parbhani
27	BPMR-145 (Ch)	VNMKV, Parbhani
28	BM-2002-1(Ch)	VNMKV, Parbhani
29	BM-2003-2(Ch)	VNMKV, Parbhani
30	PKVM-4 (Ch)	Dr. PDKV, Akola
31	PKVM-8802 (Ch)	Dr. PDKV, Akola
32	PKV Green Gold (Ch)	Dr. PDKV, Akola
33	Vaibhav (Ch)	MPKV, Rahuri
34	Utkarsh (Ch)	MPKV, Rahuri

3.5.1.3 Days required for shattering

Total number of days taken from the date of sowing to the shattering of pods in field. The lines were classified into three categories as early (< 75.00 days), medium (76.00 to 84.00 days) and late (> 85.00 days)

3.5.1.4 Plant height (cm)

The height of the fully matured plant from the base of the plant to the tip of the inflorescence measured in cm for plant height. The lines were classified into three categories as dwarf (<41.00 cm), medium (41.00 to 55.00 cm) and tall (> 56.00 cm) (Jadhav, R. A. 2019. *Ph.D. Thesis*. VNMKV, Parbhani).

3.5.2 Yield contributing characters:

3.5.2.1 Number of primary branches per plant

Total number of branches arising from the main stem at harvest was recorded. Based on the number of primary branches genotypes were classified as more number of primary branches (> 4.00), medium (3.00-4.00) and less number of branches (< 3.00).

3.5.2.2 No. of pods per cluster

The number of pods in individual cluster were counted from the selected plants and mean calculated. Based on the number of pods per cluster the genotypes were classified as less number of pods per cluster (< 4.00), Moderate (4.00-5.00) and high (> 5.00).

3.5.2.3 Number of pods per plant

The total number of seed bearing pods in the selected plants were counted at maturity and mean calculated. Genotypes were classified on the base of number of pods per plant into following three categories *viz.* less (<25.00), medium (26.00-38.00) and high (> 39.00).

3.5.2.4 Length of Pod (cm)

Ten randomly selected pods from each of the selected plants were taken and the lengths of each five pods measured in centimeter. Genotypes were classified on the base of length of pod (cm) into following three categories *viz.* short (< 7.00 cm), medium (7.00-9.00 cm) and long (> 9.00 cm).

3.5.2.5 No. of Seeds per Pod

The randomly selected five pods from each of the selected plants were taken and the number of seeds per pod was counted. Based on the number of seeds per pod the genotypes were classified as less seeded (< 13.00), Moderate (13.00-15.00) and more seeded (> 15.00).

3.5.2.6 100 Seed Weight (g)

The weight of 100-seeds drawn at random was recorded and expressed in gram. Based on the observation of 100 seed weight (g) genotypes were grouped in to following three categories *viz.* small sized (< 5.00 g), medium sized (5.00-6.00 g) and bold sized (> 6.00 g).

3.5.2.7 Seed yield per plant (g)

Total weight of seed from the selected five plants were recorded and expressed on per plant basis in grams.

3.5.2.8 Biological yield per plant (g)

After harvesting and sun drying of all the selected five plants were weighted separately in gram and averaged. Genotypes were classified on the base of biological yield (g) into following three categories *viz.* low (< 25.00 g), medium (26.00-40.00 g) and high (> 41.00 g).

3.5.2.9 Harvest index (%)

Economic yield was the seeds obtained from five observational plants. The plants were dried and weighted to constitute biological yield. The biological yield

(total dry matter after harvesting and sun drying) and seed or grain yield of each plant was recorded in grams and the harvest index was calculated as follows:

Harvest index (%) = Grain yield (gm)/Biological yield (gm) x 100

Genotypes were classified on the base of harvest index % into following three categories *viz.* low (< 25.00 %), medium (26.00-35.00 %) and high (> 36.00 %).

3.5.3 Seed quality characters:

3.5.3.1 Germination percentage (%)

Germination percentage was recorded by using rolled towel paper method. The 100 seeds were placed in four replications on moist towel paper, rolled properly and kept in seed germinator at constant temperature (25^{o}C) and relative humidity(80%). Final germination recorded on 8th day and germination expressed in percentage (ISTA 1999).

3.5.3.2 Hard seed (%)

Final germination recorded on 8th day and present of hard seeds in test expressed in percentage (ISTA 1999).

3.5.3.3 Time for opening of pods (hrs)

The 5 pods of each entry were kept in petriplates which had dipped in water and recorded the time of opening of pods in hours.

3.5.3.4 Seedling length (cm)

The germinated ten seedlings were taken and counted the length in cm.

3.5.3.5 Vigour index - I

Seedling vigour index I was calculated as per formula given by ISTA (1976)

VI - I = Germination percentage (%) x Mean seedling length (cm)

3.5.3.6 Seedling dry weight (g)

The same samples used for seedling length were dried in oven at 80°c for 24 hrs and allowed to cool for 30 minutes. The mean dry weight of the seedlings was recorded and expressed in grams.

3.5.3.7 Vigour index - II

Seedling vigour index II was calculated as per formula given by ISTA (1976).

VI - II = Germination percentage (%) x Mean seedling dry weight (g)

3.5.3.8 Seed hardness (Kg/cm^2)

Random ten seeds of each genotypes were tested to record the seed hardness in Kg/cm^2 through seed hardness tester.

3.5.3.9 Alpha amylase (mg/g)

The α-amylase enzyme activity was assayed as per the procedure given by Bernfed (1955).

Reagents:

1. 95% Ethanol
2. Distilled water
3. 1 N NaOH
4. 100 ml volumetric flask
5. 1 N Acetic acid
6. Water bath
7. Iodine-Potassium iodide solution
8. Spectrophotometer
9. Standard amylase

Composition of reaction mixtures:

A. 1 N NaOH solution: Dissolve 40 g of NaOH in 1000 ml distilled water.

B. 1 N Acetic acid solution: Dilute 57.5 ml glacial acetic acid to 1000 ml using distilled water.

C. Iodine- Potassium iodide solution: Dissolve 0.26 g of iodine in 10 ml of potassium iodide solution containing 2.6 g of KI.

D. Standard amylase solution: Take 40 mg of pure potato starch (amylase) in a 100 ml volumetric flask and add 1 ml of 95% ethanol and 9.0 ml of 1 N NaOH. Shake well and boil over water bath for 10 minutes and make up the solution to 100 ml using distilled water.

Procedure:

1. Weigh 100 mg well powdered milled mungbean in to 100 ml volumetric flask. (1g powder used in this experiment)
2. Add 1 ml 95% ethanol and 9 ml of 1 N NaOH.
3. Heat the sample for 10 minutes in boiling water bath, cool it and make up the volume to 100 ml by adding distilled water.
4. Pipette out 5 ml from the 100 ml solution into another 100 ml volume flask.
5. Add 1 ml 1 N acetic acid and then 2 ml iodide solution and make the volume to 100 ml.
6. Shake, stand for 20 minutes and determine the percent transmittance at 620 nm using a colorimeter.
7. Prepare a series of standard starch solution containing 0, 20, 40, 60, 80 and 100 % amylase as in the steps 1 to 5.
8. Read the transmittance of the standards at 620 nm and plot a standard graph.
9. Amylase content of the sample was determined in reference to the standard curve and expressed on percent basis.

Making of amylase standards:

1. Pipette out 1, 2, 3, 4, and 5 ml of the standard amylase into 100 ml volumetric flasks in three replications.

2. Keep one flask as blank without adding anything.

3. Add 1 ml 1 N acetic acid and 2 ml I-KI solution to all the flasks including blank.

4. Make up all the flasks to 100 ml using distilled water and cover all the flasks with a black cloth or aluminium foil to prevent direct light exposure as I-KI disintegrates on exposure to light.

5. Keep for 20 minutes and take reading at 620 nm in a spectrophotometer.

6. The standards including blank, correspond to 0%, 4%, 8%, 12%, 16% and 20% of amylase.

7. Draw a standard curve using the absorbance reading.

8. A calibration curve was established with standard maltose (0.2 to 2.0 ml. of distilled water) and used to convert the colorimeter reading into mg of maltose. The activity was expressed as up of maltose liberated mg-1 of protein.

Calculation

One unit of α–amylase is expressed as mg of maltose released per min. per gram of sample (mg/g).

3.5.3.10 Dehydrogenase (µg/g)

The dehydrogenase activity of mungbean seed was assessed by method suggested by Thimaya (1990).

Reagents:

1. Prepare 2, 3, 5–Triphenyl Tetrazolium Chloride (TTC solution of 3% concentration).

2. Take 3 gm TTC in 100 ml of distilled water and volume up to 100 ml. and store in amber colour bottle.

3. Take Methanol- 10 ml in each test tube (%)

4. Prepare glucose 1% solution by taking 1 gm glucose dissolved in 100 ml volumetric flask by using distilled water and final volume was made up to 100 ml.

5. Prepare standard Triphenyl Formazan (TPF) of 100 ppm concentration by using 100 mg of standard Triphenyl Formazan dissolved in 100 ml of distilled water and volume was made up to 100 ml.

Materials:

1. Air tight screw cap test tubes

2. Absorbance

3. Incubator

4. Amber colour bottle

5. Beaker

Procedure:

1. Take 1 gm of mungbean seed powder sample in air tight screw cap test tube.

2. Add 0.2 ml TTC in each test tube.

3. After sometimes, add 0.5 ml of glucose in each test tube.

4. Solution was incubated at 28 + 0.5 ^{0}C for 24 hrs.

5. Add 10 ml methanol in each test tube and shake vigorously. Pink colour supernatant liquid was occurred.

6. The absorbance was recorded at 485 nm.

7. Extrapolate the amount of TPF formed standard curve drawn in the range of 10 - 90 ug TPF ml-1.

8. Result expressed in ug TPF h-1 g-1 mungbean.

Calculation

One unit of dehydrogenase is expressed as ug TPF h-1 g-1 standard curve released per min. per gm. of sample (ug/g). (Autade, A. D. 2018. *Ph.D. Thesis*. VNMKV, Parbhani).

3.6 Statistical analysis:

The statistical analysis of data was carried out as per the standardmethod suggested by Panse and Sukhatme (1989).

The analysis of variance for each character was carried out as indicated below

Table 3.2: Analysis of variance for experimental design

Source of variation	d. f.	Sum squares	Mean sum of squares	Expected M.S.
Replications	(r–1)	SS_1	M_1	$\sigma^2 e + g\sigma^2 r$
Genotypes	(g–1)	SS_2	M_2	$\sigma^2 e + r\sigma^2 g$
Error	(r–1)(g–1)	SS_3	M_3	$\sigma^2 e$
Total	(rg–l)	--	--	--

Where,

r = Number of replications

g = Number of genotypes

σ^2 e = Error variance

σ^2 r = Variance due to replications

σ^2 g = Variance due to genotypes

The different sum of squares were divided by their respective degrees of freedom to obtain mean squares were tested against error mean square employing 'F' test.

Various calculations are carried out as under:

i) CF (Correction Factor) = GT^2/N

ii) TSS (Total SS) = $\Sigma \Sigma X^2$-CF

iii) RSS = $\Sigma RT^2/g$-CF

iv) GSS = $\Sigma T^2/r$-CF

v) ESS = TSS-RSS-GSS

vi) EMS = ESS/(g-1) (r-1)

vii) F (Calculated) = GMS/EMS

Table 3.3: Scales for Path Coefficients (Lenka and Mishra 1973)

Value of Direct or Indirect Effects	Rate or Scale
0.00 to 0.09	Negligible
0.10 to 0.19	Low
0.20 to 0.29	Moderate
0.30 to 0.99	High
More than 1.00	Very high

3.7 Correlation analysis:

The simple correlation is estimated by Pearson method.

CHAPTER -IV

RESULTS AND DISCUSSION

CHAPTER - IV

RESULTS AND DISCUSSION

Yield is a complex character and dependent on many component traits. Hence it is necessary to have knowledge on the extent of association between yield and yield contributing characters. Expression of various traits often varies with breeding materials and environments. Therefore, the information on character association between the traits themselves and with the yield for the specific breeding material being used at a particular location is important for breeding high yielding genotypes. The success of any breeding programme depends upon the quantum of genetic variability present in the population. Wider range of genetic variability helps in selecting desired genotypes.

Seed dormancy is an important character in mungbean, where rains often occur at the time of harvest, non dormant cultivars frequently germinate *in-situ* on the standing crop. The significance of seed dormancy lies in the ability of the seed to overcome the unfavorable conditions so as to remain viable till the commencement of favorable environment. Seed dormancy is a state in which seeds fail to germinate even under favorable conditions of (moisture, temperature and oxygen for germination) (Wareing, 1963).

The pre-harvest germination of the mungbean causes considerable losses due to sprouting of seeds in pods. Sometime losses due to pre harvest sprouting will be as high as 60-70% (Durga & Kumar, 1997). Seed quality in mungbean can be deteriorated substantially by *in-situ* germination under unpredictable rainfed environments. The *in-situ* germination after showers of rains at the time of harvesting leads to loss of seed quality in mungbean. This drawback can be overcome by inducing fresh seed dormancy. Mungbean seeds though protected inside the pods are susceptible to pre-harvest sprouting (PHS) following rainfall due to lack of fresh seed dormancy (FSD) which deteriorates the quality of the seed.

For the success of the breeding programme first pre-requisite is to pool the genotypes from diverse eco-geographical regions and further

studying the extent of genetic diversity, for yield, yield attributes and innovative trait like seed dormancy for meaningful utilization of the donors in the breeding programme. In the integrated structure of a plant, most of the characters are inter-related. Hence, direct selection based on yield alone is not very effective and it has been pointed out that it would be more meaningful if the structure of yield is probed through its components rather than directly.

The knowledge of genetic variability and relationship among various quantitative characters is helpful in deciding the selection criteria to bring out the possible improvement. Genetic variation of important traits can be used for crop improvement only when it is considered in relation to non-genetic variation. Number of studies in mungbean by several workers revealed wide variation for various agronomic traits. Yield is a genetically controlled complex character and is determined by number of component traits which are also quantitatively inherited.

The present investigation was undertaken with assess the dormancy in mungbean, the entitled **"Dormancy Studies in *in-situ* Germination in Mungbean (*Vigna radiata* L.)".** The observations of yield contributing characters *viz.* days to 50% flowering, days to maturity, days to shattering, number of primary branches, number of pods per cluster, number of pods per plant, length of pods (cm), number of seeds per pod and seed yield per plant (g) were taken at field whereas, seed quality parameters *viz.,* germination percentage, seedling length (cm), seedling dry wt. (g), vigour index I (%), vigour index II (%) and biochemical parameters viz., α-amylase and dehydrogenase activities were completed in laboratories of Seed Technology, Department of Agricultural Botany and Agri. Chemistry and Soil Science, Department of Agricultural Chemistry and Soil Science, VNMKV, Parbhani in *kharif* 2020 and *kharif* 2021 seasons and results are presented in the form of summarized data on yield and their attributes and quality characters of seed, which are statistically analyzed and presented in this chapter under different headings.

4.1 Analysis of variance

4.2 Range and mean performance of genotypes

4.3 Estimation of correlation

Table 4.1: Analysis of variance for randomized block design for different characters in an individual season and over a pooled mean in mungbean

Sr. No.	Characters	Location	Source of variation		
			Replication	Genotypes	Error
			d. f. (1)	d. f. (33)	d. f. (33)
1	Days to 50% flowering	*kh*-2020	3.31	4.92**	1.01
		kh-2021	0.72	6.64**	1.02
		Pool	2.01	5.78**	1.01
2	Days to maturity	*kh*-2020	0.49	9.96**	5.80
		kh-2021	0.53	10.27**	6.35
		Pool	0.51	10.11**	6.08
3	Days to shattering	*kh*-2020	3.31	20.58**	0.85
		kh-2021	3.37	44.14**	0.94
		Pool	3.33	32.36**	0.89
4	Plant height (cm)	*kh*-2020	120.18	260.27**	16.19
		kh-2021	115.25	239.65**	15.57
		Pool	117.71	249.96**	15.88
5	No. of primary branches	*kh*-2020	0.83	1.98**	0.04
		kh-2021	0.92	2.37**	0.03
		Pool	0.42	2.17**	0.05
6	No. of pods/cluster	*kh*-2020	0.17	0.74**	0.06
		kh-2021	0.13	0.71**	0.04
		Pool	0.15	0.72**	0.05
7	No. of pods/plant	*kh*-2020	7.18	64.63**	1.98
		kh-2021	9.94	60.31**	2.44
		Pool	8.56	62.47**	2.21
8	Length of pods (cm)	*kh*-2020	0.12	7.36**	0.09
		kh-2021	0.13	7.37**	0.05
		Pool	0.11	7.36**	0.07
9	No. of seeds/ pod	*kh*-2020	0.08	4.85**	0.45
		kh-2021	0.16	4.96**	0.27
		Pool	0.12	4.90**	0.36

Table: 4.1 Contd…

Sr. No.	Characters	Location	Source of variation		
			Replication	Genotypes	Error
			d. f. (1)	d. f. (33)	d. f. (33)
10	100 seed wt. (g)	*kh*-2020	0.01	0.86**	0.00
		kh-2021	0.01	0.74**	0.00
		Pool	0.01	0.80**	0.00
11	Seed yield/plant (g)	*kh*-2020	1.25	12.07**	0.64
		kh-2021	1.17	11.39**	0.87
		Pool	0.71	11.73**	0.75
12	Biological yield/plant (g)	*kh*-2020	2.44	32.42**	2.32
		kh-2021	3.33	29.09**	1.79
		Pool	2.89	30.75**	2.06
13	Harvest index (%)	*kh*-2020	19.20	130.57**	7.22
		kh-2021	17.48	107.28**	5.97
		Pool	18.34	118.92**	6.60
14	Germination %	*kh*-2020	13.24	53.55**	4.33
		kh-2021	0.06	47.63**	3.79
		Pool	6.65	50.59**	4.06
15	Hard seed %	*kh*-2020	0.30	125.22**	5.35
		kh-2021	0.40	111.35**	4.22
		Pool	0.35	118.28**	4.78
16	Pod opening time (hrs)	*kh*-2020	0.06	1253.4**	0.04
		kh-2021	0.04	1107.0**	0.03
		Pool	0.05	1180.2**	0.04
17	Seedling length (cm)	*kh*-2020	0.36	13.47**	8.22
		kh-2021	12.77	14.69**	6.31
		Pool	6.56	14.08**	7.27
18	Vigour Index I	*kh*-2020	3469.27	290725.22**	1685.56
		kh-2021	3633.13	304445.25**	1765.15
		Pool	3554.00	297585.23**	1681.15

*,**- Significant at 5 per cent and 1 per cent level respectively

Table: 4.1 Contd…

Sr. No.	Characters	Location	Source of variation		
			Replication	Genotypes	Error
			d. f. (1)	d. f. (33)	d. f. (33)
19	Seedling dry wt. (g)	***kh*-2020**	0.00	0.02**	0.00
		***kh*-2021**	0.00	0.02**	0.00
		Pool	0.00	0.02**	0.00
20	Vigour index II	***kh*-2020**	2.85	321.65**	13.01
		***kh*-2021**	3.24	366.03**	14.44
		Pool	3.07	343.84**	13.22
21	Seed hardness (Kg/cm^2)	***kh*-2020**	0.00	0.32**	0.03
		***kh*-2021**	0.07	0.38**	0.03
		Pool	0.04	0.35**	0.03
22	α-amylase (mg/g)	***kh*-2020**	1969.94	13106.36**	17.49
		***kh*-2021**	926.49	12021.11**	23.30
		Pool	1448.21	12563.73**	20.40
23	Dehydrogenase (µg/g)	***kh*-2020**	17.50	8659.77**	39.77
		***kh*-2021**	22.62	8174.37**	46.79
		Pool	20.06	8417.07**	43.28

*,**- Significant at 5 per cent and 1 per cent level, respectively

4.1 Analysis of variance

The mean values of observations recorded were subjected to analysis of variances for randomized block design in individual season & over pooled (Table 4.1) revealed that mean squares due to genotypes found significant for all the characters in all environments.

The variations due to genotypes were significant for all the characters under study both at 5% and 1% probability levels in both seasons. The significant differences in characters indicate the presence of variability in experimental material.

Table 4.2: Range of genotypes for different characters in mungbean

Sr. No.	Characters	GM	*Kh*-2020		*Kh*-2021		Pool	
			Mean	Range	Mean	Range	Mean	Range
1	Days to 50 % flowering	37.6	37.4	35.5-41.0	37.8	34.5-41.5	37.6	35.0-41.3
2	Days to maturity	69.5	69.4	65.5-74.0	69.6	65.0-75.5	69.5	65.3-74.8
3	Days to shattering	78.9	78.9	68.5-84.5	78.8	67.5-85.5	78.9	68.0-85.0
4	Plant height (cm)	74.4	72.6	51.9-95.0	76.2	54.6-102.6	74.4	53.2-98.8
5	No. of primary branches	4.2	4.1	2.5-6.8	4.3	2.4-7.2	4.2	2.5-7.0
6	No. of pods/cluster	4.0	3.9	2.8-5.2	4.1	3.0-5.7	4.0	2.9-5.5
7	No. of pods/plant	16.5	16.3	8.7-34.8	16.8	9.5-36.4	16.5	9.4-35.6
8	Length of pods (cm)	7.9	7.9	5.5-12.0	7.9	5.4-11.6	7.9	5.4-11.8
9	No. of seeds/ pod	12.5	12.6	9.2-15.8	12.4	9.6-15.0	12.5	9.4-15.1
10	100 seed wt. (g)	3.8	3.8	2.8-5.1	3.8	2.6-5.1	3.8	2.8-5.1
11	Seed yield/plant (g)	7.9	7.8	5.3-11.8	8.0	5.5-11.9	7.9	5.4-11.7
12	Biological yield/plant (g)	19.8	20.3	13.4-29.9	19.4	13.6-33.2	19.8	14.4-31.6
13	Harvest index (%)	29.1	28.5	19.4-45.6	29.7	20.4-44.6	29.1	20.3-45.6
14	Germination %	86.7	86.2	72.0-94.0	87.2	73.5-94.3	86.7	72.8-93.8
15	Hard seed %	4.0	4.0	1.8-6.3	4.1	2.3-6.5	4.0	2.0-6.4
16	Pod opening time (hrs)	32.6	33.6	0.50-83.0	31.6	0.50-78.0	32.6	0.8-80.8
17	Seedling length (cm)	35.7	35.3	28.1-39.5	36.0	30.2-40.4	35.7	29.1-39.9
18	Vigour index I	3103.4	3057.6	2173.9-3708.3	3149.2	2363.0-3772.7	3103.4	2272.3-3740.5
19	Seedling dry wt. (g)	1.0	0.9	0.7-1.1	1.0	0.7-1.2	1.0	0.7-1.1
20	Vigour index II	82.9	81.2	55.5-103.4	84.5	53.4-109.4	82.9	57.6-106.4
21	Seed hardness (Kg/cm2)	4.4	4.4	3.5-5.7	4.5	3.5-5.3	4.4	3.5-5.2
22	Alpha amylase (mg/g)	404.3	403.1	231.0-529.5	405.5	241.5-535.5	404.3	236.3-532.5
23	Dehydrogenase (ug/g)	456.3	456.0	229.8-490.9	456.7	245.2-490.9	456.3	240.0-490.4

Where – **M**: Mean and **GM**: Grand Mean

4.2 Range and Mean performance of genotypes

While interpreting the results obtained negative values were considered as favorable for the characters *viz.,* days to 50 per cent flowering, days to maturity and days to shattering.

However, positive values were considered as favorable for the characters *viz.,* plant height (cm), number of primary branches, number of pods per cluster, number of pods per plant, length of pods (cm), number of seeds per pod, 100 seed wt.(g), seed yield per plant (g), biological yield per plant (g) and harvest index(%).

The analysis of variance due to various sources of variation in *kharif* 2020 and 2021 for yield attributing characters *viz.,* plant height (cm), number of primary branches, number of pods per cluster, number of pods per plant, length of pods (cm), number of seeds per pod, 100 seed wt.(g), seed yield per plant (g), biological yield per plant (g) and harvest index(%) and seed quality parameters *viz.,* germination (%), hard seed (%), days to opening pod (hrs), seedling length (cm), vigour index I (%), vigour index II (%), seedling dry wt. (g), seed hardness (Kg/cm^2), α-amylase (mg/g) and dehydrogenase (ug/g) are presented in Table 4.1 and grand mean sum of squares presented in Table 4.2.

The results pertaining to mean performance of genotypes in individual as well as pooled environments for different yield contributing characters and seed quality characters are tabulated in tables from 4.3a to 4.3l. The character wise mean performance of genotypes is presented here under following sub headings.

4.2.1: Morphological characters

4.2.2 Yield contributing characters

4.2.3 Seed quality characters

4.2.1: Morphological characters

4.2.1.1: Days to 50% flowering

The trait of days to 50 % flowering is an irreversible and major character which contributes to earliness.

The days to 50 % flowering found varied range from 35.5 to 41.0 days with mean value 37.5 days, 34.5 to 41.5 days with mean value 37.8 days and 35.0 to 41.3 days with mean value 37.7 days in *kharif* 2020, *kharif* 2021 and in pooled mean respectively. The grand mean value for this trait has recorded 37.6 days (Table 4.2).

The genotypes BM-2019-1, AKM-1609, Phule M 818-8, AKM-1606 and check PKV Green Gold showed (35.5 days) earliness and genotype TBM-6 (41.0 days) showed late for day to 50 % flowering in *kharif* 2020. In *kharif* 2021 and in pooled mean a genotype AKM-1609 recorded early and TBM-6 late in this trait.

Among the checks, mean values for days to 50% flowering were recorded from 35.5 to 39.5 days in *kharif* 2020, 34.5 to 39.5 days in *kharif* 2021 and 35.0 days to 39.5 days in pooled mean in the genotypes PKV Green Gold and PKVM-4 respectively. In all genotypes and checks AKM 1609 (35 days) found early and TBM 6 (41.3 days) found late in days to 50 % flowering (Table 4.3a).

On the basis of days to 50 % flowering the genotypes were classified as early (< 35.00 days), medium (35.00-40.00 days) and late (> 40.00 days).

Early	**Medium**	**Late**
(< 35.00 days)	(35.00 to 40.00 days)	(> 40.00 days)
PKV Green Gold (ch)	AKM-12-24	Phule M 817-13
--	BM-2019-1	TBM-6
--	AKM-1609	TBM-10
--	AKM-1602	--
--	AKM-12-23	--

Table 4.3 a: Mean performance of genotypes for days to 50% flowering and days to maturity over two seasons

Sr. No.	Genotypes	Days to 50 % flowering			Days to maturity		
		Kh-2020	*Kh*-2021	Pool	*Kh*-2020	*Kh*-2021	Pool
1	Phule M 707-5	38.5	39.5	39.0	73.0	73.0	73.0
2	AKM-12-14	37.0	37.5	37.3	65.5	66.5	66.0
3	Phule M 602-9	38.5	38.5	38.5	66.5	67.5	67.0
4	AKM-12-24	36.5	35.5	36.0	71.0	69.5	70.3
5	BM-2019-1	**35.5**	36.5	36.0	71.5	70.5	71.0
6	Phule M 702-1	37.0	38.5	37.8	67.5	66.5	67.0
7	AKM-1609	**35.5**	**34.5**	**35.0**	65.5	66.0	65.8
8	AKM-1603	37.5	37.5	37.5	67.0	68.5	67.8
9	AKM-1602	36.5	35.5	36.0	65.5	66.5	66.0
10	Phule M 816-10	38.5	39.5	39.0	70.0	70.5	70.3
11	Phule M 817-13	40.5	**41.5**	41.0	73.0	72.5	72.8
12	TBM-4	40.0	40.5	40.3	71.5	71.5	71.5
13	TBM-6	**41.0**	**41.5**	**41.3**	70.5	71.5	71.0
14	AKM-12-28	37.5	36.5	37.0	71.0	70.5	70.8
15	TBM-10	40.5	**41.5**	41.0	70.5	69.5	70.0
16	TBM-127	37.5	38.5	38.0	68.5	69.0	68.8
17	Phule M 809-12	38.5	37.5	38.0	71.0	70.5	70.8
18	AKM-12-23	**35.5**	36.0	35.8	70.5	70.0	70.3
19	Phule M 818-8	**35.5**	39.5	37.5	**65.5**	**65.0**	**65.3**
20	Phule M 809-10	37.5	38.5	38.0	71.0	70.5	70.8
21	Phule M 402-2-1	38.5	38.5	38.5	68.5	67.5	68.0
22	Phule M 504-20-27	36.5	37.5	37.0	69.5	70.5	70.0
23	AKM-1606	**35.5**	36.5	36.0	67.5	68.0	67.8
24	AKM-1605	36.5	37.5	37.0	70.0	70.5	70.3

Table 4.3 a: Contd….

Sr. No.	Genotypes	Days to 50 % flowering			Days to maturity		
		Kh-2020	*Kh*-2021	Pool	*Kh*-2020	*Kh*-2021	Pool
25	AKM-1608	37.5	37.0	37.3	69.0	69.5	69.3
26	**BM-4 (Ch)**	36.5	37.5	37.0	71.0	71.5	71.3
27	**BPMR-145 (Ch)**	38.5	37.5	38.0	70.5	71.0	70.8
28	**BM-2002-1(Ch)**	37.5	36.5	37.0	69.0	69.5	69.3
29	**BM-2003-2(Ch)**	36.5	37.5	37.0	67.5	66.5	67.0
30	**PKVM-4 (Ch)**	39.5	39.5	39.5	70.5	71.5	71.0
31	**PKVM-8802 (Ch)**	36.5	37.5	37.0	68.5	68.0	68.3
32	**PKV-Green Gold (Ch)**	**35.5**	**34.5**	**35.0**	70.0	70.5	70.3
33	**Vaibhav (Ch)**	38.5	37.5	38.0	**74.0**	**75.5**	**74.8**
34	**Utkarsh (Ch)**	36.0	36.0	36.0	69.5	71.5	70.5
Mean		**37.5**	**37.8**	**37.7**	**69.4**	**69.6**	**69.6**
SE±		1.00	1.01	1.0	0.90	2.51	1.7
CD		2.88	2.91	2.9	2.58	7.24	4.9

4.2.1.2: Days to Maturity

The analyzed data revealed that, days to maturity in mean found varied range from 34.5 to 41.5 days with mean value 37.8 days in *Kharif* 2020 and 35.0 to 41.3 days with mean value 37.7 days, in *Kharif* 2021 whereas in pooled mean it found from 35.5 to 41.0 days with mean value 37.5 days respectively. The grand mean value for this trait was recorded 37.6 days (Table 4.2).

The genotypes AKM-12-14, AKM-1609, AKM-1602 and Phule M 818-8 (65.5 days) showed earliness and Phule M 817-13 (73.00 days) showed late for days to maturity in *kharif* 2020. In *kharif* 2021 a genotype Phule M 818-8 noted early maturity (65.00 days) and genotype TBM-4 for late maturity(71.5 days) and in pooled mean same genotypes were recorded earliness and late maturity i.e. 65.3 days and 71.5 days respectively.

Among the checks in pooled mean values for days to maturity, genotype BM-2003-2 found early (67.0) and check Vaibhav found late (74.8) Table 4.3a.

The genotypes are classified for trait of days to maturity in following three category.

Early	**Medium**	**Late**
(<62.00 days)	(62.00 to 74.00 days)	(> 74.00 days)
Nil	AKM-12-14	Vaibhav Ch.
--	Phule M 602-9	--
--	AKM-1609	--
--	AKM-1602	--
--	Phule M 818-8	--

Table 4.3 b: Mean performance of genotypes for days to shattering and plant height (cm) over two seasons

Sr. No.	Genotypes	Days to shattering			Plant height (cm)		
		Kh-2020	*Kh*-2021	Pool	*Kh*-2020	*Kh*-2021	Pool
1	Phule M 707-5	82.5	83.5	83.0	**51.9**	**54.6**	**53.2**
2	AKM-12-14	**68.5**	**67.5**	**68.0**	58.0	63.9	60.9
3	Phule M 602-9	69.5	68.5	69.0	66.2	69.0	67.6
4	AKM-12-24	84.5	83.5	84.0	76.5	78.8	77.7
5	BM-2019-1	84.5	83.5	84.0	82.9	87.4	85.2
6	Phule M 702-1	76.5	77.5	77.0	81.7	83.3	82.5
7	AKM-1609	75.5	75.0	75.3	55.9	66.4	61.2
8	AKM-1603	78.0	77.0	77.5	65.7	70.7	68.2
9	AKM-1602	75.5	74.5	75.0	70.8	78.5	74.6
10	Phule M 816-10	83.0	83.5	83.3	55.6	59.8	57.7
11	Phule M 817-13	84.0	84.5	84.3	64.3	68.9	66.6
12	TBM-4	81.5	81.0	81.3	63.4	68.6	66.0
13	TBM-6	79.0	79.5	79.3	68.8	71.2	70.0
14	AKM-12-28	79.5	80.5	80.0	56.2	58.9	57.5
15	TBM-10	78.5	79.5	79.0	69.7	74.2	72.0
16	TBM-127	76.5	75.5	76.0	68.5	76.8	72.6
17	Phule M 809-12	83.5	84.0	83.8	76.8	84.8	80.8
18	AKM-12-23	84.0	84.5	84.3	84.2	88.9	86.6
19	Phule M 818-8	69.5	68.5	69.0	58.5	62.4	60.5
20	Phule M 809-10	79.5	78.5	79.0	78.8	83.6	81.2
21	Phule M 402-2-1	81.0	81.5	81.3	**95.0**	**102.6**	**98.8**
22	Phule M 504-20-27	83.0	83.5	83.3	78.8	84.2	81.5
23	AKM-1606	76.0	75.5	75.8	72.3	74.7	73.5
24	AKM-1605	76.5	75.5	76.0	75.8	78.9	77.4

Table 4.3 b: Contd….

Sr. No.	Genotypes	Days to shattering			Plant height (cm)		
		Kh-2020	*Kh*-2021	Pool	*Kh*-2020	*Kh*-2021	Pool
25	AKM-1608	77.0	76.5	76.8	83.9	86.6	85.3
26	**BM-4 (Ch)**	80.5	81.5	81.0	80.2	83.8	82.0
27	**BPMR-145 (Ch)**	80.0	79.5	79.8	78.3	80.2	79.3
28	**BM-2002-1(Ch)**	75.5	76.0	75.8	86.4	82.7	84.6
29	**BM-2003-2(Ch)**	77.5	77.0	77.3	75.1	79.6	77.3
30	**PKVM-4 (Ch)**	80.0	80.5	80.3	94.5	91.2	92.9
31	**PKVM-8802 (Ch)**	76.5	75.5	76.0	72.2	75.4	73.8
32	**PKV-Green Gold (Ch)**	81.5	80.5	81.0	64.9	67.6	66.3
33	**Vaibhav (Ch)**	**84.5**	**85.5**	**85.0**	64.0	61.4	62.7
34	**Utkarsh (Ch)**	80.5	82.5	81.5	91.5	92.0	91.7
Mean		**78.9**	**78.8**	**78.9**	**72.6**	**76.2**	**74.4**
SE±		0.92	1.83	1.4	4.02	4.07	4.29
CD		2.66	5.28	4.0	11.58	11.71	12.87

4.2.1.3: Days to shattering

The analyzed data recorded varied range character of days to shattering from 68.5 to 84.5 days with mean value 78.9 days in *kharif* 2020, 67.5 to 85.5 days with mean 78.8 days in *kharif* 2021 and in pooled mean of 68.0 to 85.0 days with grand mean value 78.9 days (Table 4.2).

The genotype AKM-12-14 (68.5 days) showed earliness in day to shattering, while Vaibhav Ch. found late (84.5 days) for shattering in *kharif* 2020 whereas in *kharif* 2021 and in pooled mean the same genotypes i.e. AKM-12-14 and check Vaibhav showed results in earliness (67.5 days) and (68.0 days) whereas (85.5 days) and (85.0 days) in late days of shattering respectively (Table 4.3b).

The genotypes are classified for trait of days to shattering in following three categories.

Early	Medium	Late
(< 75.00 days)	(76.00 to 84.00 days)	(> 85.00 days)
AKM-12-14	Phule M 702-1	Vaibhav Ch.
Phule M 602-9	AKM-1603	--
AKM-1602	AKM-1609	--
Phule M 818-8	AKM-1606	--
--	AKM-1605	--

4.2.1.4: Plant height (cm)

Plant height is an irreversible and major morphological character which contributes to yield. The analyzed data of this study revealed the plant height (cm) observation has ranged from 51.9 to 95.0 cm with mean value 72.6 cm in *kharif* 2020, 54.6 to 102.6 cm with mean value 76.2 cm in *kharif* 2021 and 53.2 to 98.8 cm in pooled mean with grand mean value 74.4 cm (Table 4.2).

The trait of plant height in cm, on the basis of pooled mean, genotype Phule M 402-2-1 (98.8 cm) recorded tallest plant height, followed by check varieties PKVM-4 (92.9 cm) and Utkarsh (91.7 cm) whereas genotype Phule M 707-5 (53.2 cm) recorded dwarf plant height among all the studied genotypes, followed by AKM-12-28 (57.5 cm) and Phule M 816-10 (57.7 cm). The genotypes Phule M 818-8 (60.5 cm), AKM-12-14 (60.9 cm), AKM-1609 (61.2 cm), TBM-4 (66.0cm), Phule M 817-13 (66.6 cm), Phule M 602-9 (67.6 cm) and checks Vaibhav (62.7 cm) and PKV Green Gold (66.3 cm) were recorded medium range of plant height i.e. between 60-70 cm (Table 4.3b).

4.2.2: Yield contributing characters

4.2.2.1: Number of primary branches

Number of primary branches per plant is a major morphological character which is directly contributes to yield.

Analysis of data on number of primary branches revealed range values in all studied genotypes were found 2.5 to 6.8 with mean value 4.1in *kharif* 2020, 2.4 to 7.2 with mean value 4.3 in *kharif* 2021 and 2.5 to 7.0 in pooled mean with grand mean 4.2 (Table 4.2).

Among the genotypes, on the basis of pooled mean values Phule M 818-8 (6.4), Phule M 817-13 (6.1), AKM-12-14(5.7), AKM-12-28(5.4), Phule M 809-10(4.8), Phule M 702-1(4.7), Phule M 402-2-1(4.4) and AKM-12-23 (4.2) showed maximum number of primary branches. In the check varieties BM 2002-1(7.0) denoted maximum and PKV Green Gold (3.8) minimum number of primary branches however, genotypes Phule M 602-9 (2.5), TBM-10 (2.7) and AKM-1602(2.9) showed less number of primary branches. In the observation of checks, BM-2002-1 (7.0) noted more and PKV Green Gold (3.8) less number of primary branches (Table 4.3c).

The genotypes are classified for trait of number of primary branches in following three categories.

Less	**Medium**	**More**
(< 3.00)	(3.00 to 4.00)	(> 4.00)
Phule M 602-9	Phule M 707-5	AKM-12-14
AKM-1602	AKM-12-24	Phule M 702-1
TBM-10	BM-2019-1	Phule M-817-13
--	AKM-1609	AKM-12-28
--	AKM-1603	Phule M 818-8

Table 4.3 c: Mean performance of genotypes for days to No. of primary branches & No. of pods/cluster over two seasons

Sr. No.	Genotypes	No. of Primary branches			No. of pods/cluster		
		Kh-2020	*Kh*-2021	Pool	*Kh*-2020	*Kh*-2021	Pool
1	Phule M 707-5	3.8	3.7	3.8	**2.8**	**3.0**	**2.9**
2	AKM-12-14	5.6	5.8	5.7	4.4	4.6	4.5
3	Phule M 602-9	**2.5**	**2.4**	**2.5**	2.8	3.0	2.9
4	AKM-12-24	3.1	3.3	3.2	4.6	5.0	4.8
5	BM-2019-1	3.1	3.2	3.2	3.4	3.7	3.6
6	Phule M 702-1	4.6	4.8	4.7	3.5	3.7	3.6
7	AKM-1609	3.9	3.7	3.8	3.7	4.0	3.9
8	AKM-1603	3.2	3.0	3.1	4.3	4.5	4.4
9	AKM-1602	2.8	2.9	2.9	3.6	3.9	3.8
10	Phule M 816-10	3.6	3.9	3.8	4.3	4.1	4.2
11	Phule M 817-13	5.9	6.2	6.1	3.6	3.7	3.7
12	TBM-4	3.9	4.0	4.0	3.6	3.3	3.5
13	TBM-6	3.8	3.9	3.9	3.8	4.0	3.9
14	AKM-12-28	5.2	5.6	5.4	3.5	3.9	3.7
15	TBM-10	2.6	2.7	2.7	3.7	3.9	3.8
16	TBM-127	3.8	3.9	3.9	3.9	4.1	4.0
17	Phule M 809-12	4.6	4.8	4.7	**5.2**	**5.7**	**5.5**
18	AKM-12-23	4.0	4.3	4.2	3.7	3.8	3.8
19	Phule M 818-8	6.2	6.6	6.4	5.1	5.0	5.1
20	Phule M 809-10	4.6	4.9	4.8	3.8	3.9	3.9
21	Phule M 402-2-1	4.2	4.6	4.4	3.4	3.6	3.5
22	Phule M 504-20-27	3.3	3.5	3.4	4.4	4.8	4.6
23	AKM-1606	3.7	3.8	3.8	4.5	4.6	4.6
24	AKM-1605	3.6	4.0	3.8	3.6	4.0	3.8

Table 4.3 c: Contd….

Sr. No.	Genotypes	No. of primary branches			No. of pods/cluster		
		Kh-2020	*Kh*-2021	Pool	*Kh*-2020	*Kh*-2021	Pool
25	**AKM-1608**	3.4	3.6	3.5	5.0	4.7	4.9
26	**BM-4 (Ch)**	3.8	4.0	3.9	4.5	4.8	4.7
27	**BPMR-145 (Ch)**	4.6	4.9	4.8	3.3	3.5	3.4
28	**BM-2002-1(Ch)**	**6.8**	**7.2**	**7.0**	3.5	3.7	3.6
29	**BM-2003-2(Ch)**	5.2	5.3	5.2	4.4	4.2	4.3
30	**PKVM-4 (Ch)**	4.8	5.0	4.9	4.4	4.6	4.5
31	**PKVM-8802 (Ch)**	4.0	4.1	4.0	4.3	4.1	4.2
32	**PKV-Green Gold (Ch)**	3.8	3.9	3.8	4.5	4.5	4.5
33	**Vaibhav (Ch)**	4.0	4.3	4.2	3.6	3.9	3.8
34	**Utkarsh (Ch)**	4.3	4.5	4.4	3.2	3.4	3.3
Mean		**4.1**	**4.3**	**4.2**	**3.9**	**4.1**	**4.0**
SE±		0.20	0.22	0.2	0.24	0.19	0.2
CD		0.59	0.64	0.6	0.69	0.54	0.6

4.2.2.2: Number of pods/cluster

The number of pods per cluster is an important factor which has direct effect on seed yield. The number of pods per cluster observed varied range from 2.8 - 5.2 with mean 3.9 in *kharif* 2020, 3.0 – 5.7 with mean 4.1 in *kharif* 2021 and 2.9 – 5.5 with mean value 4.0 in pooled mean. The grand mean recorded 4.0 for the trait of number of pods per cluster (Table 4.2).

The analysis of data on number of pods per cluster in pooled mean showed the genotype Phule M 809-12 (5.5) has highest number of pods per cluster followed by Phule M 818-8 (5.1) while genotypes Phule M 707-5 and Phule M 602-9 (2.9) were recorded lowest number of pods per cluster. However, the three genotypes namely AKM 1608 (4.9), Phule M 818-8 (5.1) and Phule M 809-12 (5.5) showed higher number of pods per cluster than the best check BM-4 (4.7) (Table 4.3c).

In checks BM-4 recorded highest number of pods per cluster (4.7) and variety Utkarsh showed lowest number of pods per cluster (3.3).

On the basis of number of pods per cluster the genotypes were classified as high (> 5.00), moderate (4.00-5.00) and less (< 4.00).

Less	**Moderate**	**High**
(< 4.00)	(4.00 to 5.00)	(> 5.00)
Phule M 707-5	TBM-127	Phule M 809-12
Phule M 602-9	Phule M 816-10	Phule M 818-8
Utkarsh Ch.	PKVM-8802 Ch.	--
BPMR-145 Ch.	BM-2003-2 Ch.	--
TBM-4	AKM-1603	--

Table 4.3 d: Mean performance of genotypes for days to number of pods per plant and length of pods (cm) over two seasons.

Sr. No.	Genotypes	No. of pods/plant			Length of pods (cm)		
		Kh-2020	*Kh*-2021	Pool	*Kh*-2020	*Kh*-2021	Pool
1	Phule M 707-5	**8.7**	10.0	**9.4**	11.3	11.7	11.5
2	AKM-12-14	29.6	25.4	27.5	6.8	6.6	6.7
3	Phule M 602-9	9.7	**9.5**	9.6	5.4	5.6	5.5
4	AKM-12-24	11.2	10.9	11.1	7.2	6.8	7.0
5	BM-2019-1	10.8	11.2	11.0	8.8	8.6	8.7
6	Phule M 702-1	10.2	10.5	10.4	7.1	7.3	7.2
7	AKM-1609	15.9	16.0	16.0	6.7	6.9	6.8
8	AKM-1603	17.8	15.4	16.6	5.8	5.9	5.9
9	AKM-1602	13.1	17.6	15.4	7.5	8.1	7.8
10	Phule M 816-10	17.2	16.3	16.8	6.0	5.8	5.9
11	Phule M 817-13	18.8	16.8	17.8	11.8	11.6	11.7
12	TBM-4	12.6	12.0	12.3	7.6	7.4	7.5
13	TBM-6	15.6	16.5	16.1	7.4	7.3	7.3
14	AKM-12-28	18.0	19.8	18.9	5.7	6.0	5.9
15	TBM-10	14.2	13.1	13.7	6.1	6.3	6.2
16	TBM-127	10.2	12.4	11.3	10.9	12.4	11.7
17	Phule M 809-12	17.3	18.8	18.1	10.7	9.8	10.2
18	AKM-12-23	14.9	16.3	15.6	7.1	7.4	7.3
19	Phule M 818-8	**34.8**	**36.4**	**35.6**	9.3	9.1	9.2
20	Phule M 809-10	13.2	14.4	13.8	8.4	7.8	8.1
21	Phule M 402-2-1	14.9	16.1	15.5	7.5	7.3	7.4
22	Phule M 504-20-27	12.8	10.6	11.7	7.8	8.0	7.9
23	AKM-1606	18.2	19.9	19.1	6.1	6.3	6.2
24	AKM-1605	16.8	17.0	16.9	6.0	6.0	6.0

Table 4.3 d: Contd….

Sr. No.	Genotypes	No. of pods/plant			Length of pods (cm)		
		Kh-2020	*Kh*-2021	Pool	*Kh*-2020	*Kh*-2021	Pool
25	AKM-1608	19.0	17.8	18.4	**5.5**	**5.4**	**5.4**
26	**BM-4 (Ch)**	21.8	23.6	22.7	6.8	6.5	6.6
27	**BPMR-145 (Ch)**	16.4	18.8	17.6	8.0	7.7	7.9
28	**BM-2002-1(Ch)**	10.2	11.6	10.9	9.2	9.6	9.4
29	**BM-2003-2(Ch)**	25.3	22.3	23.8	11.0	10.8	10.9
30	**PKVM-4 (Ch)**	15.7	18.5	17.1	7.1	7.0	7.1
31	**PKVM-8802 (Ch)**	20.0	23.0	21.5	8.8	9.0	8.9
32	**PKV-Green Gold (Ch)**	22.8	23.1	23.0	7.2	7.2	7.2
33	**Vaibhav (Ch)**	14.2	17.0	15.6	9.7	8.5	9.1
34	**Utkarsh (Ch)**	11.1	12.9	12.0	**12.0**	**11.6**	**11.8**
Mean		**16.3**	**16.8**	**16.5**	**7.9**	**7.9**	**7.9**
SE±		1.40	1.56	1.5	0.30	0.23	0.57
CD		4.04	4.49	4.3	0.87	0.67	1.71

4.2.2.3: Number of pods/plant

The number of pods per plant is an also important factor which has direct effect on seed yield.

The analyzed data on number of pods per plant observation showed the range values from 8.7 to 34.8 with mean value 16.3, 9.5 to 36.4 with mean value 16.8 and 9.4 to 35.6 with mean value 16.5 in *Kharif* 2020, *Kharif* 2021 and in pooled mean respectively. The grand mean value for this trait recorded 16.5 (Table 4.2).

The data revealed that there was significant difference in number of pods per plant of studied genotypes. On the basis of pooled mean in a character of number of pods per plant predicted the genotype Phule M 818-8 (35.6) recorded highest number of pods per plant, followed by AKM-12-14 (27.5), AKM-1606 (19.1),

AKM-12-28 (18.9) and Phule M 809-12 (18.1) while genotype Phule M 707-5 (9.4) showed lowest number of pods per plant.

The check variety BM-2003-2 (23.8) showed maximum number of pods per plant, followed by PKV Green Gold (23.00), BM-4(22.7) and PKVM-8802(21.5) whereas BM-2002-1 (10.9), Utkarsh (12.0) and Vaibhav (15.6) recorded minimum number of pods per plant (Table 4.3d).

4.2.2.4: Length of pods (cm)

The length of pods has also direct effect on the number of seeds per pod which has relation to seed yield per plant.

The data on trait of length of pod in centimeter found varied range from 5.4 to 12.0 cm, 5.4 to 11.6 cm and 5.4 to 11.8 cm in *Kharif* 2020, *Kharif* 2021 and in pooled mean respectively. The mean values for *kharif* 2020, *kharif* 2021 and pooled mean were found same i.e. 7.9 cm and grand mean value has also found 7.9 cm in the trait of length of pod in centimeter (Table 4.2).

On the basis of length of pods (cm) genotypes were classified on following three categories *viz.,* short (< 7.00 cm), medium (7.00-9.00 cm) and long (> 9.00 cm).

Among the studied genotypes, on the basis of pooled mean observation it revealed that, genotypes Phule M 817-13 & TBM-127 (11.7 cm) recorded highest length of pod, followed by Phule M 707-5 (11.5 cm), Phule M 809-12 (10.2 cm) and Phule M 818-8 (9.2 cm). The genotype AKM-1608 (5.4 cm) recorded lowest length of pods, followed by Phule M 602-9 (5.5 cm), AKM-1603, Phule M 816-10 and AKM-12-28(5.9 cm), AKM-1605 (6.0 cm), TBM-10 and AKM-1606 (6.2 cm), AKM-12-14 (6.7 cm), AKM-1609 (6.8 cm) and AKM-12-24 (7.00 cm). The grand mean value of this experiment was found 7.9 cm (Table 4.3d).

In this study among the checks, Utkarsh (11.8 cm) recorded highest length of pod, followed by BM-2003-2 (10.9 cm) whereas, BM-4 (6.6 cm) recorded lowest length of pod.

On the basis of length of pods (cm) genotypes were classified on following three categories

Short	Medium	Long
(< 7.00 cm)	(7.00 to 9.00 cm)	(> 9.00 cm)
AKM-1608	AKM-12-24	Phule M 707-5
AKM-12-28	PKVM-4 Ch.	Phule M 817-13
Phule M 602-9	Phule M 702-9	TBM-127
AKM-1603	TBM-6	Phule M 809-12
Phule M 816-10	AKM-12-23	Phule M 818-8

4.2.2.5: Number of seeds/pod

The number of seeds per pod has direct effect on seed yield. Analyzed data showed the range values of genotypes on the basis of mean from 9.2 to 15.8 with mean 12.6 in the season of *kharif* 2020, 9.6 to 15.0 with mean 12.4 in *kharif* 2021 and 9.4 to 15.1 with mean 12.5 in pooled mean were recorded. The grand mean for this trait recorded 12.5 (Table 4.2).

Table 4.3 e: Mean performance of genotypes for No. of seeds per pod and 100 seed weight (g) over two seasons

Sr. No.	Genotypes	No. of seeds/ pod			100 seed wt. (g)		
		Kh-2020	*Kh*-2021	Pool	*Kh*-2020	*Kh*-2021	Pool
1	Phule M 707-5	14.5	14.2	14.4	4.0	4.0	4.0
2	AKM-12-14	10.2	10.1	10.2	3.9	4.0	4.0
3	Phule M 602-9	10.5	10.0	10.3	4.0	4.1	4.0
4	AKM-12-24	13.0	12.8	12.9	3.7	3.7	3.7
5	BM-2019-1	10.8	10.0	10.4	5.0	4.5	4.7
6	Phule M 702-1	11.6	12.2	11.9	3.7	3.7	3.7
7	AKM-1609	11.9	12.2	12.1	4.1	4.1	4.1
8	AKM-1603	13.4	13.2	13.3	3.2	3.3	3.2
9	AKM-1602	11.2	11.0	11.1	3.1	3.0	3.1
10	Phule M 816-10	**15.8**	14.3	**15.1**	3.3	3.4	3.4
11	Phule M 817-13	15.1	14.7	14.9	4.2	4.2	4.2
12	TBM-4	12.2	11.8	12.0	5.0	**5.1**	**5.1**
13	TBM-6	14.5	14.2	14.4	3.9	4.0	4.0
14	AKM-12-28	12.2	12.4	12.3	3.4	3.7	3.6
15	TBM-10	13.8	14.6	14.2	3.2	3.5	3.4
16	TBM-127	14.5	14.7	14.6	4.9	4.4	4.6
17	Phule M 809-12	11.3	11.8	11.6	3.7	3.4	3.6
18	AKM-12-23	13.8	13.9	13.9	3.8	4.0	3.9
19	Phule M 818-8	13.0	12.9	13.0	4.2	4.1	4.2
20	Phule M 809-10	13.0	11.9	12.5	3.6	3.6	3.6
21	Phule M 402-2-1	12.4	12.0	12.2	3.9	3.5	3.7
22	Phule M 504-20-27	12.4	12.9	12.7	4.2	4.0	4.1
23	AKM-1606	**9.2**	**9.6**	**9.4**	**2.8**	3.1	2.9
24	AKM-1605	11.6	13.0	12.3	2.9	3.0	2.9

Table 4.3 e: Contd….

Sr. No.	Genotypes	No. of seeds/ pod			100 seed wt. (g)		
		Kh-2020	*Kh*-2021	Pool	*Kh*-2020	*Kh*-2021	Pool
25	AKM-1608	10.0	9.6	9.8	2.9	**2.6**	**2.8**
26	**BM-4 (Ch)**	11.8	10.2	11.0	2.9	3.0	3.0
27	**BPMR-145 (Ch)**	11.2	11.4	11.3	4.1	4.0	4.1
28	**BM-2002-1(Ch)**	12.2	12.4	12.3	4.7	4.7	4.7
29	**BM-2003-2(Ch)**	14.5	**15.0**	14.8	5.0	4.8	4.9
30	**PKVM-4 (Ch)**	12.1	12.3	12.2	3.1	3.2	3.2
31	**PKVM-8802 (Ch)**	13.1	13.0	13.1	4.1	4.2	4.2
32	**PKV-Green Gold (Ch)**	13.0	12.5	12.8	3.6	3.3	3.5
33	**Vaibhav (Ch)**	13.1	11.6	12.4	3.7	3.6	3.6
34	**Utkarsh (Ch)**	14.4	14.2	14.3	**5.1**	5.0	5.1
Mean		**12.6**	**12.4**	**12.5**	**3.8**	**3.8**	**3.8**
SE±		0.67	0.52	0.94	0.07	0.06	0.34
CD		1.93	1.49	2.82	0.21	0.16	1.02

Among the studied genotypes, Phule M 816-10 (15.1) recorded highest number of seeds per pod i.e. more seeded genotype, followed by Phule M 817-13 (14.9), TBM-127 (14.6), Phule M 707-5 and TBM-6 (14.4). The genotype AKM-1606 (9.4) recorded lowest number of seeds per pod among all tested genotypes i.e. low seeded genotype, followed by AKM-1608 (9.8), AKM-12-14 (10.2), Phule M 602-9 (10.3) and BM-2019-1(10.4). In checks BM-4 (11.0), BPMR-145 (11.3), BM-2002-1 (12.3), PKVM-4 (12.2), PKV Green Gold (12.8) and Vaibhav (12.4) were found in less number of seeds per pod category whereas checks BM-2003-2 (14.8), PKVM-8802 (13.1) and Utkarsh (14.3) were found in moderate category of seeds per pod (Table 4.3e).

On the base of number of seeds per pod were categorized under following groups *viz.*, less seeded (< 13.00), moderate (13-15) and more seeded (> 13.00).

Less	Moderate	More
(< 13.00)	(13.00 to 15.00)	(> 15.00)
AKM-1606	Phule M 818-8	Phule M 816-10
AKM-1608	PKVM-8802 Ch.	--
AKM-12-24	AKM-1603	--
Phule M 602-9	AKM-12-23	--
Bm-2019-1	TBM-10	--

4.2.2.6: 100 seed wt. (g)

The 100 seed wt. in grams (test weight) is an important factor which has direct effect on seed yield. The 100 seed wt. (g) found range values in mean data observation from 2.8-5.1 g, 2.6-5.1 g and 2.8-5.1 g in *kharif* 2020, *kharif* 2021 and in pooled mean respectively. The mean value for *kharif* 2020, *kharif* 2021 and in pooled mean was found 3.8 g and grand mean also found 3.8 g of 100 seed weight (Table 4.2).

Among the tested genotypes, on the basis of pooled mean it revealed that, genotype TBM-4 (5.1 g) recorded highest wt. of 100 seeds, followed by BM-2003-2 (4.9 g) and BM-2002-1 (4.7 g) and the genotype AKM-1608 (2.8 g) recorded lowest 100 seeds wt., followed by AKM-1606 and AKM-1605 (2.9 g) (Table 4.3e).

In the checks for the trait of 100 seed wt. (g) all checks were observed under the category of moderate and bold seeded variety.

On the basis of 100 seed weight (g), genotypes were distributed under three classes i.e. small size seed wt. (< 3.00 g), medium size (3.00-4.00 g) and bold size seed wt (> 5.00 g).

Small	Medium	Bold
(< 3.00 g)	(3.00 to 4.00 g)	(> 4.00 g)
AKM-1606	AKM-1602	TBM-4
AKM-1608	AKM-1603	BM-2003-2 Ch.
AKM-1605	PKVM-4 Ch.	BM-2002-1 Ch.
BPMR-145 Ch.	Phule M 816-10	Utkarsh Ch.
--	TBM-10	TBM-127

4.2.2.7: Seed yield/plant (g)

The analyzed data of this trait showed the significant differences in seed yield per plant (g). In the trait of seed yield per plant (g) data revealed the mean values of ranges from 5.3 to 11.8 g with mean value 7.8 g, 5.5 to 11.9 g with mean 8.0 g and 5.4 to 11.7 g with mean 7.9 g in *kharif* 2020, *kharif* 2021 and in pooled mean respectively whereas the grand mean value has found 7.9 g for this character (Table 4.2).

The character of seed yield per plant (g), recorded seed yield per plant from 5.3 g (Phule M 602-9) to 11.8 g (AKM-12-14) in *kharif* 2020, 5.5 g (Phule M 602-9) to 11.9 g (BM-2003-2) in *kharif* 2021 and of 5.4 g (Phule M 602-9) to 11.7 g (BM-2003-2) in pooled mean.

The genotype Phule M 817-13 (11.7g) recorded maximum seed yield per plant along with the best check for this character BM-2003-2 (11.7 g), followed by genotype AKM-12-14 (11.5 g), check PKVM-8802 (11.1 g) and Phule M 818-8 (11.0 g). The genotype Phule M 602-9 recorded minimum seed yield per plant (5.4 g) followed by Phule M 702-1(5.6 g), Phule M 504-20-27(5.7 g), AKM-12-24, AKM-1602 and Phule M 809-10 (5.9 g) (Table 4.3f).

4.2.2.8: Biological yield/plant (g)

Among all genotypes, biological yield per plant (g) observed the range in *kharif* 2020, *kharif* 2021 and pooled mean from 13.4 to 29.9 g with 20.3 g mean value, 13.6 to 33.2 g with mean 19.4 and 14.4 to 31.6 g with mean of 19.8 g respectively. The grand mean value for this observation was found 19.8 g (Table 4.2).

All the tested genotypes, TBM-10 (22.8 g) recorded high biological yield followed by TBM-6 (22.2 g), Phule M 816-10 (21.8 g), AKM-1602 (21.7 g). The biological yield found low in the genotype AKM-1609 (14.4 g), followed by Phule M 817-13 (15.1g), Phule M 602-9 (16.9 g), Phule M 702-1 (17.9 g), AKM-1606 (18.1 g), TBM-127 (18.2 g), Phule M 809-12 (18.3 g), Phule M 818-8 (18.5 g),AKM-1608 (18.6 g), Phule M 402-2-1(19.0g), Phule M 707-5(19.2 g), AKM-12-23 (19.3g), Phule M 809-10 (19.6 g) and BM-2019-1 (20.0 g).

As in checks, result of biological yield (g) showed that, the Utkarsh has (31.6 g) high biological yield, followed by Vaibhav (28.5 g), PKVM-4 (26.5 g), BPMR- 145 (20.3 g) and rest of the checks were observed below the 20.0 g in biological yield (Table 4.3f).

Table 4.3 f: Mean performance of genotypes for seed yield per plant (g) and biological yield per plant (g) over two seasons

Sr. No.	Genotypes	Seed yield/plant (g)			Biological yield/plant (g)		
		Kh-2020	*Kh*-2021	Pool	*Kh*-2020	*Kh*-2021	Pool
1	Phule M 707-5	6.8	8.0	7.4	20.3	18.2	19.2
2	AKM-12-14	**11.8**	11.2	11.5	22.6	18.5	20.5
3	Phule M 602-9	**5.3**	**5.5**	**5.4**	17.5	16.3	16.9
4	AKM-12-24	5.9	5.8	5.9	21.5	19.5	20.5
5	BM-2019-1	6.8	6.5	6.6	21.5	18.6	20.0
6	Phule M 702-1	5.5	5.8	5.6	17.0	18.8	17.9
7	AKM-1609	9.9	9.1	9.5	15.3	**13.6**	**14.4**
8	AKM-1603	8.2	8.6	8.4	21.9	19.3	20.6
9	AKM-1602	5.8	6.0	5.9	23.0	20.4	21.7
10	Phule M 816-10	8.6	8.8	8.7	22.8	20.7	21.8
11	Phule M 817-13	11.6	11.8	11.7	14.8	15.4	15.1
12	TBM-4	7.3	7.7	7.5	23.2	18.4	20.8
13	TBM-6	8.7	9.0	8.8	23.7	20.7	22.2
14	AKM-12-28	8.9	9.1	9.0	22.0	20.1	21.1
15	TBM-10	7.5	7.9	7.7	24.1	21.4	22.8
16	TBM-127	7.4	7.2	7.3	17.8	18.7	18.2
17	Phule M 809-12	7.4	7.2	7.3	19.9	16.8	18.3
18	AKM-12-23	8.1	8.0	8.0	19.5	19.1	19.3
19	Phule M 818-8	11.2	10.8	11.0	19.6	17.4	18.5
20	Phule M 809-10	5.8	6.0	5.9	20.8	18.5	19.6
21	Phule M 402-2-1	6.1	6.0	6.0	16.6	21.3	19.0
22	Phule M 504-20-27	5.6	5.9	5.7	23.2	17.9	20.6
23	AKM-1606	6.2	6.1	6.2	20.0	16.1	18.1
24	AKM-1605	6.0	6.2	6.1	21.4	19.1	20.3

Table 4.3 f: Contd….

Sr. No.	Genotypes	Seed yield/plant (g)			Biological yield/plant (g)		
		Kh-2020	*Kh*-2021	Pool	*Kh*-2020	*Kh*-2021	Pool
25	AKM-1608	5.5	5.9	5.7	19.4	17.8	18.6
26	**BM-4 (Ch)**	8.5	9.2	8.9	20.4	18.3	19.3
27	**BPMR-145 (Ch)**	9.5	9.9	9.7	18.7	22.0	20.3
28	**BM-2002-1(Ch)**	6.1	6.2	6.2	14.6	18.8	16.7
29	**BM-2003-2(Ch)**	11.5	**11.9**	**11.7**	13.7	18.6	16.1
30	**PKVM-4 (Ch)**	6.6	6.9	6.7	27.3	25.6	26.5
31	**PKVM-8802 (Ch)**	10.9	11.3	11.1	**13.4**	14.1	13.8
32	**PKV-Green Gold (Ch)**	9.9	10.7	10.3	13.6	16.0	14.8
33	**Vaibhav (Ch)**	7.2	7.5	7.3	27.8	29.2	28.5
34	**Utkarsh (Ch)**	8.2	8.7	8.5	**29.9**	**33.2**	**31.6**
Mean		**7.8**	**8.0**	**7.9**	**20.3**	**19.4**	**19.8**
SE±		2.30	2.68	2.5	1.52	1.34	1.79
CD		2.30	2.68	2.5	4.39	3.85	5.37

4.2.2.9: Harvest index (%)

The analysis of data showed the significant differences in harvest index % among the genotypes. In the trait of harvest index % , mean values were observed the range from 19.4 to 45.6 % with mean value 28.5 %, 20.4 to 44.6 % with mean 29.7 % and 20.3 to 45.6 % with mean 29.1 % in *kharif* 2020, *kharif* 2021 and in pooled mean respectively. The grand mean value found 29.1 % for this character (Table 4.2).

In this experiment among all the 34 entries, genotype Phule M 818-8 (45.6 %) recorded high harvest index % followed by check variety PKVM-8802

(44.6 %), genotype Phule M 817-13 (43.7 %), check PKV-Green Gold (41.1 %). The check PKVM-4 (20.3 %) recorded low harvest index % followed by Vaibhav (20.5%) and Utkarsha (21.2 %). The genotypes AKM-1602 (21.4 %), Phule M 504-20-27 (22.1 %), AKM-12-24 (22.3 %), Phule M 809-10 (23.0 %), AKM-1605 (23.1 %), AKM -1608 (23.4 %), Phule M 702-1 (23.9 %), Phule M 602-9 (24.2 %), Phule M 402-1 (24.4 %) and BM-2019-1 (24.9 %) were also found low in harvest index percentage (Table 4.3g).

The genotypes were classified under following three groups as low (< 25.00 %), medium (26.00-35.00 %) and high (> 36.00 %) in harvest index percentage.

Low	**Medium**	**High**
(<25.00 %)	(26.00 to 35.00 %)	(>36.00 %)
PKVM-4 Ch.	Phule M 707-5	AKM-12-14
Vaibhav Ch.	AKM-1603	AKM-1609
Utkarsh Ch.	TBM-4	Phule M 817-13
AKM-1602	Phule M 816-10	Phule M 818-8
Phule M 504-20-27	TBM-6	BM-2003-2 Ch.

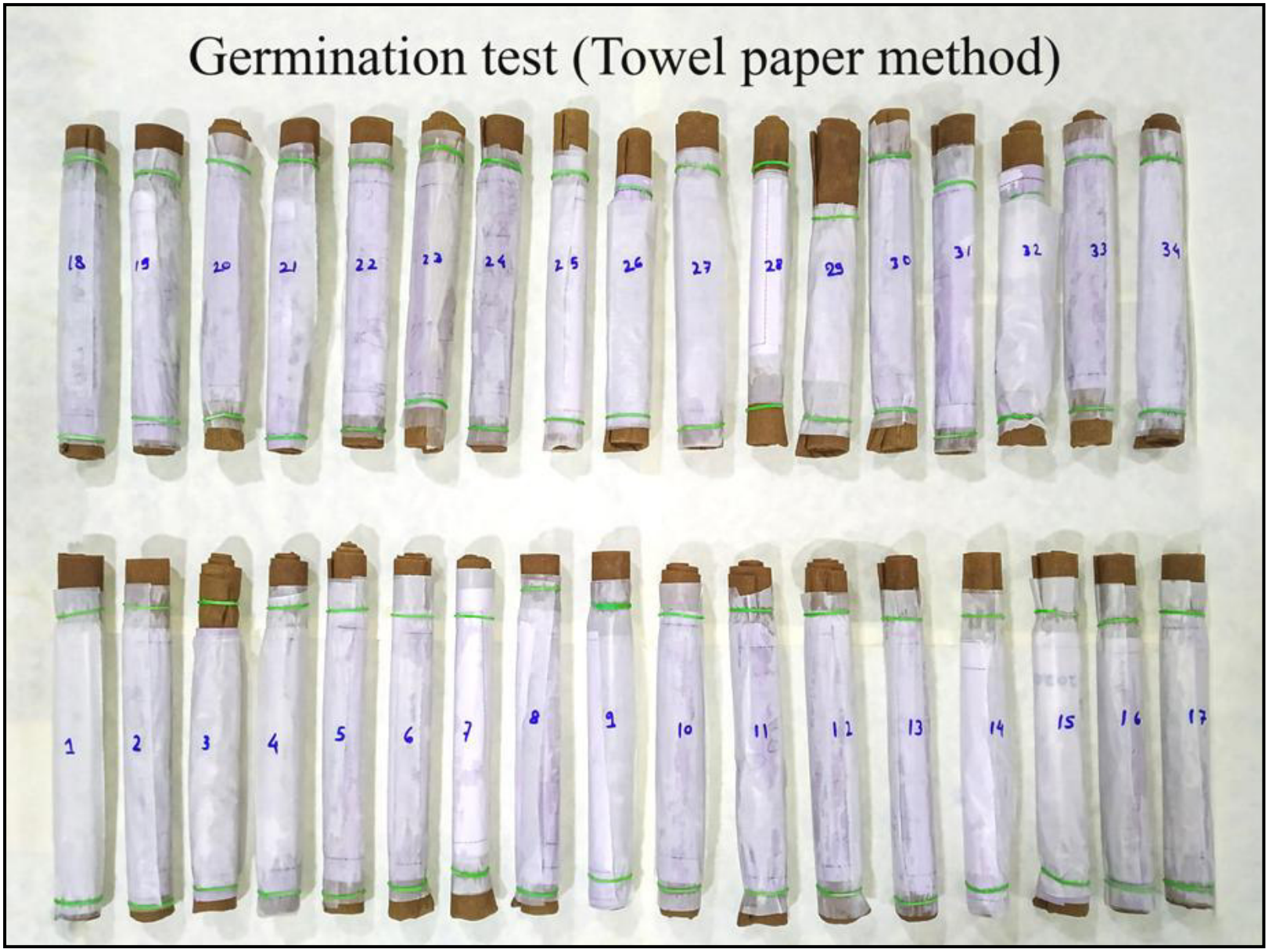

Plate 2: Germination test by 'Rolled Towel Paper Method'

Plate 3: Evaluation of germination percentage

Table 4.3 g: Mean performance of genotypes for harvest index (%) and germination percentage over two seasons

Sr. No.	Genotypes	Harvest index (%)			Germination %		
		Kh-2020	*Kh*-2021	Pool	*Kh*-2020	*Kh*-2021	Pool
1	Phule M 707-5	25.1	30.5	27.8	88.5	87.5	88.0
2	AKM-12-14	37.9	41.7	39.8	82.5	82.5	82.5
3	Phule M 602-9	23.2	25.2	24.2	80.5	84.0	82.3
4	AKM-12-24	21.7	22.9	22.3	85.8	87.5	86.6
5	BM-2019-1	23.9	25.9	24.9	85.5	86.0	85.8
6	Phule M 702-1	24.4	23.5	23.9	86.8	87.5	87.1
7	AKM-1609	39.4	40.2	39.8	85.0	86.5	85.8
8	AKM-1603	27.2	30.7	29.0	77.5	78.5	78.0
9	AKM-1602	20.1	22.6	21.4	85.5	87.3	86.4
10	Phule M 816-10	27.3	29.9	28.6	86.8	87.0	86.9
11	Phule M 817-13	43.8	43.5	43.7	88.0	88.5	88.3
12	TBM-4	24.0	29.3	26.7	78.0	80.5	79.3
13	TBM-6	26.8	30.2	28.5	**72.0**	**73.5**	**72.8**
14	AKM-12-28	28.8	31.2	30.0	76.8	77.5	77.1
15	TBM-10	23.7	26.8	25.3	80.0	80.5	80.3
16	TBM-127	29.3	27.8	28.5	86.5	87.8	87.1
17	Phule M 809-12	27.1	29.9	28.5	85.5	87.0	86.3
18	AKM-12-23	29.4	29.4	29.4	86.5	87.8	87.1
19	Phule M 818-8	44.6	**46.6**	**45.6**	92.3	93.5	92.9
20	Phule M 809-10	21.7	24.4	23.0	86.0	87.0	86.5
21	Phule M 402-2-1	26.8	21.9	24.4	87.5	89.0	88.3
22	Phule M 504-20-27	19.4	24.8	22.1	86.3	87.8	87.0
23	AKM-1606	23.8	27.5	25.6	85.5	87.3	86.4
24	AKM-1605	21.7	24.4	23.1	91.5	93.0	92.3

Table 4.3 g: Contd….

Sr. No.	Genotypes	Harvest index (%)			Germination %		
		Kh-2020	*Kh*-2021	Pool	*Kh*-2020	*Kh*-2021	Pool
25	AKM-1608	22.1	24.8	23.4	85.5	86.8	86.1
26	**BM-4 (Ch)**	29.4	33.5	31.5	86.0	87.5	86.8
27	**BPMR-145 (Ch)**	33.6	31.0	32.3	92.3	92.8	92.5
28	**BM-2002-1(Ch)**	29.4	24.9	27.2	91.5	93.3	92.4
29	**BM-2003-2(Ch)**	**45.6**	38.9	42.2	**94.0**	93.5	93.8
30	**PKVM-4 (Ch)**	**19.4**	21.2	**20.3**	93.3	**94.3**	**93.8**
31	**PKVM-8802 (Ch)**	44.9	44.4	44.6	92.3	91.5	91.9
32	**PKV-Green Gold (Ch)**	42.1	40.1	41.1	86.5	87.0	86.8
33	**Vaibhav (Ch)**	20.6	**20.4**	20.5	92.0	91.5	91.8
34	**Utkarsh (Ch)**	21.6	20.8	21.2	92.5	92.8	92.6
Mean		**28.5**	**29.7**	**29.1**	**86.2**	**87.2**	**86.7**
SE±		2.68	2.44	2.95	2.08	1.95	2.35
CD		7.73	7.03	8.85	5.98	5.60	7.05

4.2.3: Seed quality characters

4.2.3.1: Germination percentage

Germination percentage among all the genotypes and checks recorded varied range from 72.8 % to 93.8 % with mean of 86.7 % in pooled, while range from 72.0 % to 94.0 % with mean 86.2% and 73.5 % to 94.3 % with mean 87.2 % in *kharif* 2020 and in *kharif* 2021 respectively. The grand mean recorded 86.7 % of germination percentage in this important seed quality character (Table 4.2).

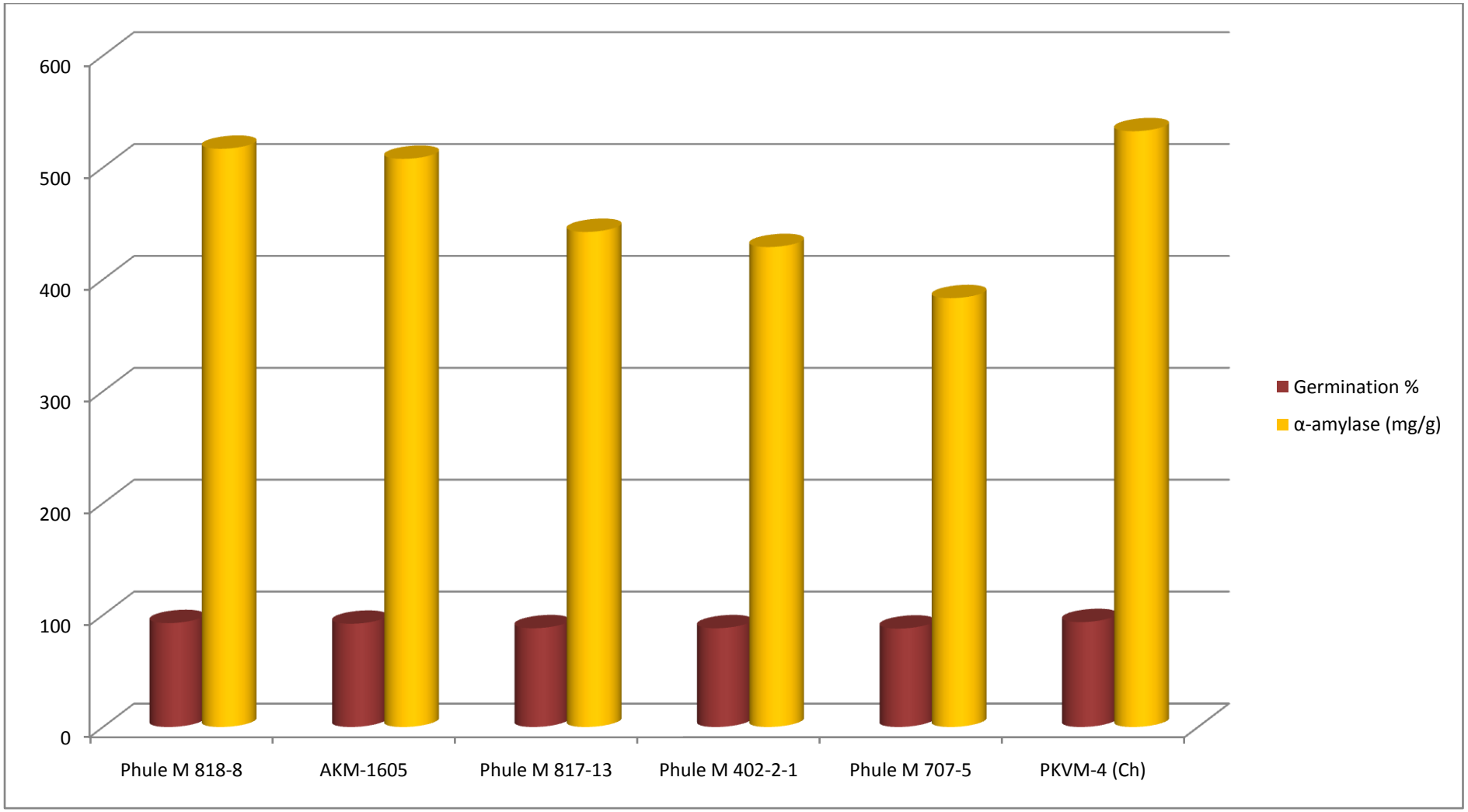

Fig. 1: Effect of α-amylase on germination percentage of top five genotypes with best check

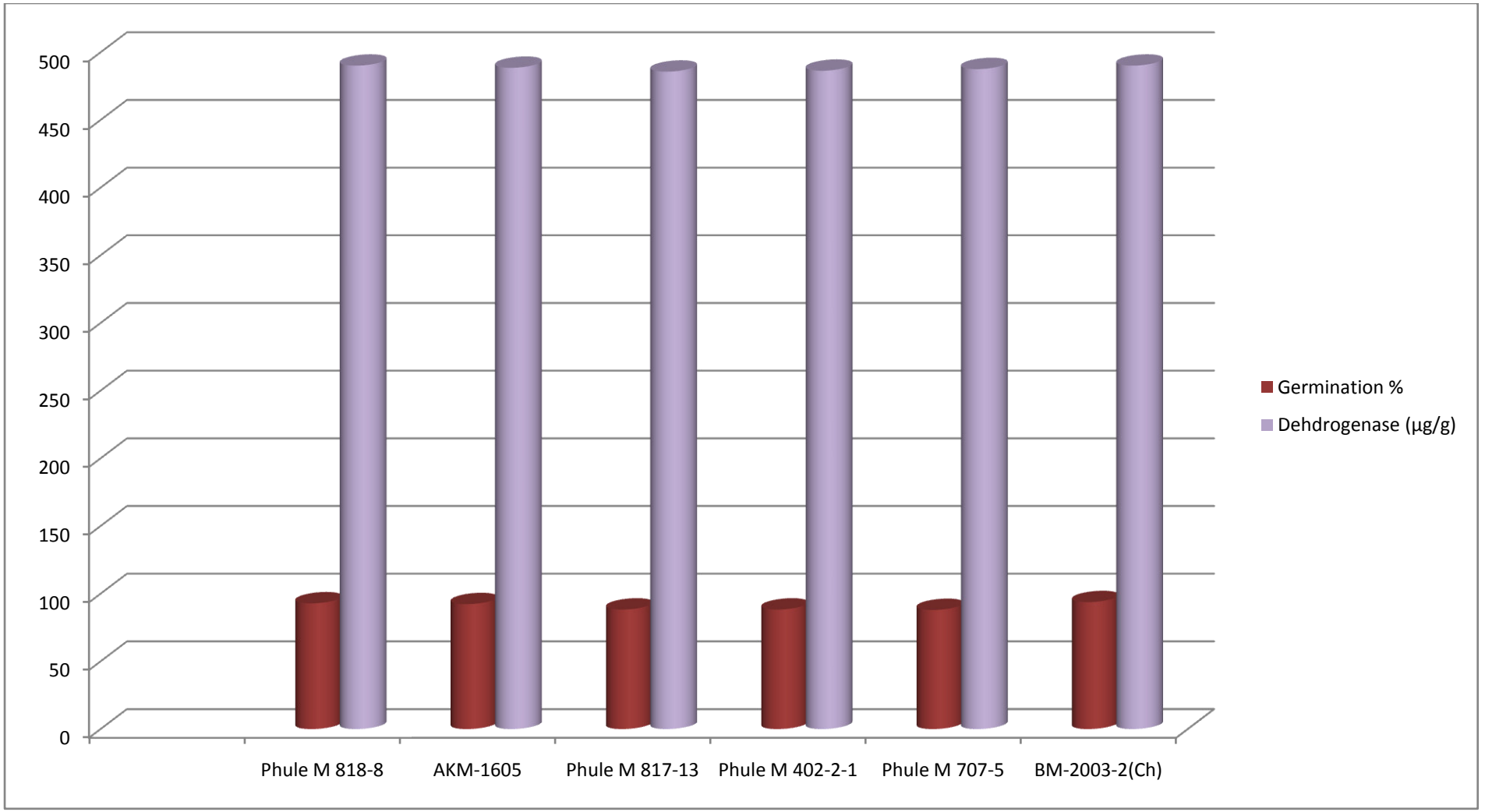

Fig. 2: Effect of dehydrogenase on germination percentage of top five genotypes with best check

Among the genotypes on the basis of pooled mean, Phule M 818-8 (92.9 %) recorded highest germination percentage followed by AKM-1605 (92.3 %), Phule M 817-13 and Phule M 402-2-1 (88.3 %) and Phule M 707-5 (88.0 %) while genotype, TBM-6 (72.8 %) recorded lowest germination percentage followed by AKM-1228 (77.1 %), AKM-1603 (78.0 %), TBM-4 (79.3 %) and TBM-10 (80.3 %).

In the checks, PKVM-4 and BM-2003-2 (93.8 %) expressed highest germination percentage, followed by Utkarsh (92.6 %), BPMR145 (92.5 %) and BM-2002-1 (92.4 %). In all the 34 entries, in which 25 were genotypes and 9 were checks, only one genotype i.e. TBM-6 showed the significant low results as compare with Minimum Seed Certification Standard (MSCS) regarding the germination percentage trait (Table 4.3g).

Germination test method by Towel Paper in laboratory and its evaluation have shown in Plate 2 and 3 while germination percentage of top five genotypes with the best check influenced by α-amylase and dehydrogenase are graphically depicted in Fig. 1 and 2.

4.2.3.2: Hard seed percentage

As per the observation recorded in germination test, the hard seed percentage found varied range from 1.8 to 6.3 % with mean 4.0 % in *kharif* 2020, 2.3 to 6.5 % with mean 4.1 % in *kharif* 2021 and 2.0 to 6.4 % with mean 4.0 % in pooled mean. The grand mean value is recorded 4.0 % in this trait (Table 4.2).

Among the genotypes, AKM-1605 (6.37 %) recorded more hard seed percentage in seed germination test, followed by Phule M 818-8 (5.87 %), Phule M 707-5 (5.62 %), Phule M 504-20-27 (5.50 %), Phule M 402-2-1 and AKM-1606 (5.25 %) while genotypes Phule M 809-10 (2.12 %), AKM-1609 and AKM-1603 (2.37 %), Phule M 809-12 (2.50 %), Phule M 602-9 (2.62 %) and TBM-10 (2.99 %) were recorded the low hard seed percentages.

The result on hard seed percentage in checks, the following varieties showed maximum percentage of hard seed % *viz.* BM-2003-2 (6.00 %), BM-2002-1 (5.37 %) and BPMR-145 (5.00 %) whereas, BM-4 (2.00 %), PKV Green Gold and

Utkarsh (3.62 %) noted minimum percentage of hard seed in seed germination test (Table 4.3h).

Table 4.3 h: Mean performance of genotypes for hard seed % and pod opening time (hrs.) over two seasons.

Sr. No.	Genotypes	Hard seed %			Pod opening time(hrs.)		
		Kh-2020	*Kh*-2021	Pool	*Kh*-2020	*Kh*-2021	Pool
1	Phule M 707-5	5.5	5.8	5.62	29.50	32.00	30.8
2	AKM-12-14	2.8	3.3	3.00	5.00	5.50	5.3
3	Phule M 602-9	2.5	2.8	2.62	1.00	1.50	1.3
4	AKM-12-24	3.5	3.3	3.37	25.00	22.50	23.8
5	BM-2019-1	4.5	4.8	4.62	20.00	16.50	18.3
6	Phule M 702-1	4.3	3.8	4.00	38.50	35.00	36.8
7	AKM-1609	2.5	2.3	2.37	44.50	48.00	46.3
8	AKM-1603	2.5	2.3	2.37	**1.00**	**0.50**	**0.8**
9	AKM-1602	4.8	5.0	4.87	**0.50**	**1.00**	**0.8**
10	Phule M 816-10	4.5	4.8	4.62	28.50	32.00	30.3
11	Phule M 817-13	4.0	3.5	3.75	37.50	35.00	36.3
12	TBM-4	3.8	4.5	4.12	0.50	1.00	0.8
13	TBM-6	3.3	2.7	2.99	1.00	1.50	1.3
14	AKM-12-28	3.0	3.3	3.12	4.50	6.00	5.3
15	TBM-10	3.5	3.8	3.62	5.00	3.50	4.3
16	TBM-127	4.3	4.0	3.12	45.00	41.50	43.3
17	Phule M 809-12	2.3	2.8	2.50	39.50	41.00	40.3
18	AKM-12-23	4.8	4.5	4.62	35.00	30.50	32.8
19	Phule M 818-8	5.5	6.3	5.87	70.50	68.00	69.3
20	Phule M 809-10	2.0	2.3	2.12	54.50	49.00	51.8
21	Phule M 402-2-1	5.5	5.0	5.25	40.00	35.50	37.8
22	Phule M 504-20-27	5.8	5.3	5.50	30.50	25.00	27.8
23	AKM-1606	5.0	5.5	5.25	45.50	40.50	43.0
24	AKM-1605	**6.3**	**6.5**	**6.37**	5.00	4.50	4.8

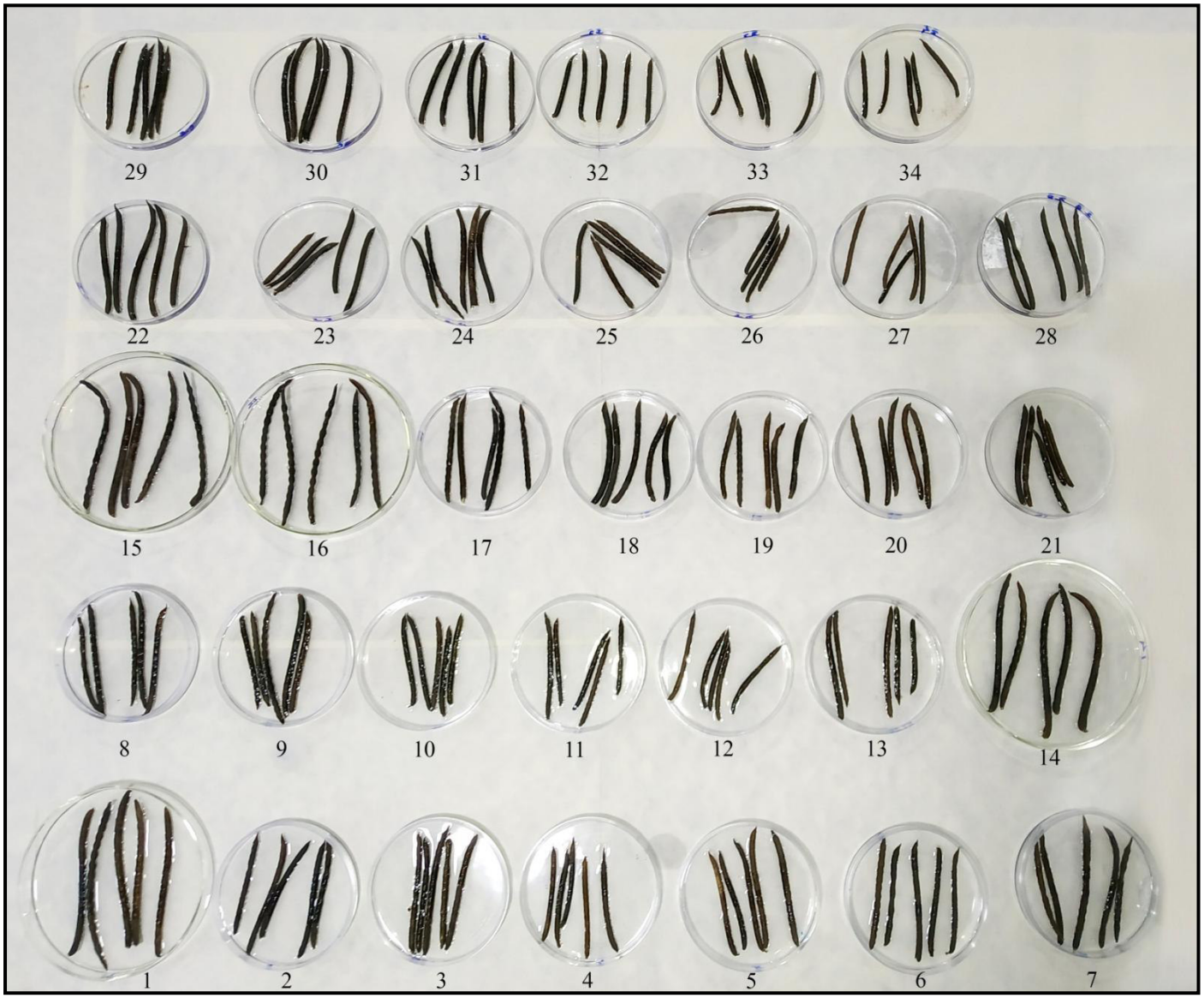

Plate 4: Evaluation of dormancy in mungbean by *in-situ* germination at laboratory (Pre-Harvest Sprouting)

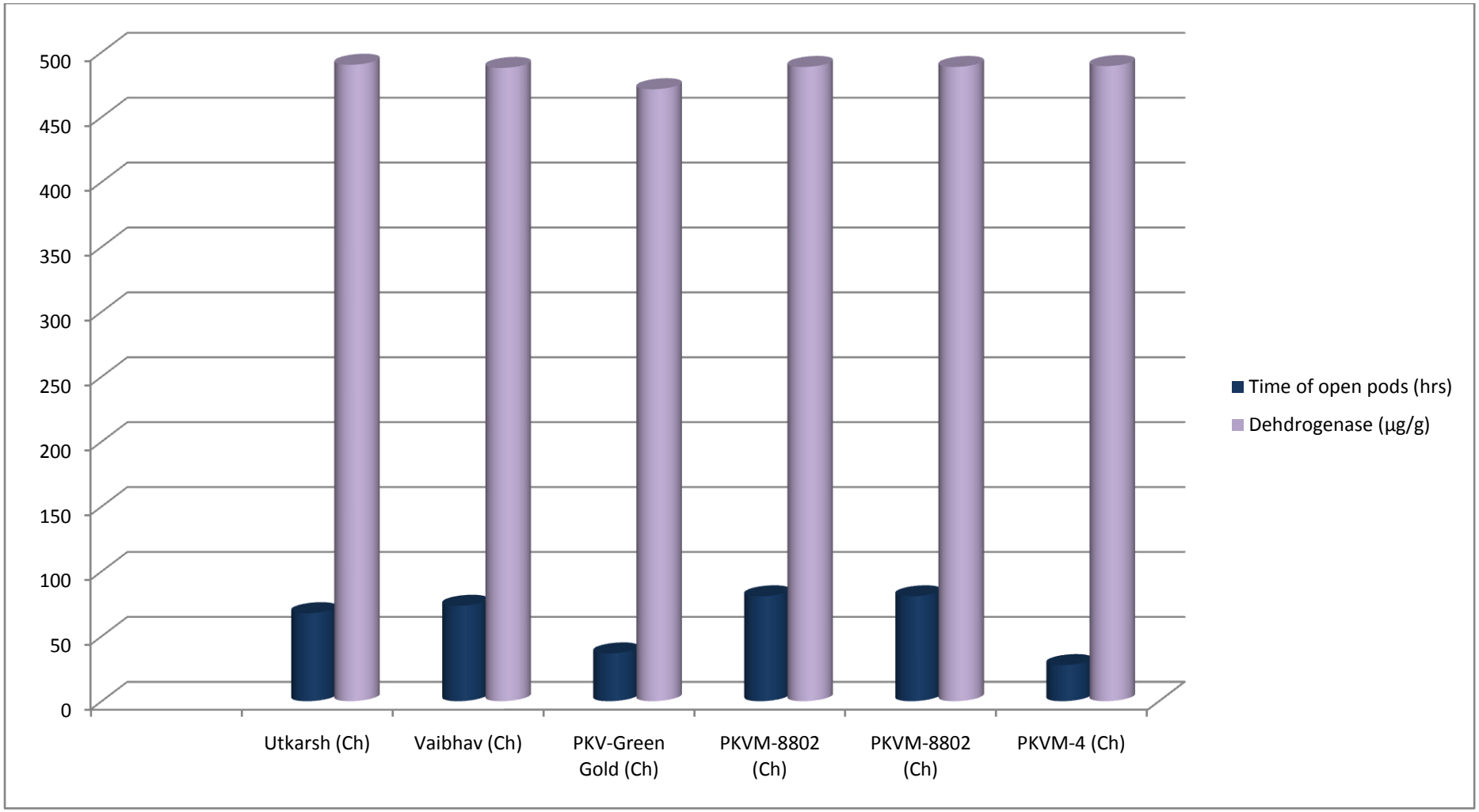

Fig. 4: Effect of dehydrogenase on time of opening of pods of top five genotypes with best check

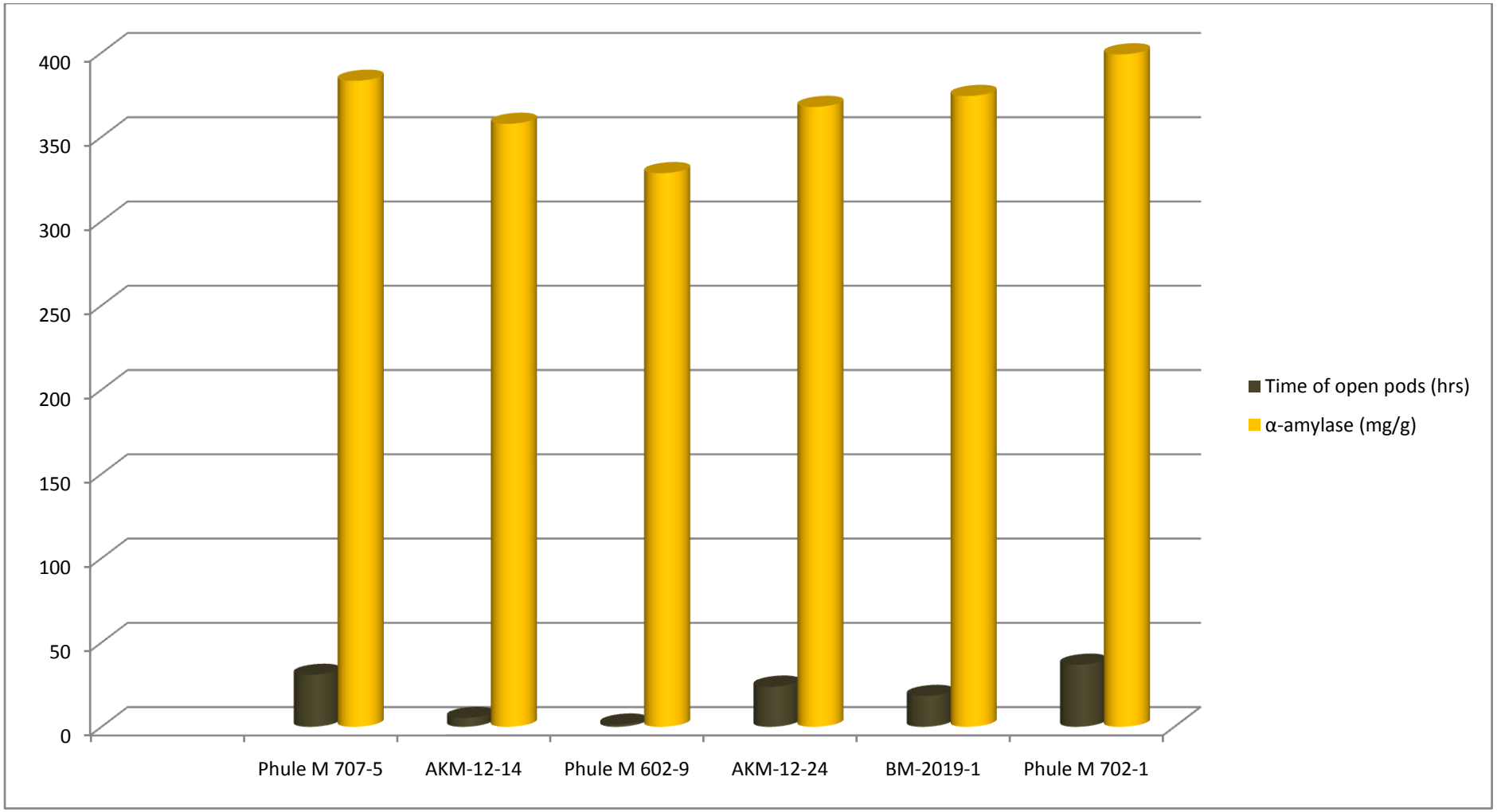

Fig. 3: Effect of α-amylase on time of opening of pods of top five genotypes with best check

Table 4.3 h: Contd….

Sr. No.	Genotypes	Hard seed %			Pod opening time (hrs.)		
		Kh-2020	*Kh*-2021	Pool	*Kh*-2020	*Kh*-2021	Pool
25	AKM-1608	3.3	2.8	3.00	55.00	49.50	52.3
26	**BM-4 (Ch)**	**1.8**	**2.3**	**2.00**	35.00	30.50	32.8
27	**BPMR-145 (Ch)**	5.3	4.8	5.00	74.50	70.00	72.3
28	**BM-2002-1(Ch)**	5.5	5.3	5.37	10.00	7.50	8.8
29	**BM-2003-2(Ch)**	5.8	6.3	6.00	67.50	60.00	63.8
30	**PKVM-4 (Ch)**	4.5	4.8	4.62	30.00	25.50	27.8
31	**PKVM-8802 (Ch)**	3.5	4.3	3.87	**83.50**	**78.00**	**80.8**
32	**PKV-Green Gold (Ch)**	3.8	3.5	3.62	35.50	38.00	36.8
33	**Vaibhav (Ch)**	4.8	4.3	4.50	75.00	72.00	73.5
34	**Utkarsh (Ch)**	3.8	3.5	3.62	70.00	65.50	67.8
Mean		**4.0**	**4.1**	**4.0**	**33.6**	**31.6**	**32.6**
SE±		0.06	0.05	0.05	0.12	0.03	0.31
CD		0.18	0.15	0.16	278.91	120.83	0.93

4.2.3.3: Pod opening time (hrs)

The Fresh Seed Dormancy (FSD) of mungbean has assessed in this observation by *in-situ* germination study *i.e*. time of opening of pods (hrs). Evaluation of dormancy in mungbean by *in-situ* germination at laboratory (Pre-Harvest Sprouting) has shown in Plate 4.

Time to opening of pods (hrs) range values were observed from 0.5 to 83.0 hrs with mean 33.6 hrs. in *kharif* 2020, 0.5 to 78.0 hrs with mean 31.6 hrs in *kharif* 2021 and 0.8 to 80.8 hrs with mean value 32.6 hrs in pooled mean. The grand mean value for time of opening the pod was found 32.6 hrs (Table 4.2).

On the basis of pooled mean data the following genotypes recorded very short time for open the pods *viz.,* AKM-1603, AKM-1602 and TBM-4 (0.8 hrs), Phule M 602-9 and TBM-6 (1.3 hrs), TBM-10 (4.3 hrs), AKM-1605 (4.8 hrs). These genotypes required nearly half day to open the pods, means these lines were found favorable in *in-situ* germination, i.e. less fresh seed dormant genotypes (Plate 5).

The following genotypes and checks observed moderate time for opening the pods *viz.,* Phule M 707-5 (30.8 hrs), AKM-12-14 (5.3 hrs), AKM-12-24 (23.8 hrs), BM-2019-1 (18.3 hrs), Phule M 702-1 (36.8 hrs), AKM-1609 (46.3 hrs), Phule M 816-10 (30.3 hrs), Phule M 817-13 (36.3 hrs), AKM-12-28 (5.3 hrs), Phule M 809-12 (40.3 hrs), AKM-12-23 (32.8 hrs), Phule M 402-2-1 (37.8 hrs), Phule M 504-20-27 (27.8 hrs), AKM-1605 (4.8 hrs), BM-4 Ch. (32.8 hrs), BM-2002-1 Ch (8.8 hrs), PKVM-4 Ch (27.8 hrs) and PKV Green Gold Ch (36.8 hrs) i.e. nearly 1-2 days time taken for opening of pods (Plate 6 & 7).

However the observation of (pre harvest sprouting) time for opening the pods following genotypes and check were found more time taken genotypes to open the pods. These are TBM-127 (43.3 hrs.), Phule M 818-8 (69.3 hrs.), Phule M 809-10 (51.8 hrs.), AKM-1606 (43.0 hrs.), AKM-1608 (52.3 hrs.), BPMR-145 Ch. (72.3 hrs.), BM-2003-2 Ch. (63.8 hrs.), PKVM-8802 Ch. (80.8 hrs.), Vaibhav Ch. (73.5 hrs.) and Utkarsh Ch. (67.8 hrs.). It means these genotypes and checks were found resistant to unpredictable rains at maturity and had fresh seed dormancy up to 2-3 days (Table 4.3h).

The time of opening of pods in hrs of top five genotypes with the best check influenced by α-amylase and dehydrogenase are graphically depicted in Fig. 3 and 4.

4.2.3.4: Seedling length (cm)

The observation of seedling length (cm) on mean data revealed the range from 28.2 to 39.5 cm with mean value 35.3 cm in *kharif* 2020, 30.2 to 40.4 cm with mean 36.0 cm in *kharif* 2021 and 29.1 to 39.9 cm with mean of 35.7 cm in pooled mean. The grand mean for this trait recorded 35.7 cm (Table 4.2).

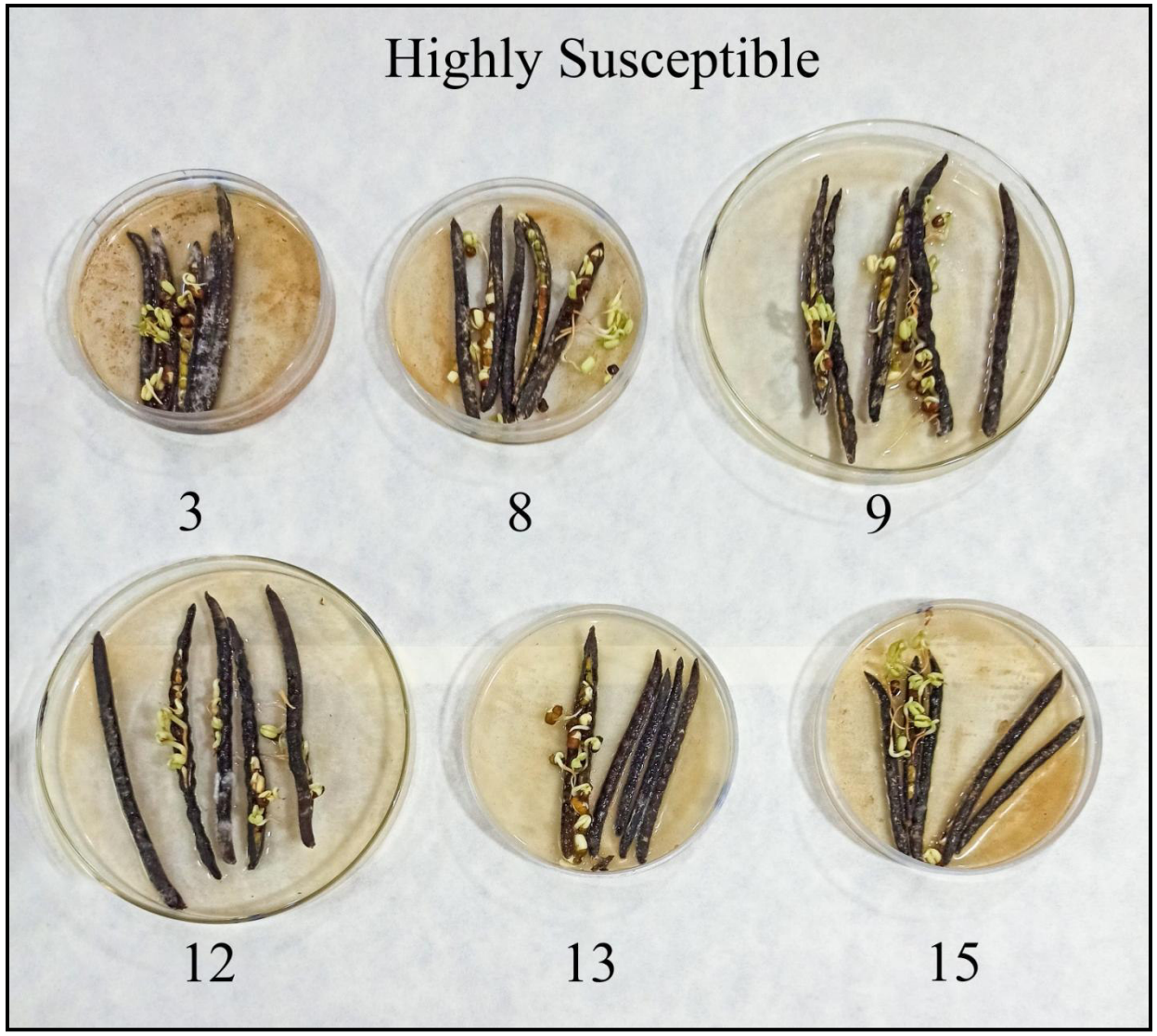

Plate 5: Highly susceptible genotypes indicated less fresh seed dormancy (FSH) by *in-situ* germination at laboratory

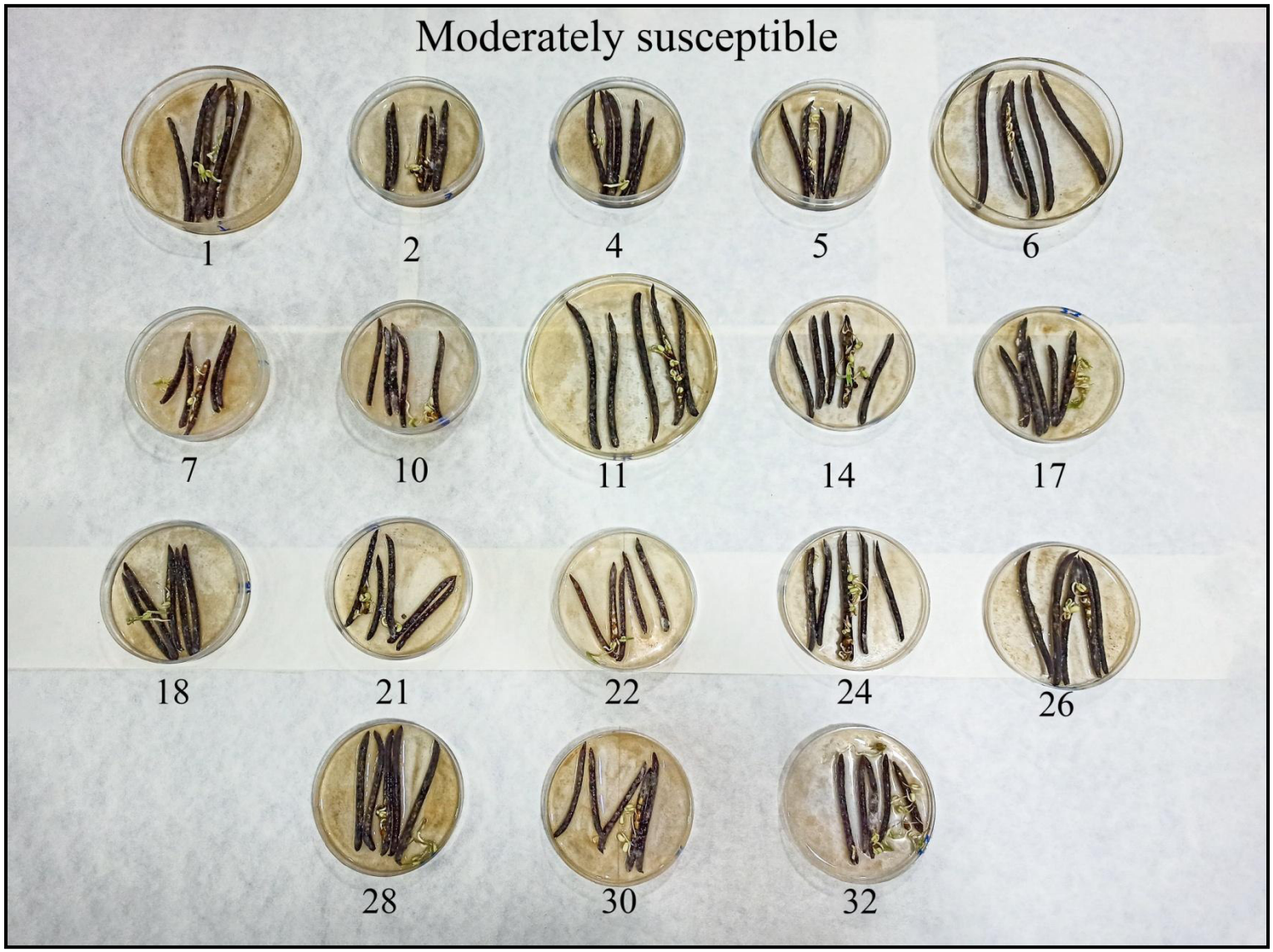

Plate 6: Moderately susceptible genotypes indicated moderate fresh seed dormancy (FSH) by *in-situ* germination at laboratory

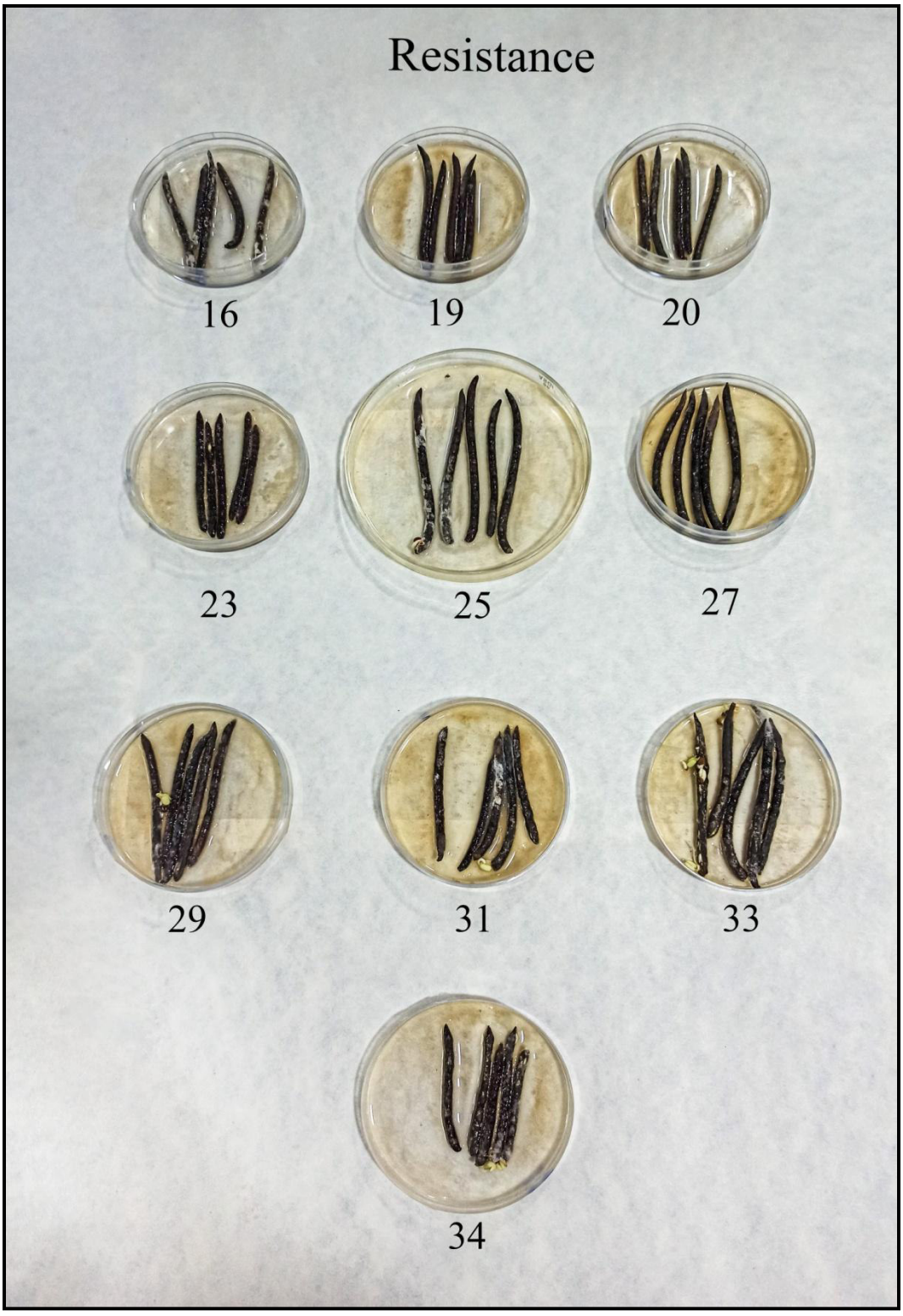

Plate 7: Resistant genotypes indicated more fresh seed dormancy (FSD) by *in-situ* germination at laboratory

Maximum seedling length (cm) among tested genotypes were recorded in AKM-1605 (39.5 cm), followed by Phule M 817-13 (38.6 cm), Phule M-818-8 (38.2 cm), Phule M 816-10 (38.0 cm) and AKM-1606 (37.3 cm) while only one genotype among all entries was found below the 30.0 cm of seedling length i.e. AKM-1603 (29.1 cm).

In this study, out of nine checks highest seedling length (cm) observed in BM-2003-2 (39.9 cm) followed by BM-2002-1 (39.5 cm), Vaibhav (38.9 cm), BPMR-145 (38.3 cm) and Utkarsh (37.9 cm) (Table 4.3i).

Table 4.3 i: Mean performance of genotypes for Seedling length (cm) and vigour Index I over two seasons

Sr. No.	Genotypes	Seedling length (cm)			Vigour index I		
		Kh-2020	*Kh*-2021	Pool	*Kh*-2020	*Kh*-2021	Pool
1	Phule M 707-5	34.5	35.5	35.0	3048.8	3101.9	3075.4
2	AKM-12-14	33.3	32.0	32.6	2743.1	2635.9	2689.5
3	Phule M 602-9	30.5	32.1	31.3	2455.3	2696.4	2575.8
4	AKM-12-24	35.2	34.8	35.0	3014.1	3045.0	3029.6
5	BM-2019-1	34.2	36.7	35.4	2919.8	3153.6	3036.7
6	Phule M 702-1	35.7	36.8	36.3	3097.0	3220.0	3158.5
7	AKM-1609	35.3	37.4	36.4	3002.2	3235.1	3118.7
8	AKM-1603	**28.1**	**30.2**	**29.1**	**2173.9**	2370.7	**2272.3**
9	AKM-1602	35.4	35.1	35.3	3026.7	3062.5	3044.6
10	Phule M 816-10	37.6	38.4	38.0	3261.8	3344.3	3303.0
11	Phule M 817-13	38.5	38.8	38.6	3388.0	3429.4	3408.7
12	TBM-4	31.0	32.5	31.8	2418.0	2616.3	2517.1
13	TBM-6	33.0	32.2	32.6	2376.0	**2363.0**	2369.5
14	AKM-12-28	32.8	32.2	32.5	2517.4	2491.6	2504.5
15	TBM-10	32.7	33.0	32.8	2612.0	2656.5	2634.3
16	TBM-127	35.7	35.3	35.5	3088.1	3097.6	3092.8
17	Phule M 809-12	34.5	34.1	34.3	2949.8	2968.4	2959.1
18	AKM-12-23	35.4	34.8	35.1	3062.1	3053.7	3057.9
19	Phule M 818-8	37.8	38.5	38.2	3487.1	3599.8	3543.4
20	Phule M 809-10	34.6	35.7	35.2	2975.6	3105.9	3040.8
21	Phule M 402-2-1	34.0	36.7	35.4	2975.0	3266.3	3120.7
22	Phule M 504-20-27	36.3	37.4	36.8	3126.6	3281.9	3204.2
23	AKM-1606	38.7	35.9	37.3	3304.6	3132.3	3218.4
24	AKM-1605	38.5	40.5	39.5	3522.8	3766.5	3644.6

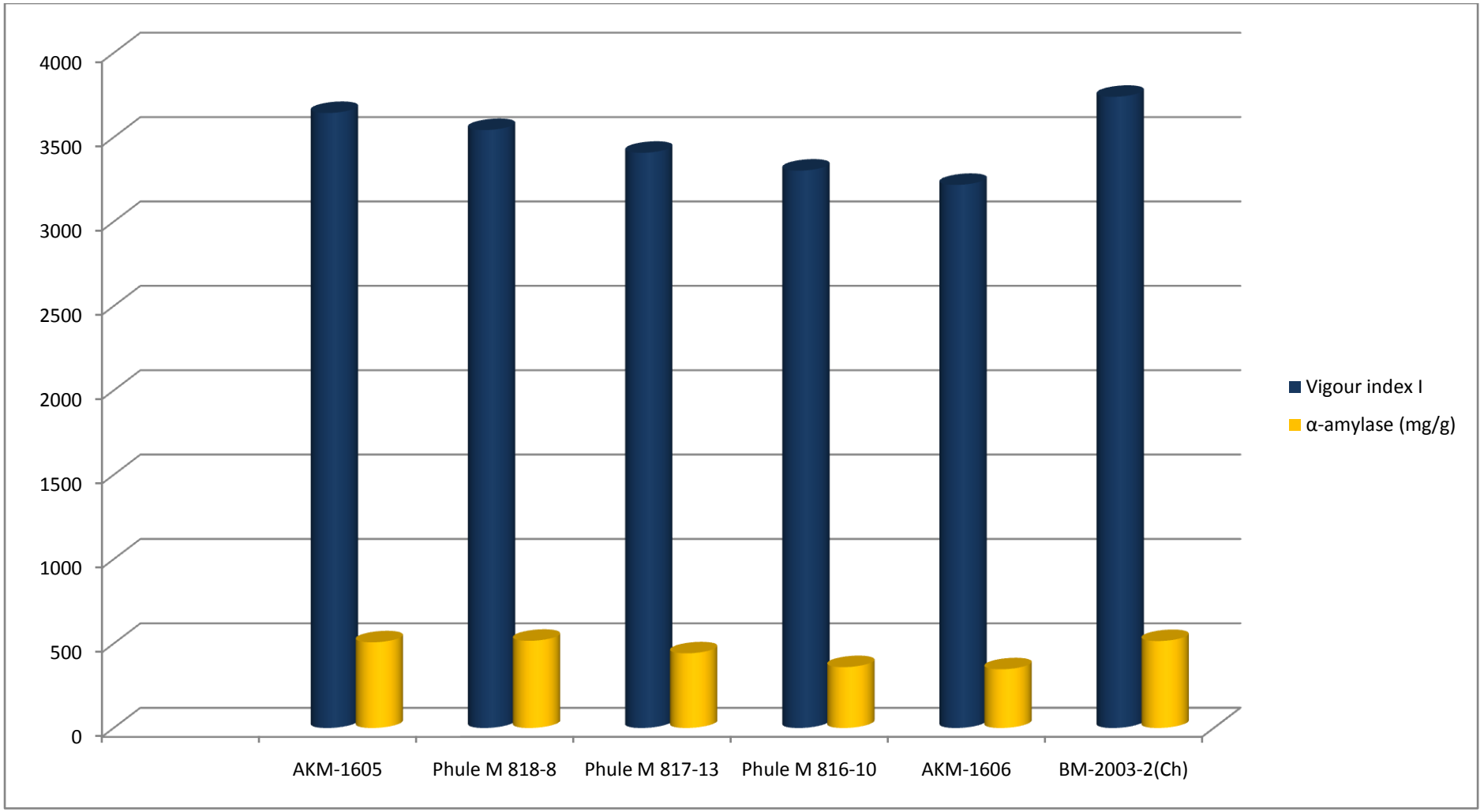

Fig. 5: Effect of α-amylase on vigour index I of top five genotypes with best check

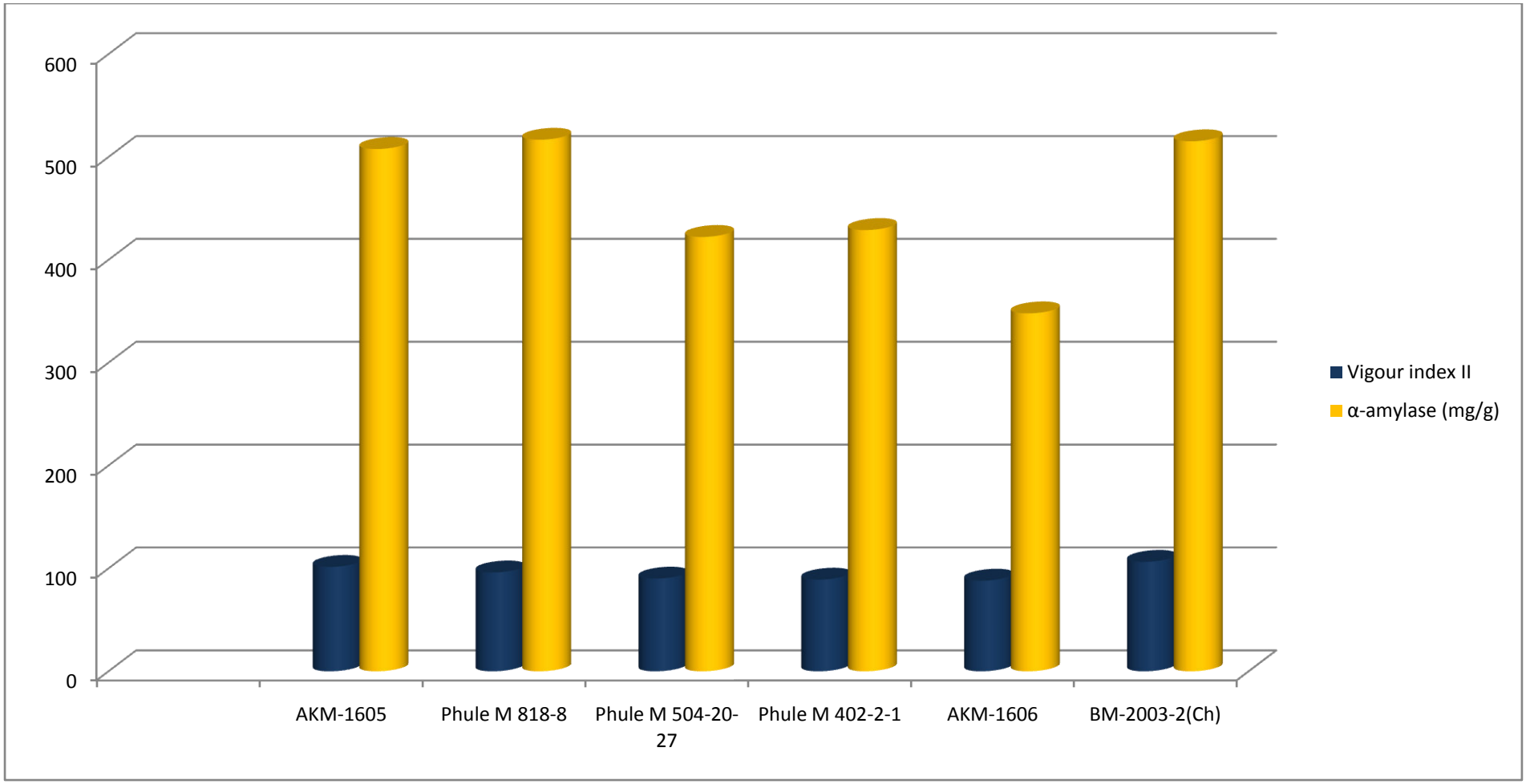

Fig. 7: Effect of α-amylase on vigour index II of top five genotypes with best check

Table 4.3 i: Contd….

Sr. No.	Genotypes	Seedling length (cm)			Vigour index I		
		Kh-2020	*Kh*-2021	Pool	*Kh*-2020	*Kh*-2021	Pool
25	AKM-1608	34.0	34.8	34.4	2907.0	3014.6	2960.8
26	**BM-4 (Ch)**	34.5	36.5	35.5	2967.0	3193.8	3080.4
27	**BPMR-145 (Ch)**	37.8	38.9	38.3	3482.4	3603.3	3542.9
28	**BM-2002-1(Ch)**	38.7	40.3	39.5	3536.5	3761.7	3649.1
29	**BM-2003-2(Ch)**	**39.5**	**40.4**	**39.9**	**3708.3**	**3772.7**	**3740.5**
30	**PKVM-4 (Ch)**	37.6	35.7	36.6	3501.5	3360.0	3430.8
31	**PKVM-8802 (Ch)**	36.7	37.8	37.3	3385.6	3458.7	3422.1
32	**PKV-Green Gold (Ch)**	34.5	34.6	34.6	2984.3	3010.2	2997.2
33	**Vaibhav (Ch)**	38.3	39.5	38.9	3519.0	3614.3	3566.6
34	**Utkarsh (Ch)**	37.0	38.7	37.9	3422.5	3589.4	3506.0
Mean		**35.3**	**36.0**	**35.7**	**3057.6**	**3149.2**	**3103.4**
SE±		2.87	2.51	3.14	96.93	42.01	97.2
CD		8.25	7.23	9.42	278.91	120.83	291.60

4.2.3.5: Vigour index I

The data revealed that the vigour index I recorded positive significant with germination percentage. Germination percentage values were more than the Minimum Seed Certification Standard (MSCS) in all genotypes and checks in this study except only one genotype.

The range values for vigour index I for all entries of experiment were found 2272.3 to 3740.5 in pooled mean, 2173.9 to 3708.3 in *kharif* 2020 and 2363.0 to 3772.7 in *kharif* 2021 with grand mean value 3103.4 (Table 4.2).

In this study, AKM-1605 (3644.6) genotype recorded the highest vigour index I, followed by Phule M 818-8 (3543.4), Phule M 817-13 (3408.7), Phule M 816-10 (3303.0), AKM-1606 (3218.4) and Phule M 504-20-27 (3204.2). However, genotype AKM-1603 (2272.3) recorded the lowest vigour index I in all the genotypes followed by TBM-6 (2369.5), AKM-12-28 (2504.5), TBM-4 (2517.1) and

Phule M 602-9 (2575.8). In checks, BM-2003-2 (3740.5) found the highest and PKV Green Gold (2997.2) found the lowest vigour index I (Table 4.3i).

The vigour index I of top five genotypes with the best check influenced by α-amylase and dehydrogenase are graphically depicted in Fig. 5&6.

Table 4.3 j: Mean performance of genotypes for seedling dry wt. (g) and vigour Index II over two seasons

Sr. No.	Genotypes	Seedling dry wt. (g)			Vigour index II		
		Kh-2020	*Kh*-2021	Pool	*Kh*-2020	*Kh*-2021	Pool
1	Phule M 707-5	1.0	0.9	1.0	86.7	80.5	83.6
2	AKM-12-14	0.7	0.8	0.8	59.4	64.4	61.9
3	Phule M 602-9	0.7	0.7	**0.7**	**55.5**	59.6	**57.6**
4	AKM-12-24	1.0	1.0	1.0	84.0	86.6	85.3
5	BM-2019-1	0.9	1.0	1.0	80.4	82.6	81.5
6	Phule M 702-1	1.0	1.0	1.0	85.0	83.1	84.1
7	AKM-1609	0.8	1.0	0.9	67.6	84.8	76.2
8	AKM-1603	0.9	0.7	0.8	66.7	**53.4**	60.0
9	AKM-1602	0.9	0.9	0.9	75.2	81.1	78.2
10	Phule M 816-10	1.0	1.0	1.0	84.1	86.1	85.1
11	Phule M 817-13	1.0	1.0	1.0	88.9	86.7	87.8
12	TBM-4	0.8	0.8	0.8	59.7	66.0	62.8
13	TBM-6	0.8	0.9	0.8	59.8	63.2	61.5
14	AKM-12-28	0.9	0.9	0.9	65.2	67.0	66.1
15	TBM-10	0.9	0.9	0.9	69.6	70.8	70.2
16	TBM-127	1.0	1.0	1.0	83.9	86.9	85.4
17	Phule M 809-12	0.8	0.9	0.9	71.8	75.7	73.8
18	AKM-12-23	0.9	0.9	0.9	77.9	82.5	80.2
19	Phule M 818-8	1.0	1.1	1.0	93.2	99.1	96.1
20	Phule M 809-10	1.0	1.0	1.0	84.3	83.5	83.9
21	Phule M 402-2-1	1.0	1.0	1.0	86.6	91.7	89.1
22	Phule M 504-20-27	1.0	1.1	1.0	88.0	92.1	90.1
23	AKM-1606	1.0	1.1	1.0	84.6	91.6	88.1
24	AKM-1605	1.1	1.1	1.1	99.7	103.2	101.5

Table 4.3j: Contd….

Sr. No.	Genotypes	Seedling dry wt. (g)			Vigour index II		
		Kh-2020	*Kh*-2021	Pool	*Kh*-2020	*Kh*-2021	Pool
25	AKM-1608	1.0	1.0	1.0	83.8	88.5	86.1
26	**BM-4 (Ch)**	0.9	0.9	0.9	76.5	82.3	79.4
27	**BPMR-145 (Ch)**	1.0	1.1	1.0	91.3	97.4	94.4
28	**BM-2002-1(Ch)**	1.1	1.1	1.1	98.8	103.5	101.2
29	**BM-2003-2(Ch)**	**1.1**	**1.2**	**1.1**	**103.4**	**109.4**	**106.4**
30	**PKVM-4 (Ch)**	1.0	1.0	1.0	89.5	93.3	91.4
31	**PKVM-8802 (Ch)**	1.0	1.0	1.0	90.4	95.2	92.8
32	**PKV-Green Gold (Ch)**	0.9	0.9	0.9	76.1	80.0	78.1
33	**Vaibhav (Ch)**	1.1	1.1	1.1	99.4	103.4	101.4
34	**Utkarsh (Ch)**	1.0	1.1	1.0	94.4	97.4	95.9
Mean		**0.9**	**1.0**	**1.0**	**81.2**	**84.5**	**82.9**
SE±		0.01	0.02	0.28	2.00	3.80	2.27
CD		0.04	0.06	0.84	5.76	10.93	6.81

4.2.3.6: Seedling dry wt. (g)

The seedling dry weight (g) showed a direct relation to the seedling length. In germination test it is observed highly positive significant relationship of seedling length (cm) and Seedling dry weight (g).

The seedling dry wt. (g) in *kharif* 2020 & *kharif* 2021 observed the range from 0.7 to 1.1 g and 0.7 to 1.2 g respectively while in pooled mean from 0.9 to 1.0 g with grand mean value 1.0 g (Table 4.2).

The genotype *viz.,* AKM-1605, checks BM-2002-1, BM-2003-2 and Vaibhav recorded highest seedling dry weight (1.1 g) while genotype Phule M 602-9 (0.7 g) recorded the lowest seedling dry weight. The seedling dry weight of 1.0 g of each were recorded by the following genotypes *viz.* Phule M 707-5, AKM-12-24, BM-2019-1, Phule M 702-1, Phule M 816-10, Phule M 817-13, TBM-127, Phule M 818-8, Phule 809-10, Phule 402-2-1, Phule 504-20-27, AKM-1606, AKM-1608

whereas the genotypes AKM-1609, AKM-1602, AKM-1228, TBM-10, Phule M 809-12 and AKM-12-23 recorded the 0.9 g. and AKM-12-14, AKM-1603, TBM-4 and TBM-6 recorded 0.8 g of seedling dry wt.

However, among all the nine checks, three checks *viz*. BM-2002-1, BM-2003-2 and Vaibhav were recorded 1.1 g, BPMR-145, PKVM-4, PKVM-8802 and Utkarsha 1.0 g. and BM-4 and PKV Green Gold were recorded 0.9 g seedling dry wt. (Table 4.3j).

4.2.3.7: Vigour index II

The data revealed that the vigour index II recorded positive significant with seedling dry weight in grams.

The observation of vigour index II found the range values from 57.6 to 106.4 in pooled mean whereas, in two seasons i.e. in *kharif* 2020 and *kharif* 2021 predicted the range from 55.5 to 103.4 and 53.4 to 109.4 respectively. The grand mean value has noted 82.9 by analyzed data (Table 4.2).

The genotype AKM-1605 (101.5) recorded highest vigour index II, followed by genotypes Phule M 818-8 (96.1), Phule M 504-20-27 (90.1), Phule M 402-2-1 (89.1), AKM-1606 (88.1) and AKM-1608 (86.1) whereas, genotype Phule M 602-9 (57.6) recorded the lowest vigour index II.

Checks varieties BM-2003-2 (106.4) and Vaibhav (101.4) recorded the highest vigour index II whereas PKV Green Gold (78.1) and BM-4 (79.4) recorded lowest vigour index II among all checks (Table 4.3j).

The vigour index II of top five genotypes with the best check influenced by α-amylase and dehydrogenase are graphically depicted in Fig. 7&8.

4.2.3.8: Seed hardness (Kg/cm^2)

In the observation of seed hardness (Kg/cm^2) character range values recorded from 3.5 to 5.2 Kg/cm^2 in pooled mean while in both seasons i.e. in *kharif* 2020 & *kharif* 2021 were 3.5 to 5.7 Kg/cm^2 and 3.5 to 5.3 Kg/cm^2 respectively. The grand mean value for this trait was found 4.4 Kg/cm^2 (Table 4.2).

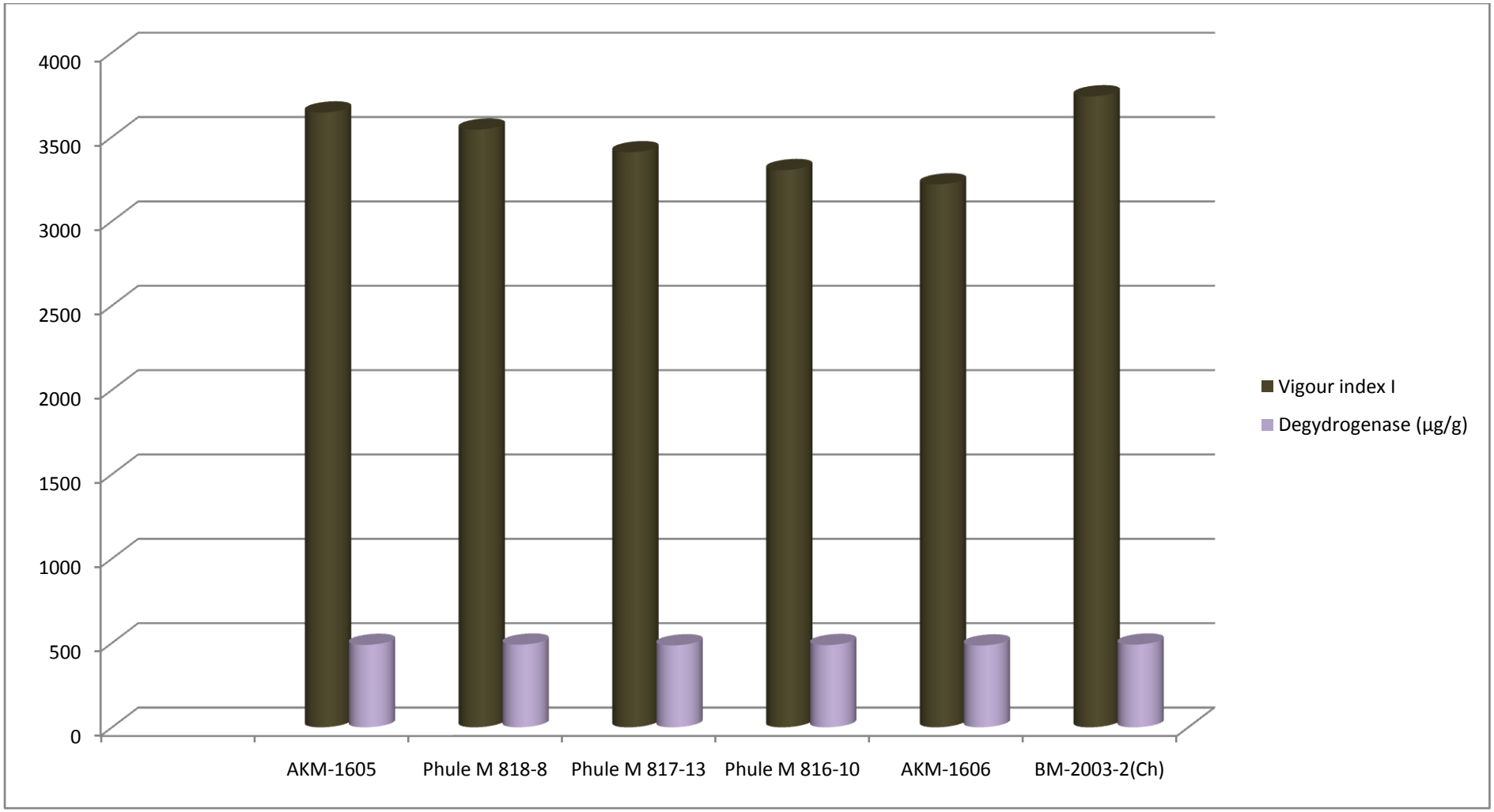

Fig. 6: Effect of dehydrogenase on vigour index I of top five genotypes with best check

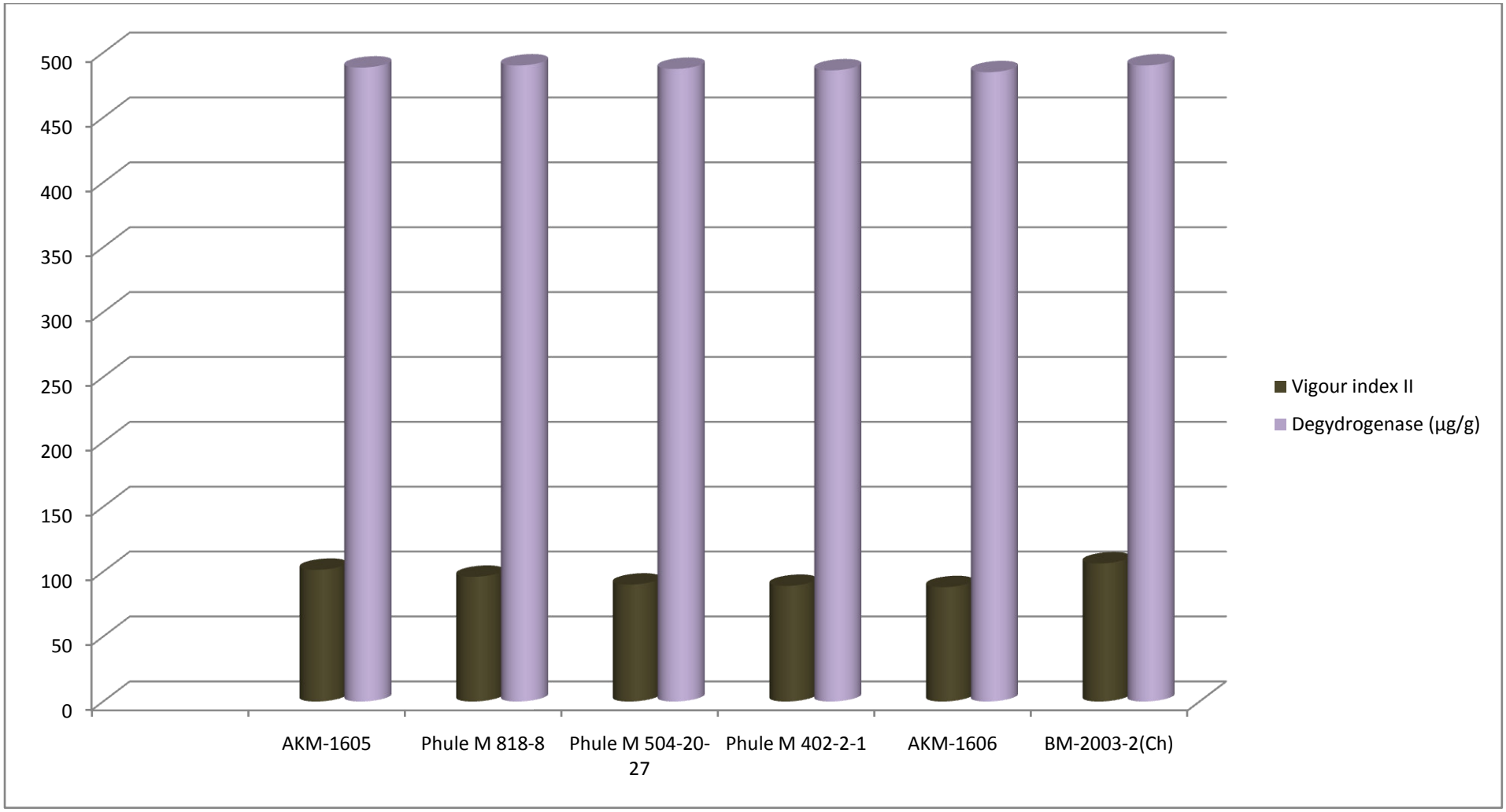

Fig. 8: Effect of dehydrogenase on vigour index II of top five genotypes with best check

Table 4.3 k: Mean performance of genotypes for seed hardness (Kg/cm^2) and α-amylase (mg/g) over two seasons

Sr. No.	Genotypes	Seed hardness (Kg/cm^2)			α-amylase (mg/g)		
		Kh-2020	*Kh*-2021	Pool	*Kh*-2020	*Kh*-2021	Pool
1	Phule M 707-5	**5.7**	4.8	**5.2**	387.0	379.5	383.3
2	AKM-12-14	4.8	5.0	4.9	354.0	361.5	357.8
3	Phule M 602-9	4.8	4.8	4.8	319.5	337.5	328.5
4	AKM-12-24	4.5	4.8	4.6	366.0	369.5	367.8
5	BM-2019-1	4.8	4.8	4.8	372.0	376.5	374.3
6	Phule M 702-1	4.3	4.0	4.1	396.0	402.0	399.0
7	AKM-1609	4.8	5.0	4.9	325.5	333.0	329.3
8	AKM-1603	5.0	4.8	4.9	295.5	307.5	301.5
9	AKM-1602	4.3	4.3	4.3	327.0	330.0	328.5
10	Phule M 816-10	4.0	4.3	4.1	357.0	364.5	360.8
11	Phule M 817-13	4.8	**5.3**	5.0	436.5	448.5	442.5
12	TBM-4	4.8	**5.3**	5.0	294.0	288.0	291.0
13	TBM-6	4.3	4.3	4.3	**231.0**	**241.5**	**236.3**
14	AKM-12-28	4.5	4.8	4.6	265.5	276.0	270.8
15	TBM-10	4.8	4.8	4.8	313.5	318.0	315.8
16	TBM-127	4.3	4.3	4.3	423.5	412.5	418.0
17	Phule M 809-12	4.5	4.5	4.5	358.5	369.0	363.8
18	AKM-12-23	4.3	4.3	4.3	429.0	423.0	426.0
19	Phule M 818-8	4.0	4.0	4.0	521.5	512.0	516.8
20	Phule M 809-10	4.3	4.5	4.4	408.0	414.0	411.0
21	Phule M 402-2-1	4.0	4.3	4.1	423.0	435.0	429.0
22	Phule M 504-20-27	4.0	3.5	3.8	426.0	418.5	422.3
23	AKM-1606	4.0	4.0	4.0	343.5	352.5	348.0
24	AKM-1605	4.0	3.8	3.9	510.5	505.0	507.8

Table 4.3 k: Contd….

Sr. No.	Genotypes	Seed hardness (Kg/cm^2)			α-amylase (mg/g)		
		Kh-2020	*Kh*-2021	Pool	*Kh*-2020	*Kh*-2021	Pool
25	AKM-1608	4.3	4.5	4.4	432.0	428.5	430.3
26	**BM-4 (Ch)**	4.3	4.3	4.3	455.0	425.5	440.3
27	**BPMR-145 (Ch)**	**3.5**	**3.5**	**3.5**	508.5	510.5	509.5
28	**BM-2002-1(Ch)**	4.3	4.3	4.3	509.5	510.0	509.8
29	**BM-2003-2(Ch)**	4.3	4.8	4.5	510.0	520.5	515.3
30	**PKVM-4 (Ch)**	4.0	4.0	4.0	**529.5**	**535.5**	**532.5**
31	**PKVM-8802 (Ch)**	4.5	4.3	4.4	485.5	478.5	482.0
32	**PKV-Green Gold (Ch)**	4.3	4.3	4.3	412.5	425.5	419.0
33	**Vaibhav (Ch)**	4.0	4.3	4.1	471.0	478.5	474.8
34	**Utkarsh (Ch)**	4.5	4.8	4.6	508.5	499.5	504.0
Mean		**4.4**	**4.5**	**4.4**	**403.1**	**405.5**	**404.3**
SE±		0.18	0.16	0.45	4.18	4.82	4.45
CD		0.52	0.49	1.35	12.03	13.89	13.35

The analyzed data revealed that, seed hardness (Kg/cm^2) found maximum in genotypes Phule M 707-5 (5.2 Kg/cm^2) followed by Phule M 817-13 & TBM-4 (5.0 Kg/cm^2), AKM-12-14, AKM-1609 & AKM-1603 (4.9 Kg/cm^2) and Phule M 602-9, BM-2019-1, TBM-10 (4.8 Kg/cm^2).

Minimum seed hardness (Kg/cm^2) was found in the genotypes Phule M 504-20-27 (3.8 Kg/cm^2) followed by AKM-1605 (3.9 Kg/cm^2), Phule M 818-8 and AKM-1606 (4.0 Kg/cm^2).

In the checks, Utkarsh (4.6 Kg/cm^2), BM-2003-2 (4.5 Kg/cm^2) and PKVM-8802 (4.4 Kg/cm^2) was found maximum seed hardness while BPMR-145 (3.5 Kg/cm^2), PKVM-4 (4.0 Kg/cm^2) and Vaibhav (4.1 Kg/cm^2) were recorded minimum seed hardness (Table 4.3k).

Plate 8: Evaluation of α-amylase in mungbean at laboratory

4.2.3.9: α-amylase (mg/g)

In mungbean aleurone layer is present around endosperm of seed. During seed germination this aleurone layer degenerate and secret α-amylase which is responsible for degradation of carbohydrates, proteins and other food materials of endosperm and make it available to growing embryo.

On the basis of analyzed data, observation of α-amylase among all the genotypes found range from 236.3 to 532.5 mg/g in pooled mean value of both seasons while in *kharif* 2020 it noticed from 231.0 to 529.5 mg/g and in *kharif* 2021 from 241.5 to 490.9 mg/g. The grand mean value of this trait was found 404.3 mg/g (Table 4.2).

Among all the genotypes α-amylase recorded maximum in the Phule M 818-8 (516.8 mg/g) followed by genotypes AKM-1605 (507.8 mg/g), Phule M 817-13 (442.5 mg/g), AKM-1608 (430.3 mg/g), Phule M 402-2-1 (429.0 mg/g) and AKM-1223 (426.0 mg/g). The genotype TBM-6 (236.3 mg/g) recorded minimum α-amylase among tested genotypes followed by AKM-12-28 (270.8 mg/g), TBM-4 (291.0 mg/g), AKM-1603 (301.5 mg/g) and TBM-10 (315.8 mg/g).

The checks PKVM-4 (532.5 mg/g), BM-2003-2 (515.3 mg/g), BM-2002-1 (509.8 mg/g), BPMR-145 (509.5 mg/g), PKVM-8802 (482.0 mg/g l), Vaibhav (474. 8 mg/g), BM-4 (440.3 mg/g) and PKV Green Gold (419.0 mg/g) were found high concentration of α-amylase (Table 4.3k).

The activity of evaluation of α-amylase in mungbean at laboratory has depicted in Plate 8.

4.2.3.10: Dehydrogenase (µg/g)

The ranged values for Dehydrogenase (µg/g) for all entries of experiment were found 240.0 to 490.4 µg/g in pooled mean, 229.8 to 490.9 µg/g in *kharif* 2020 and 245.2 to 490.9 µg/g in *Kharif* 2021 with grand mean value 456.3 µg/g (Table 4.2).

The maximum dehydrogenase content recorded in genotypes Phule M 818-8 (490.16 µg/g) followed by AKM-1605 (488.57 µg/g), Phule M 707-5, Phule M

816-10 and Phule M 504-20-27 (487.53 µg/g), AKM-1602 (486.78 µg/g) and Phule M 402-2-1 (486.40 µg/g). However, the genotype Phule M 809-12 (240.04 µg/g) recorded minimum dehydrogenase content and followed by Phule M 809-10 (377.65 µg/g) and TBM-127 (379.15 µg/g). These three genotypes were recorded lower dehydrogenase content in all tested genotypes.

The observations of dehydrogenase activity content in checks, following results wereobserved. The checks Utkarsh (490.35 µg/g), BM-2003-2 (490.17 µg/g), PKVM-4 (489.32 µg/g), PKVM-8802 (488.66 µg/g), BPMR-145 (488.47 µg/g), BM-2002-1 (488.38 µg/g), Vaibhav (487.91 µg/g) and PKV Green Gold (471.48 µg/g) were found high concentration of dehydrogenase content while only one check BM-4 (229.80 µg/g) recorded low concentration of dehydrogenase content among all genotypes and checks of this study (Table 4.3l).

The activity of evaluation of dehydrogenase in mungbean at laboratory has depicted in Plate 9 and 10.

Table 4.3 l: Mean performance of genotypes for dehydrogenase (µg/g) over two Seasons

Sr. No.	Genotypes	Dehydrogenase (µg/g)		
		Kh-2020	*Kh*-2021	Pool
1	Phule M 707-5	487.2	488.09	487.62
2	AKM-12-14	473.2	474.53	473.87
3	Phule M 602-9	473.0	474.15	473.59
4	AKM-12-24	477.2	480.94	479.05
5	BM-2019-1	481.1	474.78	477.95
6	Phule M 702-1	480.4	479.81	480.09
7	AKM-1609	415.9	416.69	416.32
8	AKM-1603	475.3	477.74	476.51
9	AKM-1602	486.2	487.34	486.78
10	Phule M 816-10	487.3	487.72	487.53
11	Phule M 817-13	484.7	486.78	485.74
12	TBM-4	473.8	474.34	474.06
13	TBM-6	466.2	474.72	470.48
14	AKM-12-28	461.5	439.87	450.70
15	TBM-10	474.7	473.15	473.94
16	TBM-127	377.9	380.41	379.15
17	Phule M 809-12	**234.8**	**245.25**	**240.04**
18	AKM-12-23	487.9	482.25	485.08
19	Phule M 818-8	489.4	**490.92**	490.16
20	Phule M 809-10	372.3	383.02	377.65
21	Phule M 402-2-1	487.0	485.84	486.40
22	Phule M 504-20-27	487.7	487.34	487.53
23	AKM-1606	483.8	486.21	484.99
24	AKM-1605	488.7	488.47	488.57

Table 4.3 l: Contd….

Sr. No.	Genotypes	Dehydrogenase (µg/g)		
		Kh-2020	*Kh*-2021	Pool
25	AKM-1608	372.3	383.02	377.65
26	**BM-4 (Ch)**	229.8	229.78	229.80
27	**BPMR-145 (Ch)**	488.3	488.66	488.47
28	**BM-2002-1(Ch)**	489.4	487.34	488.38
29	**BM-2003-2(Ch)**	490.9	489.41	490.17
30	**PKVM-4 (Ch)**	489.8	488.85	489.32
31	**PKVM-8802 (Ch)**	488.5	488.85	488.66
32	**PKV-Green Gold (Ch)**	469.6	473.34	471.48
33	**Vaibhav (Ch)**	488.5	487.34	487.91
34	**Utkarsh (Ch)**	**490.9**	489.79	**490.35**
Mean		**456.0**	**456.7**	**456.3**
SE±		6.30	6.84	6.57
CD		18.14	19.68	19.71

4.3: Estimation of Correlation

4.3.1: Correlation studies of genotypes on seed yield with different yield contributing characters

Pearson correlation coefficient analysis was carried out & presented in Table 4.4.1. Correlation coefficient is an important statistical constant, which indicates the degree of association among the various characters. Seed yield is a complex character and is dependent on its component characters.

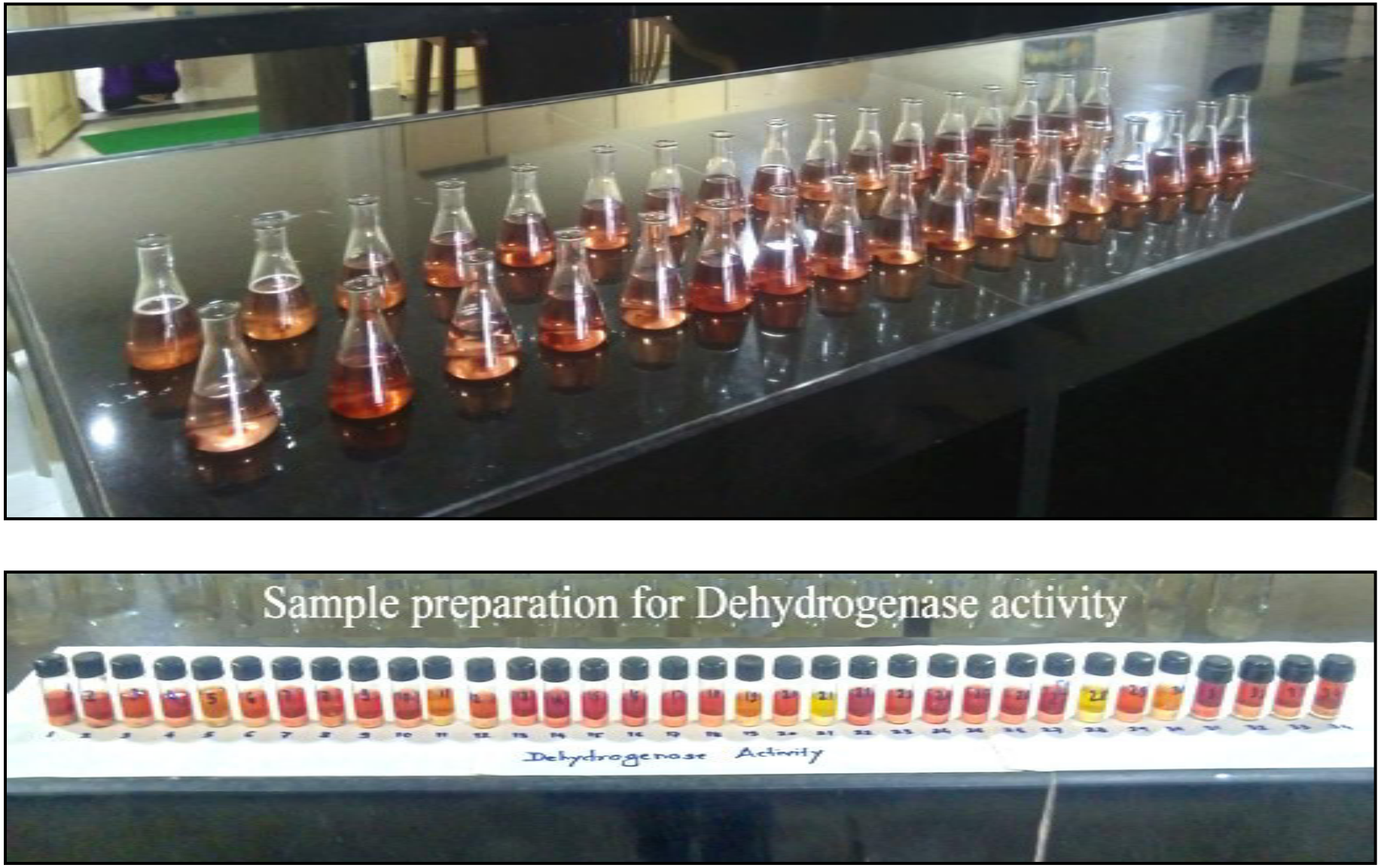

Plate 9: Preparation for dehydrogenase activity in mungbean

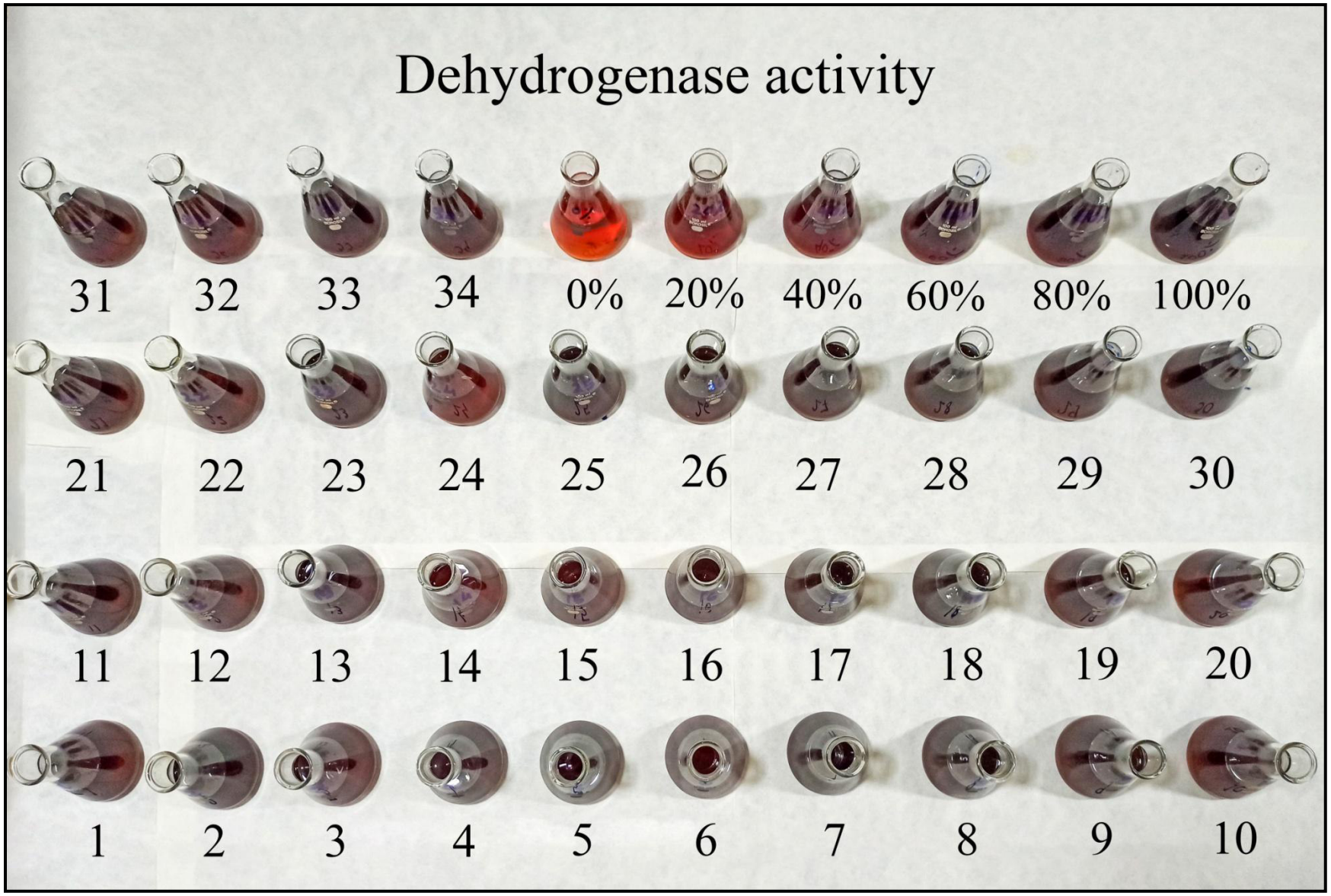

Plate 10: Evaluation of α-amylase in mungbean at laboratory

Table 4.4.1: Correlation studies of genotypes on seed yield with different yield contributing characters

	Plant height (cm)	No. of primary branches	No. of pods/cluster	No. of pods/plant	Length of pods (cm)	No. of seeds/ pod	Biological yield/plant (gm)	Harvest index (%)	Seed yield/plant (gm)
Plant height (cm)	1								
No. of primary branches	-0.001	1							
No. of pods/cluster	0.062	0.099	1						
No. of pods/plant	-0.245	0.431*	0.587**	1					
Length of pods (cm)	0.041	0.396*	-0.147	-0.072	1				
No. of seeds/ pod	-0.193	0.127	-0.163	-0.081	0.487**	1			
Biological yield/plant (gm)	0.179	-0.118	-0.134	-0.203	0.023	0.099	1		
Harvest index (%)	-0.429*	0.437**	0.231	0.702**	0.229	0.227	-0.611**	1	
Seed yield/plant (gm)	-0.453**	0.506**	0.251	0.808**	0.249	0.280	-0.206	0.887**	1

Correlation measures the actual relationship between various characters and helps the plant breeder in fixing selection criteria for grain yield in parental lines and segregating populations. Correlation coefficient reveals the type, nature and magnitude of association between any pair of characters. Phenotypic correlation is the association between two characters, which can be directly observed and is subjected to changes in the environment.

Therefore, study of relationship of characters with each other and with seed yield become more important in crop improvement programme. Hence, it is essential to find out relative contribution of each of the component characters in yield for giving due weight age during selection.

The seed yield character of the study recorded significant positive correlation with number of harvest index % (0.887), number of pods per plant (0.808) and primary branches (0.506) while it was non-significant positively correlated to the number of number of seeds per pod (0.280), pods per cluster (0.251) and length of pods cm (0.249). It also reported significant negatively correlation with plant height cm (-0.453) and non-significant negatively correlation with biological yield per plant in gram (-0.206).

In a present study seed yield is a complex trait and it is positively correlated with number of primary branches, number of pods per plant and harvest index. It revealed that increase in these yield contributing characters reflects increase in a yield and *vice-versa*. However it is observed that number of pods per cluster, length of pods and number of seeds per pod is correlated with yield in desirable direction. It means increases in number of primary branches, Number of pods per plant and harvest index % with increased seed yield per plant and *vice-versa*.

Seed yield per plant was negatively significant with plant height it means increase in plant height reduces the yield and *vice-versa* (Table 4.4.1).

The number of primary branches might be developed into more number of pod clusters which resulted in high seed yield per plant. Similar findings were earlier reported by Singh *et al.,* (1977), Kumar *et al.,* (2004), Khajudparn and Tantasawat (2011), Nand and Anuradha (2013), Ahmed *et al*., (2015), Ghimire *et al*., (2017), Kritikaand Yadav (2017), Kate *et al.,* (2017), and Keerthiga *et al.,*(2018).

The correlation of pods per plant and yield were also reported by Malhotra *et al*., (1974), Rathnaswamy *et al*., (1978), Upadhyaya *et al*., (1980), Khanpara *et al*., (2012), Das and Barua (2015) and Parihar *et al.,* (2018).

The similar results were also found with trait of harvest index % by Deore, (1983), Dixit *et al*., (2002), Haritha and Reddy Sekhar, (2002), Gupta *et al*., (2005), Gul *et al*., (2008), Vinay *et al*., (2010), Gadakh *et al*., (2013) and Dhoot *et al*., (2017). They suggested, while selecting for improvement of lines in seed yield, these characters can be keep in mind for selection.

The number of seeds per pod is an important factor which had direct effect on seed yield but due to the physiological factor and source sink relationship all pods does not contain more seeds. These results are in confirmation with the findings of Shelar (2002), Mondal *et al*. (2012) and Shinde *et al*. (2017).

Table 4.4.2: Correlation studies of genotypes on seed quality with different seed quality contributing characters

	Germination %	**Time to opening pods**	**Vigour index I**	**Vigour index II**	**α-amylase (mg/g)**	**Dehydrogenase (µg/g)**
Germination %	1					
Days to opening pods (hrs.)	0.666**	1				
Vigour index I	0.951**	0.647**	1			
Vigour index II	0.902**	0.652**	0.955**	1		
α- amylase (mg/g)	0.934**	0.636**	0.884**	0.867**	1	
Dehydrogenase (µg/g)	0.423*	-0.084	0.436*	0.405*	0.097	1

4.3.2: Correlation studies of genotypes on seed quality with different seed quality contributing characters

The enzyme α-amylase showed significant positive correlation with germination percentage (0.934), time to opening of pods (0.636), vigour index I (0.436) and vigour index II (0.405). Enzyme α-amylase estimated high range of positive correlation with germination percentage, time to opening of pods, vigour index I & II (Table 4.4.2).

This indicates the strong association of enzyme α-amylase with germination percentage, time to opening of pods, vigour index I & II. It revealed that increase in enzyme activity of α-amylase with increased germination percentage, time to opening of pods, vigour index I, vigour index II and *vice-versa*. The high concentration of α-amylase in a seed is responsible for increase in germination percentage, days to opening the pods, vigour index I and II, which indicates that high percentage of α-amylase in seed may be responsible to *in-situ* germination.

Similar results were found by Bain and Mercer (1966), Abdul-Baki and Anderson (1972) reported amylase is responsible for embryo growth which resulted into seedling growth in germinating seeds. Dyer and Movellie (1976) also reported that increase in α-amylase activity in cereal seed results in higher germination percent. Such results were also reported by Wadhawa *et al.* (1988), Shigeshi *et al.* (1991), Desai (2004), Rahman et al., (2009), Mohankumar and Manonnmani (2011), Ghavidel and Mehdi (2011), Deshmukh (2013), Chandrika *et al*., (2013), Savitha and Chandra (2013), Digumarthy Niharika *et al*., (2020), Wei Yu *et al*., (2020) and Matheus Santin Padilha *et al*., (2021).

The next enzyme dehydrogenase exhibited significant positive correlation with germination percentage (0.423), vigour index I (0.436) and vigour index II (0.405). The enzyme dehydrogenase reported non-significant negative correlation with time to days of opening pods (-0.084) while it is non-significant positively correlated with α-amylase (0.097).

Enzyme dehydrogenase showed high range of positive correlation with germination percentage, vigour index I & II however, it noticed negligible range of correlation with α-amylase. The time to opening of pods estimated negligible non-significant negative correlation with enzyme dehydrogenase activity.

It means increase in enzyme activity of dehydrogenase with increased germination percentage, vigour index I, vigour index II and *vice-versa*.

Such types of results were found by Dacha *et al*., (1999) reported dehydrogenase activity in soybean seed and corrected that this enzyme decreasing the seed moisture which is helpful for increase seed viability. Similar results were also find by Verma *et al*., (2003), Aurellia Tatipata (2010) and Biswas *et al*., (2011) reported that dehydrogenase activity influenced the seed germination, vigour and viability of seed by ageing. Reddy *et al.* (2010) also reported that dehydrogenase and β–amylase activity were decreased during ageing of wheat seed. Deshmukh *et al.,* (2013), Salimath *et al.,* (2016), Singh *et al.,* (2017) and Kittiwan Klarod *et al*., (2021) reported that germination percentage exhibited significant and positive correlation with dehydrogenase activity.

CHAPTER -V

SUMMARY AND CONCLUSION

CHAPTER V

SUMMARY AND CONCLUSION

The present investigation was undertaken with a view the "**Dormancy studies in *in-situ* Germination in Mungbean (*Vigna radiata* L.)**" at Department of Agricultural Botany, VNMKV, Parbhani during *kharif* 2020 and *kharif* 2021 with following objectives.

1. To assess the dormancy and *in-situ* germination in mungbean.
2. To study the enzyme α-amylase responsible for germination and dormancy in mungbean.
3. To study the dehydrogenase compound in mungbean regarding seed germination and dormancy.
4. Correlation studies of enzymes α-amylase and dehydrogenase with seed quality.
5. To evaluate yield and its associated traits.

The experiment arranged in randomized block design (RBD) with two replications and every treatment has four rows of 4.5 meter long with 45 cm distance in between rows. The package of practices was carried out as per recommendation for raising the good crop condition. The experimental material included in the present study comprised of 34 genotypes including checks were collected from the Agriculture Research Station, Badnapur, VNMKV, Parbhani and Pulses Research Unit, Dr. PDKV, Akola.

The observations on different morphological, yield contributing characters and seed quality characters *viz.,* days to 50 % flowering, days to maturity, days to shattering, plant height (cm), number of primary branches, number of pods per cluster, number of pods per plant, length of pods (cm), number of seeds per pod, 100 seed wt.(g), seed yield per plant (g), biological yield per plant (g), harvest index(%) and seed quality parameters *viz.,* germination (%), hard seed (%), days to opening pod (hrs.), seedling

length (cm), vigour index I, vigour index II, seedling dry wt. (g), seed hardness (Kg/cm^2), α-amylase (mg/g) and dehydrogenase (µg/g) were recorded.

The observations on field level were taken of five randomly plants for all the quantitative characters except days to 50% flowering, days to maturity and days to shattering and laboratory work has completed in the laboratory of Seed Technology, Department of Agricultural Botany, VNMKV, Parbhani and laboratory of Soil Science and Agricultural Chemistry, College of Agriculture, VNMKV, Parbhani.

The statistical analysis of data was carried out as per the standard method suggested by Panse and Sukhatme (1989). The results obtained are precisely presented and summarized below:

1. Analysis of variance revealed significant differences among the genotypes for all the characters indicated presence of genetic diversity in the experimental material used for study.

2. Among the genotypes, genotype AKM-1609 found early and TBM-6 late in days to 50 % flowering. In the character of days to maturity, Phule M 818-8, AKM-1609, AKM-12-14, AKM-1602 recorded early days to maturity as compared best check BM-2003-2 while genotypes Phule M 602-9 and Phule M 702-1 showed at par with an above best check.

3. The genotypes Phule M 817-13, AKM-12-23, AKM-12-24, BM-2019-1, Phule M 809-12, Phule M 816-10, Phule M 504-20-27, Phule M 707-5 and TBM-4 took the maximum days for the shattering among all the standard checks excepting only one check. The irreversible and major morphological character *i.e.* plant height observed the range from 53.2 to 98,8 cm in all genotypes.

4. In the yield contributing characters *viz.* number of primary branches, number of pods per cluster, number of pods per plant, the genotypes Phule M 818-8 and AKM-12-14 showed maximum number of primary branches with checks, Phule M 809-12, Phule M 818-8 and AKM-1608 in traits of number of pods per cluster and in number of pods per plant, Phule M 818-8 and AKM-12-14 recorded

superior with best check.

5. Among the genotypes, in the character of length of pods viz; Phule M 817-13, TBM-127 and Phule M 707-5 were found superior to all checks excepting only one check Utkarsh while in 100 seed wt. genotype TBM-4 showed at par with best check Utkarsh. Regarding the observation of number of seeds per pod, genotypes Phule M 816-10 and Phule M 817-13 were estimated the higher seeds per pod as compare with best check BM-2003-2.

6. Seed yield per plant character revealed the genotype Phule M 817-13 has at par with the best check BM-2003-2 while genotypes AKM-12-14 and Phule M 818-8 were recorded the better in seed yield per plant character while in biological yield in grams genotypes TBM-10, TBM-6, Phule M 816-10, AKM-1602 and AKM-12-28 resulted superior in grams. In the character of harvest index % genotype Phule M 818-8 recorded the highest HI with best check PKVM-8802.

7. On the observation of germination percentage, in both seasons, out of 25 studied genotypes following five genotypes *viz.* Phule M 818-8, AKM-1605, Phule M 817-13, Phule M 402-2-1 and Phule M 707-5 were found superior in germination percentage while 19 genotypes were also found satisfactory in germination percentage i.e. an above the Minimum Seed Certification Standard (MSCS) and only one genotype TBM-6 was found in both the seasons below the MSCS level. All the standard checks in this study were also estimated the best germination percentage in both the seasons over the MSCS level. In the germination percentage test maximum percentage of hard seeds was found in AKM-1605 and minimum in Phule M 504-20-27 genotypes.

8. This observation showed helpful to assess the fresh seed dormancy (FSD) in *in-situ* germination of mungbean by measuring the time of opening of pods in hrs and noted the range from 0.8 to 80.8 hrs. The genotype Phule M 818-8 taken highest time to opening of pods, followed by AKM-1608, Phule M 809-10, AKM-1609 and TBM-127 i.e. nearly 2-3 days for opening of pods means it may dormant for *in-situ* germination. The remaining genotypes required nearly half

day to open the pods, means these lines were found favorable in to germinate in pods i.e. indicated less FSD. Regarding the standard checks, PKVM-8802, Vaibhav, BPMR-145, Utkarsh and BM-2003-2 were found more time taking variety for the opening of pods means it has sufficient FSD and BM-2002-1, PKVM-4, BM-4 and PKV Green Gold indicated less FSD.

9. Maximum seedling length (cm) and vigour index I among tested genotypes were recorded highest in AKM-1605, Phule M 817-13, Phule M-818-8, Phule M 816-10 and AKM-1606 and lowest in AKM-1603. In this study, out of nine checks PKV Green Gold expressed higher and BM-2003-2 lower in seedling length (cm) and vigour index I respectively.

10. The seedling dry weight (g) is significantly positive correlated with vigour index II. In this character genotype AKM-1605 recorded maximum seedling dry weight and vigour index II and Phule M 602-9 recorded minimum which indicates relationship in between these two traits.

11. The seed hardness (Kg/cm^2) measured by seed hardness instrument and found highest in genotypes Phule M 707-5, Phule M 817-13, TBM-4, AKM-12-14, AKM-1609 & AKM-1603 and the lowest in the genotypes Phule M 504-20-27, AKM-1605, Phule M 818-8 and AKM-1606. The checks Utkarsh, BM- 2003-2 and PKVM- 8802 found highest seed hardness.

12. The enzymatic activity of the enzyme α-amylase in mungbean seed exhibited the highly positive correlation with the characters germination percentage, vigour index I and II, and dehydrogenase also exhibited the positive correlation with germination percentage and vigour index I and II.

The results obtained in this study are discussed on the availability research findings.

CONCLUSION

It is concluded from the present study that , the genotypes (Phule M 817-13,AKM 12-14, Phule M 818-8) recorded high seed yield along with better seed quality parameters, so these genotypes must be use in future breeding programme for the development of new high yielding lines/ strains along with better seed quality parameters.

The enzymes α-amylase recorded the positive association with germination %, time to opening of pods, vigour index I and II however dehydrogenase with germination %, vigour index I and II.

The observation of time of opening the pods may also be helpful for assessment of FSD in mungbean.

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LITERATURE CITED

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APPENDIX

APPENDIX-I

Weekly meteorological data during field experiment at Parbhani for Year 2020-21

WK	Period	RF	Temperature oC		Humidity (%)		EVP (mm)	BSS (Hrs.)	WS (Kmph)
			Max	Min	RH1	RH2			
1	1-7 Jan.	3.4	27.0	15.0	83	52	2.7	5.7	4.1
2	8-14 Jan.	0.0	28.0	12.9	78	43	3.3	6.9	3.4
3	15-21 Jan.	0.0	29.0	13.9	78	42	3.2	7.8	3.4
4	22-28 Jan.	0.0	31.2	13.8	81	33	4.1	8.9	3.1
5	29-4 Feb.	1.3	28.9	13.7	77	40	4.3	8.1	5.2
6	5-11 Feb.	0.0	28.6	16.5	75	50	3.5	5.6	5.1
7	12-18 Feb.	0.0	31.5	13.1	78	31	5.0	8.8	3.6
8	19-25 Feb.	0.0	33.6	14.3	78	24	7.0	9.5	3.7
9	26-4 Mar	0.0	33.0	12.3	66	24	6.1	8.0	3.3
10	5-11 Mar.	9.0	32.9	15.9	75	30	7.7	8.9	4.2
11	12-18 Mar.	2.8	34.3	17.8	67	27	7.3	9.2	4.1
12	19-25 Mar.	8.8	35.3	16.8	71	23	7.0	9.2	3.7
13	26-1 Apr.	36.8	37.1	20.5	74	25	7.5	9.1	5.5
14	2-8 Apr.	0.0	37.7	20.6	70	25	3.8	9.7	3.8
15	9-15 Apr.	0.0	39.1	20.0	61	18	3.8	9.8	3.8
16	16-22 Apr.	0.0	40.4	23.4	54	17	9.3	9.6	3.9
17	23-29 Apr.	0.0	40.4	21.7	55	19	9.7	10.7	4.5
18	30-6 May	0.0	41.4	22.9	51	18	10.6	10.1	4.2
19	7-13 May	0.0	40.8	24.9	46	17	12.8	10.1	5.0
20	14-20 May	13.0	40.4	24.9	62	24	9.3	7.0	5.0
21	21-27 May	0.0	43.7	24.6	48	15	12.7	10.3	5.4
22	28-3 Jun.	13.6	38.8	25.7	56	31	12.3	9.6	6.5
23	4-10 Jun.	5.0	36.1	23.3	71	36	8.8	8.2	7.6
24	11-17 Jun.	148.0	32.0	23.4	85	64	3.6	4.1	5.0
25	18-24 Jun.	9.2	33.1	23.7	84	61	3.7	3.5	5.5
26	25-1 Jul.	23.7	34.5	24.0	87	54	5.2	7.2	4.1
27	2-8 Jul.	63.0	32.5	23.4	85	68	4.1	4.8	4.7
28	9-15 Jul.	103.4	32.5	23.0	84	61	3.7	6.5	4.1
29	16-22 Jul.	31.4	31.1	22.9	85	72	3.8	4.8	3.5
30	23-29 Jul.	30.1	31.4	22.9	84	64	4.0	6.4	3.0
31	30-5 Aug.	36.1	31.9	23.1	80	67	4.1	6.4	2.8

Contd…

WK	Period	RF	Temperature oC		Humidity (%)		EVP (mm)	BSS (Hrs.)	WS (Kmph)
			Max	Min	RH1	RH2			
32	6-12 Aug.	29.2	30.6	22.5	86	68	3.7	3.9	4.3
33	13-19 Aug.	42.5	27.8	22.0	94	82	1.5	0.4	4.0
34	20-26 Aug.	28.8	30.2	21.7	92	70	2.1	3.6	3.4
35	27-2 Sept.	24.2	31.1	21.6	91	64	3.3	5.9	3.6
36	3-9 Sept.	19.8	33.6	22.1	86	54	4.9	8.1	2.8
37	10-16 Sept.	53.2	31.8	22.2	91	64	3.7	5.8	3.1
38	17-23 Sept.	198.2	31.2	22.3	95	75	2.0	2.7	3.1
39	24-30 Sept.	47.2	30.4	22.1	90	64	3.2	4.0	3.1
40	1-7 Oct.	17.0	33.4	21.0	90	49	4.9	7.5	3.9
41	8-14 Oct.	85.6	31.3	21.7	89	66	3.4	4.6	2.6
42	15-21 Oct.	8.0	31.5	21.9	77	51	3.5	5.7	4.2
43	22-28 Oct.	6.4	32.0	20.7	90	47	3.7	6.1	2.5
44	29-04 Nov.	0.0	32.5	15.6	100	36	4.8	9.2	1.9
45	5-11 Nov.	0.0	31.0	10.9	85	22	5.3	9.2	2.8
46	12-18 Nov.	0.0	32.0	14.8	84	35	4.8	9.3	3.1
47	19-25 Nov.	0.0	32.2	17.2	83	43	4.2	8.2	2.5
48	26-02 Dec.	0.0	29.7	15.2	80	41	4.7	6.6	4.8
49	3-9 Dec.	0.0	31.0	9.2	86.6	27.0	4.8	9.3	2.9
50	10-16 Dec	0.0	30.3	14.8	83.1	34.9	4.1	7.2	2.8
51	17-23 Dec	0.0	28.8	10.2	89.0	36.0	4.0	7.9	2.9
52	24-30 Dec	0.0	32.7	10.8	97.9	37.9	4.4	9.3	2.8
	Total	**1098.7**							

APPENDIX-II

Weekly meteorological data during field experiment at Parbhani for Year 2021-22

WK	Period	RF	RD	Temperature °C		Humidity (%)		EVP (mm)	BSS (Hrs.)	WS (Kmph)
				Max	Min	RH1	RH2			
1	1-7 Jan.	0.0	0.0	28.8	15.4	88	51	3.7	4.3	3.8
2	8-14 Jan.	0.0	0.0	31.0	15.3	90	40	4.4	6.3	3.5
3	15-21 Jan.	0.0	0.0	31.2	15.1	82	35	4.4	7.6	3.1
4	22-28 Jan.	0.0	0.0	31.7	13.6	83	34	4.3	8.2	2.5
5	29-4 Feb.	0.0	0.0	30.3	12.9	78	29	5.2	7.4	3.4
6	5-11 Feb.	0.0	0.0	30.2	11.3	66	20	5.9	9.4	3.0
7	12-18 Feb.	1.8	0.0	32.4	14.3	76	24	5.6	8.7	2.8
8	19-25 Feb.	14.5	2.0	30.3	13.0	93	40	4.5	7.7	3.4
9	26-4 Mar	0.0	0.0	36.3	15.5	67	14	7.2	9.1	2.9
10	5-11 Mar.	0.0	0.0	36.6	16.6	61	14	7.1	9.3	2.6
11	12-18 Mar.	0.0	0.0	36.8	16.8	60	21	7.5	9.0	3.0
12	19-25 Mar.	14.3	2.0	34.9	20.1	74	28	6.9	7.0	5.0
13	26-1 Apr.	0.0	0.0	39.3	16.0	57	12	9.1	9.2	3.3
14	2-8 Apr.	0.0	0.0	39.4	19.2	48	11	10.1	9.2	3.8
15	9-15 Apr.	2.0	0.0	36.3	20.5	63	25	7.0	5.5	4.4
16	16-22 Apr.	0.0	0.0	39.5	19.9	51	13	9.6	9.2	3.5
17	23-29 Apr.	0.0	0.0	39.8	21.2	46	13	9.7	9.1	4.1
18	30-6 May	8.2	1.0	38.8	22.8	61	20	8.7	8.7	4.2
19	7-13 May	0.0	0.0	38.8	24.2	59	26	8.9	8.3	4.1
20	14-20 May	3.0	0.0	37.9	25.7	60	31	9.4	7.6	7.8
21	21-27 May	0.0	0.0	39.8	25.3	50	20	11.9	8.4	7.2
22	28-3 Jun.	71.1	4.0	35.7	23.0	76	43	7.6	6.1	5.5
23	4-10 Jun.	154.4	5.0	32.9	21.0	87	60	3.3	5.7	3.5
24	11-17 Jun.	102.6	4.0	32.5	21.5	88	62	4.6	6.0	5.8
25	18-24 Jun.	9.7	2.0	32.7	19.6	86	57	4.7	5.5	5.4
26	25-1 Jul.	35.3	1.0	32.9	23.3	84	57	4.6	5.6	5.2
27	2-8 Jul.	41.1	2.0	33.4	23.8	82	54	5.3	5.9	4.2
28	9-15 Jul.	389.7	6.0	29.7	22.0	96	78	1.1	2.4	3.7
29	16-22 Jul.	126.7	4.0	30.1	22.6	92	73	3.0	5.7	4.1
30	23-29 Jul.	9.9	2.0	30.5	21.4	89	65	3.4	4.5	5.3
31	30-5 Aug.	2.4	0.0	30.9	21.6	84	63	3.3	2.7	5.8

Contd…

WK	Period	RF	RD	Temperature °C		Humidity (%)		EVP (mm)	BSS (Hrs.)	WS (Kmph)
				Max	Min	RH1	RH2			
32	6-12 Aug.	2.3	0.0	33.1	22.5	84	52	4.9	6.2	4.2
33	13-19 Aug.	48.5	4.0	29.4	22.2	89	70	3.6	4.7	4.6
34	20-26 Aug.	5.9	1.0	30.6	22.4	92	64	3.1	5.2	2.9
35	27-2 Sept.	48.8	3.0	30.0	22.7	91	68	3.0	3.4	3.1
36	3-9 Sept.	233.1	5.0	28.2	21.8	92	79	1.6	3.9	3.7
37	10-16 Sept.	44.4	3.0	30.9	22.0	91	67	3.4	6.6	4.1
38	17-23 Sept.	48.6	3.0	30.9	22.3	92	64	4.0	5.1	3.6
39	24-30 Sept.	133.9	5.0	28.9	21.8	94	75	1.6	2.2	3.6
40	1-7 Oct.	112.9	3.0	32.7	22.4	94	59	3.5	7.3	2.4
41	8-14 Oct.	3.0	0.0	33.0	21.2	92	46	4.4	7.8	2.3
42	15-21 Oct.	45.8	1.0	31.1	19.6	89	48	4.2	7.0	2.9
43	22-28 Oct.	0.0	0.0	31.5	15.9	86	30	5.0	9.4	2.1
44	29-04 Nov.	0.0	0.0	31.2	15.7	79	36	5.5	8.5	3.7
45	5-11 Nov.	0.0	0.0	30.9	14.3	85	29	5.0	7.6	3.3
46	12-18 Nov.	0.0	0.0	30.8	20.6	81	54	4.1	4.5	4.6
47	19-25 Nov.	1.2	0.0	31.7	21.7	88	49	4.0	6.5	4.3
48	26-02 Dec.	0.0	0.0	28.8	15.3	79	35	5.0	5.9	3.9
49	3-9 Dec.	4.2	1.0	28.2	16.7	87	45	3.1	3.5	3.0
50	10-16 Dec	0.0	0.0	28.7	13.2	88	35	4.7	5.9	3.0
51	17-23 Dec	0.0	0.0	28.1	9.4	91	30	3.4	7.1	2.3
52	24-30 Dec	0.0	0.0	28.2	13.6	88	44	3.1	4.9	3.0
	Total	**1704.3**	**64.0**	**64.0**						

CURRICULUM VITAE

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Academic qualification

Course / Degree	Name of the college / institute	University / Board	Year of Passing	Percentages (%) / CGPA	Class / Grade
SSC	Shivshakti Vidyalay, Kotha	Amaravati	1992	74.77	First
HSC	Rural Institute, Amaravati	Amaravati	1994	56.33	Second
B.Sc.(Agri.)	ANCA, Warora	Dr. PDKV, Akola	1998	7.67	First
M.Sc. (Seed Tech.)	PGI, Akola	Dr. PDKV, Akola	2000	7.89	First

Sandeep Raosaheb Kadam

Place: Parbhani

Date: 06/02/2023