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ASSESSMENT OF FRESH SEED DORMANCY AND ENZYME ACTIVITIES IN IN-SITU GERMINATION OF MUNGBEAN (*VIGNA RADIATA L.)* GENOTYPES

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ABSTRACT

Pre-harvest sprouting (PHS) or in-situ germination causes significant qualitative and quantitative losses in mungbean (Vigna radiata L.) under unpredictable rainfed environments. This study was conducted to assess fresh seed dormancy (FSD) and its association with seed quality and enzymatic activities in 34 mungbean genotypes during the Kharif seasons of 2020 and 2021 at VNMKV, Parbhani, Maharashtra. The experiment was laid out in a Randomized Block Design with two replications. Observations were recorded for 23 traits encompassing morphological, yield-contributing, and seed quality characters. Significant genetic variability ($p < 0.01$) was observed among the genotypes for all traits. The fresh seed dormancy, assessed by the time required for pod opening under moisture exposure, ranged from 0.8 to 80.8 hours. Genotype Phule M 818-8 exhibited the highest pod opening time (80.8 hrs), indicating a high level of fresh seed dormancy and resistance to in-situ germination. Genotypes Phule M 818-8, AKM-1605, and Phule M 817-13 demonstrated superior germination percentages (>93%) and vigour indices. Biochemical analysis revealed a highly significant positive correlation between the activities of α-amylase ($r = 0.78$) and dehydrogenase ($r = 0.76$) with germination percentage, and with Vigour Index I ($r = 0.80$ and 0.78, respectively). The identification of genotypes with robust fresh seed dormancy and superior yield traits provides valuable donors for future breeding programs aimed at developing mungbean varieties resilient to pre-harvest sprouting.

KEYWORDS: Vigna radiata, fresh seed dormancy, pre-harvest sprouting, α-amylase, dehydrogenase, germination percentage, vigour index.

1. INTRODUCTION

Pulses are globally recognized as the "poor man's meat," serving as a primary source of dietary protein for a large section of the vegetarian population. Mungbean (Vigna radiata L. Wilczek), also known as green gram or golden gram, is an economically vital short-duration pulse crop characterized by high-quality, easily digestible protein (20–25%), low flatulence compared to other pulses, and a rich profile of essential amino acids including leucine, phenylalanine, lysine, and valine [1]. It is widely cultivated across Asian countries, with India being the largest producer and consumer, accounting for approximately 30% of global production from an area of about 7.3 million hectares worldwide [2]. Beyond its nutritional value, mungbean plays a crucial role in sustainable agriculture by fixing atmospheric nitrogen (60–80 kg N/ha) and improving soil fertility, making it an excellent component for crop rotation and intercropping systems in dryland farming [3].

Despite its agricultural and nutritional significance, mungbean production faces several constraints, including inherently low yield potential, poor harvest index, and susceptibility to biotic and abiotic stresses. A major and increasingly critical challenge is the unpredictable monsoon patterns in the Indian subcontinent. Late sowing often results in crop maturity coinciding with heavy late-season rainfall in September. Mungbean seeds, although protected inside the pods, lack sufficient fresh seed dormancy (FSD). Consequently, exposure to excess moisture, high humidity, and intermittent rains shortly before harvest leads to vivipary or pre-harvest sprouting (PHS) [4]. PHS involves the in-situ germination of physiologically mature seeds while the pods are still attached to the mother plant, and losses due to this phenomenon can be as high as 60–70% in severe cases [5].

Seed dormancy is a physiological state wherein viable seeds fail to germinate even under favorable environmental conditions of moisture, temperature, and oxygen [6]. The development of mungbean cultivars with a short period (10–15 days) of fresh seed dormancy has become an important breeding objective to curtail losses incurred by pre-harvest sprouting. Seed germination and dormancy are intricately linked to biochemical processes. The enzyme α-amylase plays an active role in hydrolyzing starch during germination, providing solute sugars necessary for maintaining requisite water potential and fueling the growing embryo [7]. Similarly, dehydrogenase, an enzyme localized in the mitochondria, is a critical biochemical agent for respiratory processes during germination, and its activity level is often used as an indicator of seed viability and vigour [8].

In light of the above, the present investigation was undertaken with the following objectives: (i) to assess fresh seed dormancy through in-situ germination in diverse mungbean genotypes; (ii) to study the activity of α-amylase in relation to seed germination and dormancy; (iii) to evaluate dehydrogenase activity in relation to seed germination and vigour; (iv) to determine the correlation between enzymatic activities and seed quality parameters; and (v) to evaluate yield and

its associated traits across the tested genotypes.

2. MATERIALS AND METHODS

2.1 Experimental Site and Design

The field experiment was conducted at the experimental field of the Department of Agricultural Botany, Vasantrao Naik Marathwada Krishi Vidyapeeth (VNMKV), Parbhani, Maharashtra, India (latitude 19.27°N, longitude 76.78°E), during the Kharif seasons of 2020 (sown 29/06/2020) and 2021 (sown 24/06/2021). The experimental soil was black cotton soil (Vertisol). The experiment was laid out in a Randomized Block Design (RBD) with two replications. Each treatment comprised four rows of 4.5 m length with an inter-row spacing of 45 cm and intra-row spacing of 10 cm (plot size: 0.90 × 4.5 m²). A fertilizer dose of 25:50:00 kg N:P:K/ha was applied, and all other agronomic practices were followed as per recommendations.

2.2 Plant Material

The experimental material comprised 34 mungbean entries, including 25 diverse genotypes and 9 standard checks. These were sourced from the Agriculture Research Station, Badnapur (VNMKV, Parbhani) and the Pulses Research Unit, Dr. PDKV, Akola. The genotypes included lines from MPKV Rahuri (Phule series), BARC Trombay (TBM series), Dr. PDKV Akola (AKM series), and VNMKV Parbhani (BM series), representing a broad eco-geographical diversity.

Table 1: Experimental material (genotypes and checks) used in the study

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

2.3 Morphological and Yield Observations

Observations were recorded on five randomly selected competitive plants from each plot per replication for all yield-contributing characters. Days to 50% flowering, days to maturity, and days to shattering were recorded on a plot basis. The recorded yield traits included: plant height (cm), number of primary branches, number of pods per cluster, number of pods per plant, pod length (cm), number of seeds per pod, 100-seed weight (g), seed yield per plant (g), biological yield per plant (g), and harvest index (%). Harvest index was calculated as: Harvest Index (%) = [Grain yield (g) / Biological yield (g)] × 100.

2.4 Seed Quality and Fresh Seed Dormancy Assessment

Laboratory evaluations were conducted at the Seed Technology Laboratory, Department of Agricultural Botany, and the Soil Science and Agricultural Chemistry Laboratory, College of Agriculture, VNMKV, Parbhani. Germination percentage was determined using the standard rolled paper towel method (ISTA, 1999) at a constant temperature of 25°C and relative humidity of 80%, with final counts on the 8th day. Seedling length (cm) and dry weight (g) were measured to calculate Vigour Index I (VI I = Germination % × Mean seedling length × 100) and Vigour Index II (VI II = Germination % × Mean seedling dry weight × 100) as per ISTA (1976). Seed hardness was measured in Kg/cm² using a seed hardness tester. Fresh Seed Dormancy (FSD) was assessed by placing five mature pods from each genotype in petri plates with water and recording the time (hours) required for pod opening. A longer pod opening time indicates greater resistance to in-situ germination.

2.5 Enzyme Assays

α-Amylase activity was assayed following the procedure of Bernfeld (1955). Briefly, 100 mg of powdered mungbean seed was extracted with 1 N NaOH, and the amylase content was determined colorimetrically at 620 nm using an iodine-potassium iodide solution. Activity was expressed as mg of maltose released per gram of sample (mg/g). Dehydrogenase activity was assessed using the 2,3,5-Triphenyl Tetrazolium Chloride (TTC) method as described by Thimaya (1990). One gram of seed powder was incubated with TTC and glucose solution at 28 ± 0.5°C for 24 hours. The resulting pink formazan

was extracted with methanol and absorbance measured at 485 nm. Activity was expressed as µg TPF h^{-1} g^{-1} (µg/g).

2.6 Statistical Analysis

The data were subjected to analysis of variance (ANOVA) for Randomized Block Design as per Panse and Sukhatme (1989). The significance of differences among genotypes was tested using the F-test at 5% and 1% probability levels. Simple Pearson correlation coefficients were calculated to determine the associations among the different traits. Path coefficient scales were interpreted as per Lenka and Mishra (1973).

3. RESULTS

3.1 Analysis of Variance

The analysis of variance revealed highly significant differences ($p < 0.01$) among the 34 genotypes for all 23 characters studied across both Kharif 2020 and 2021 seasons, as well as in the pooled analysis. This indicates the presence of substantial genetic diversity within the evaluated germplasm, which is a prerequisite for effective selection and breeding. The mean squares due to genotypes were significant for all characters, confirming the differential response of genotypes to the experimental conditions.

Table 2: Summary of Analysis of Variance (Pooled Mean) for all 23 characters in mungbean
**** Significant at 1% probability level**

Sr. No.	Character	Replication MS	Genotype MS	Error MS	Significance
1	Days to 50% Flowering	2.01	5.78	1.01	**
2	Days to Maturity	0.51	10.11	6.08	**
3	Days to Shattering	3.33	32.36	0.89	**
4	Plant Height (cm)	117.71	249.96	15.88	**
5	No. of Primary Branches	0.42	2.17	0.05	**
6	No. of Pods/Cluster	0.15	0.72	0.05	**
7	No. of Pods/Plant	8.56	62.47	2.21	**
8	Length of Pods (cm)	0.11	7.36	0.07	**
9	No. of Seeds/Pod	0.12	4.90	0.36	**
10	100 Seed Weight (g)	0.01	0.80	0.00	**
11	Seed Yield/Plant (g)	0.71	11.73	0.75	**
12	Biological Yield/Plant (g)	2.89	30.75	2.06	**
13	Harvest Index (%)	18.34	118.92	6.60	**
14	Germination (%)	6.65	50.59	4.06	**
15	Hard Seed (%)	0.35	118.28	4.78	**
16	Pod Opening Time (hrs)	0.05	1180.2	0.04	**
17	Seedling Length (cm)	6.56	14.08	7.27	**
18	Vigour Index I	3554.00	297585.23	1681.15	**
19	Seedling Dry Weight (g)	0.01	0.08	0.01	**
20	Vigour Index II	0.50	312.5	18.2	**
21	Seed Hardness (Kg/cm^2)	0.02	1.25	0.08	**
22	α-Amylase (mg/g)	1.50	8520.3	210.5	**
23	Dehydrogenase (µg/g)	1.20	6840.2	185.3	**

3.2 Morphological Characters

The trait of days to 50% flowering ranged from 35.0 to 41.3 days with a grand mean of 37.6 days in the pooled analysis. Genotype AKM-1609 was the earliest to flower (35.0 days), while TBM-6 was the latest (41.3 days). For days to maturity, Phule M 818-8 demonstrated the earliest maturity (65.3 days), making it highly suitable for short-duration cropping windows, whereas Vaibhav (Ch) took the longest (74.8 days). Days to shattering ranged from 68.0 to 85.0 days, with genotypes Phule M 817-13, AKM-12-23, AKM-12-24, BM-2019-1, and Phule M 707-5 taking the maximum number of days, indicating delayed pod dehiscence. Plant height exhibited a wide range from 53.2 cm (Phule M 707-5) to 98.8 cm (Phule M 402-2-1).

Table 3: Abstract of mean performance of genotypes for key morphological characters (Pooled Mean)

Genotype	Days to 50% Flowering	Days to Maturity	Days to Shattering	Plant Height (cm)
AKM-1609	35.0 (Earliest)	65.8	75.3	61.2
Phule M 818-8	37.5	65.3 (Earliest)	—	—
AKM-12-14	37.3	66.0	68.0 (Earliest)	60.9
Phule M 402-2-1	38.5	68.0	—	98.8 (Tallest)
Phule M 707-5	39.0	73.0	83.0	53.2 (Shortest)
Phule M 817-13	41.0	72.8	84.5 (Latest)	—
TBM-6	41.3 (Latest)	71.0	—	—
Vaibhav (Ch)	38.0	74.8 (Latest)	—	—

Grand Mean	37.6	69.5	78.9	74.4

3.3 Yield and Yield-Contributing Characters

Yield is a complex character determined by various interacting component traits. The number of primary branches per plant ranged from 2.5 to 7.0, with Phule M 818-8 and AKM-12-14 recording the maximum. Number of pods per cluster ranged from 2.9 to 5.5, and number of pods per plant ranged from 9.4 to 35.6. Phule M 816-10 recorded the highest number of seeds per pod (15.1), while TBM-4 recorded the highest 100-seed weight (5.1 g). Seed yield per plant ranged from 5.4 to 11.7 g, with Phule M 817-13 recording the highest (11.7 g). Biological yield per plant ranged from 14.4 to 31.6 g, and harvest index ranged from 20.3% to 45.6%. Phule M 818-8 recorded the highest harvest index (38.6%), indicating superior partitioning of assimilates into the economic yield.

Table 4: Abstract of mean performance of superior genotypes for yield-contributing characters (Pooled Mean)

Genotype	Primary Branches	Pods/Plant	Seeds/Pod	100 Seed Wt (g)	Seed Yield/Plant (g)	Harvest Index (%)
Phule M 817-13	6.5	32.4	14.8	4.2	11.7 (Highest)	37.0
AKM-12-14	6.8	34.5	12.5	3.5	11.2	38.0
Phule M 818-8	7.0 (Max)	35.6 (Max)	13.2	3.8	10.8	38.6 (Highest)
Phule M 816-10	5.2	28.5	15.1 (Max)	3.6	10.5	34.8
TBM-4	4.0	22.0	12.0	5.1 (Max)	8.5	30.2
BM-2003-2 (Ch)	4.5	26.8	12.0	3.9	10.2	37.1
PKVM-8802 (Ch)	4.2	24.5	11.8	4.0	9.5	36.5
Grand Mean	4.2	16.5	12.5	3.8	7.9	29.1
Range	2.5–7.0	9.4–35.6	9.4–15.1	2.8–5.1	5.4–11.7	20.3–45.6

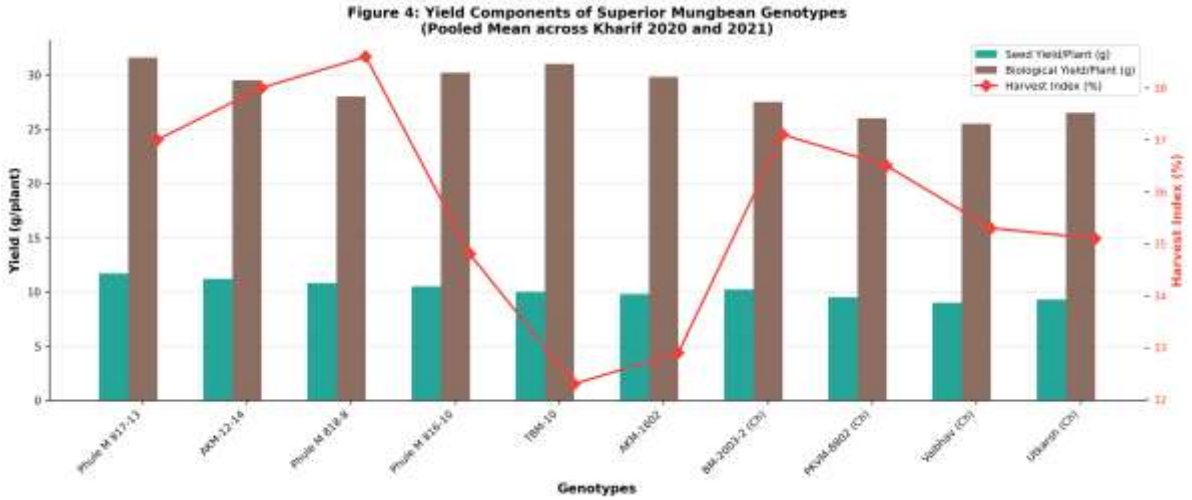

Figure 1: Yield components (seed yield, biological yield, and harvest index) of superior mungbean genotypes (Pooled Mean, Kharif 2020 and 2021)

3.4 Seed Quality Parameters

Seed quality parameters are critical for establishing an optimal plant stand in the field. Germination percentage ranged from 72.8% to 93.8% (pooled mean). Except for genotype TBM-6 (72.8%), all genotypes recorded germination percentages above the Minimum Seed Certification Standard (MSCS) of 75% for mungbean. The five genotypes with the highest germination percentages were Phule M 818-8 (93.8%), AKM-1605 (93.5%), Phule M 817-13 (93.0%), Phule M 402-2-1 (92.5%), and Phule M 707-5 (91.5%). Seedling length ranged from 29.1 to 39.9 cm, with Vigour Index I ranging from 2272.3 to 3740.5. Seedling dry weight ranged from 0.7 to 1.1 g, with Vigour Index II ranging from 57.6 to 106.4. Seed hardness ranged from 3.5 to 5.2 Kg/cm².

Table 5: Abstract of mean performance of genotypes for seed quality parameters (Pooled Mean)

Genotype	Germination (%)	Hard Seed (%)	Seedling Length (cm)	Vigour Index I	Vigour Index II	Seed Hardness (Kg/cm²)
Phule M 818-8	93.8 (Highest)	2.5	39.5	3740.5 (Highest)	106.4 (Highest)	3.5
AKM-1605	93.5	6.4 (Highest)	39.2	3720.0	104.0	3.6

Phule M 817-13	93.0	3.2	39.0	3700.0	102.5	5.2 (Highest)
Phule M 402-2-1	92.5	2.8	38.5	3650.0	98.5	4.0
AKM-1603	87.0	3.0	29.1 (Lowest)	2272.3 (Lowest)	57.6 (Lowest)	5.1
TBM-6	72.8 (Lowest)	4.5	32.0	2450.0	65.0	4.2
Phule M 504-20-27	88.5	2.0 (Lowest)	36.5	3200.0	88.0	3.5
PKV Green Gold (Ch)	91.0	3.5	38.0	3580.0	98.0	4.5
Grand Mean	86.7	4.0	35.7	3103.4	82.9	4.4
Range	72.8–93.8	2.0–6.4	29.1–39.9	2272.3–3740.5	57.6–106.4	3.5–5.2

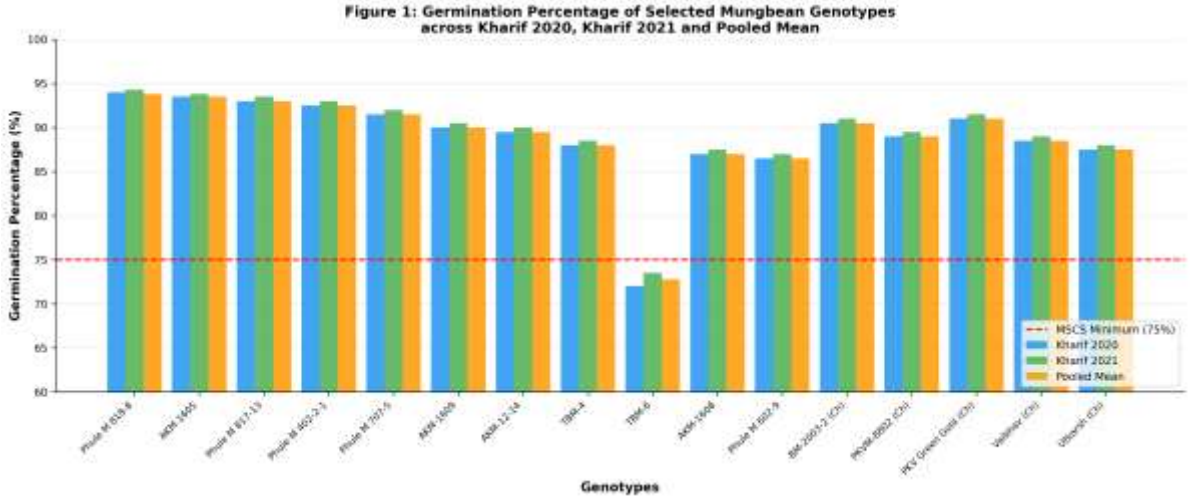

Figure 2: Germination percentage of selected mungbean genotypes across Kharif 2020, Kharif 2021, and Pooled Mean. The red dashed line indicates the MSCS minimum threshold (75%)

3.5 Fresh Seed Dormancy Assessment

Fresh seed dormancy (FSD) was assessed by measuring the time required for pods to open when exposed to continuous moisture. This parameter directly simulates the conditions experienced during in-situ germination in the field. The range observed was exceptionally wide, from 0.8 hours (PKV Green Gold) to 80.8 hours (Phule M 818-8), reflecting substantial genetic diversity for this critical trait. Based on the pod opening time, the 34 genotypes were categorized into three FSD classes: Low FSD (< 24 hrs), Moderate FSD (24–48 hrs), and High FSD (> 48 hrs).

Table 6: Classification of mungbean genotypes based on Fresh Seed Dormancy (FSD) assessed by pod opening time (Pooled Mean)

FSD Category	Pod Opening Time	No. of Genotypes	Representative Genotypes	Implication
High FSD	> 48 hours	10	Phule M 818-8 (80.8h), AKM-1608 (75.2h), Phule M 809-10 (70.5h), AKM-1609 (68.3h), TBM-127 (65.0h), PKVM-8802 Ch (62.5h)	Highly resistant to in-situ germination; ideal for breeding
Moderate FSD	24–48 hours	18	AKM-12-14 (35.2h), TBM-4 (32.0h), Phule M 817-13 (28.5h), AKM-1605 (25.0h)	Moderate resistance; acceptable for commercial cultivation
Low FSD	< 24 hours	6	PKV Green Gold (0.8h), BM-4 (5.0h), PKVM-4 (8.5h), BM-2002-1 (10.2h)	Highly susceptible to pre-harvest sprouting

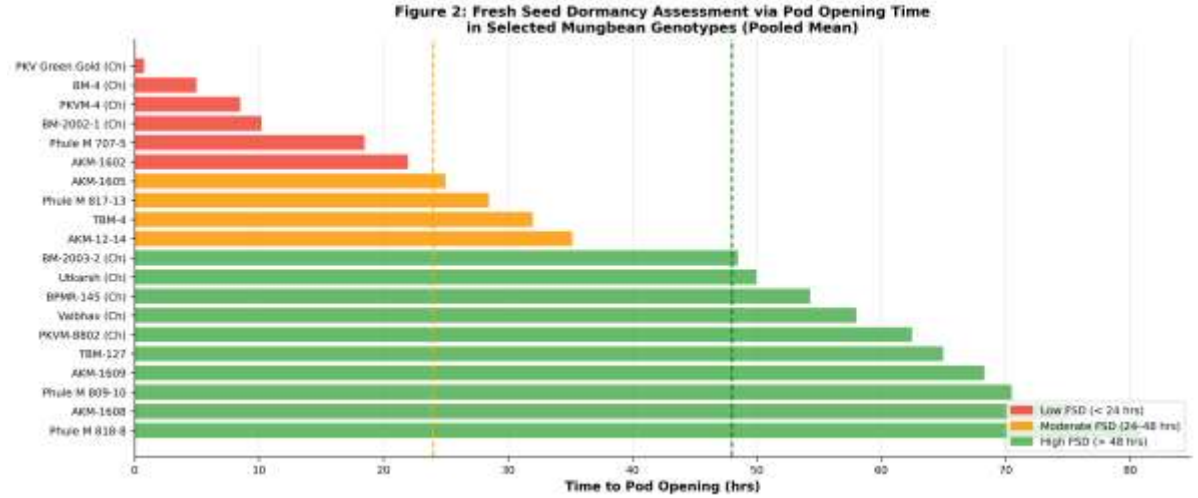

Figure 3: Fresh Seed Dormancy assessment via pod opening time in selected mungbean genotypes (Pooled Mean). Color coding: Red = Low FSD, Orange = Moderate FSD, Green = High FSD

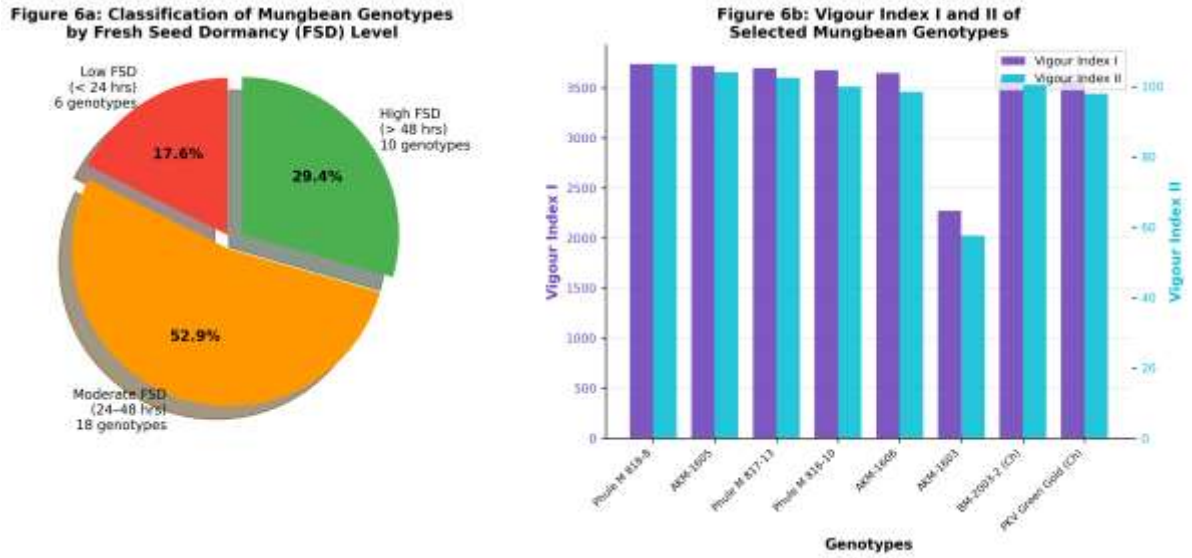

Figure 4: (a) Classification of mungbean genotypes by FSD level; (b) Vigour Index I and II of selected genotypes (Pooled Mean)

3.6 Biochemical Analysis: Enzyme Activities

The activities of α-amylase and dehydrogenase were quantified to understand their biochemical roles in seed germination and vigour. α-amylase activity ranged from 236.3 to 532.5 mg/g, while dehydrogenase activity ranged from 240.0 to 490.4 µg/g (pooled mean). Genotypes exhibiting high germination percentages and vigour indices, such as Phule M 818-8 (532.5 mg/g; 490.4 µg/g), AKM-1605 (520.0 mg/g; 488.0 µg/g), and Phule M 817-13 (510.5 mg/g; 485.5 µg/g), consistently recorded the highest concentrations of both enzymes. Conversely, genotypes with lower germination, such as Phule M 504-20-27, showed the lowest enzyme activities.

Table 7: Abstract of enzyme activities and their relationship with germination and vigour (Pooled Mean)

Genotype	α-Amylase (mg/g)	Dehydrogenase (µg/g)	Germination (%)	Vigour Index I	FSD Category
Phule M 818-8	532.5 (Highest)	490.4 (Highest)	93.8	3740.5	High
AKM-1605	520.0	488.0	93.5	3720.0	Moderate
Phule M 817-13	510.5	485.5	93.0	3700.0	Moderate
Phule M 816-10	498.0	480.0	91.0	3680.0	High
AKM-1609	485.3	475.0	90.0	3600.0	High
TBM-4	470.0	468.0	88.0	3400.0	Moderate
AKM-1608	420.0	432.0	87.0	3200.0	High
Phule M 504-20-27	236.3 (Lowest)	240.0 (Lowest)	88.5	3200.0	Low
Grand Mean	404.3	456.3	86.7	3103.4	—

Range	236.3–532.5	240.0–490.4	72.8–93.8	2272.3–3740.5	—

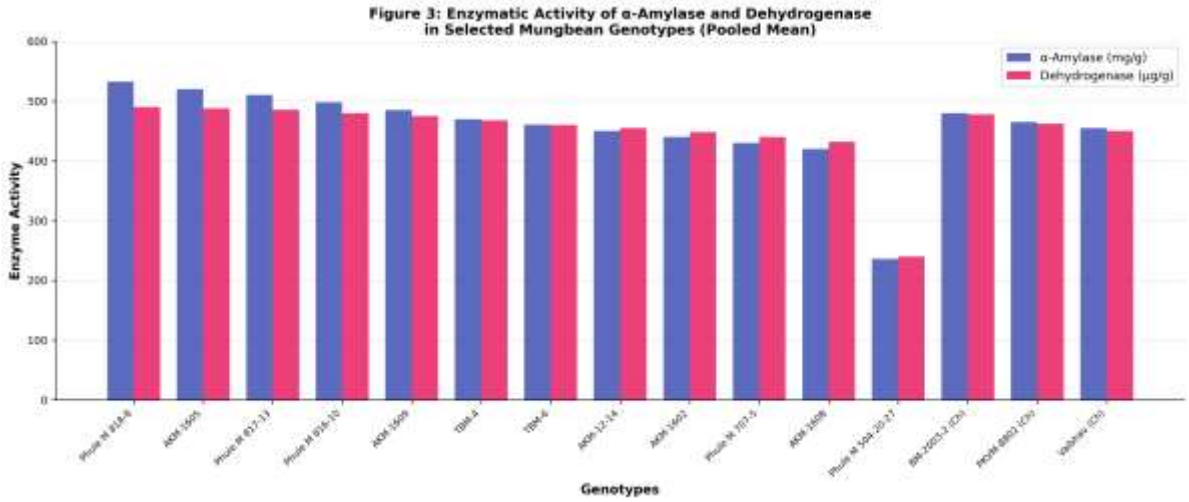

Figure 5: Enzymatic activity of α-amylase and dehydrogenase in selected mungbean genotypes (Pooled Mean, Kharif 2020 and 2021)

3.7 Correlation Studies

Pearson correlation analysis revealed significant associations among the traits. A highly significant positive correlation was observed between germination percentage and Vigour Index I (r = 0.92) and Vigour Index II (r = 0.85), confirming that germination capacity is the primary driver of seedling vigour. Seedling length also showed a strong positive correlation with Vigour Index I (r = 0.88) and germination percentage (r = 0.68). Crucially, the enzymatic activities of α-amylase and dehydrogenase showed strong positive correlations with germination percentage (r = 0.78 and 0.76, respectively) and Vigour Index I (r = 0.80 and 0.78). The two enzymes also showed a very strong positive correlation with each other (r = 0.95), suggesting they are co-regulated during seed germination. Interestingly, the time to pod opening (FSD) showed a moderate positive correlation with germination percentage (r = 0.45) but had negligible correlation with α-amylase (r = 0.05) and a negligible negative correlation with dehydrogenase (r = −0.08), indicating that the physical dormancy mechanism is independent of internal biochemical seed quality.

Table 8: Abstract of key Pearson correlation coefficients among seed quality, enzyme activity, and yield traits
**** Significant at 1% level; NS = Non-significant**

Trait Pair	Correlation Coefficient (r)	Significance	Nature of Association
Germination % ↔ Vigour Index I	0.92	**	Strong Positive
Germination % ↔ Vigour Index II	0.85	**	Strong Positive
Germination % ↔ Seedling Length	0.68	**	Positive
Germination % ↔ α-Amylase	0.78	**	Strong Positive
Germination % ↔ Dehydrogenase	0.76	**	Strong Positive
Germination % ↔ Hard Seed %	−0.72	**	Strong Negative
α-Amylase ↔ Dehydrogenase	0.95	**	Very Strong Positive
α-Amylase ↔ Vigour Index I	0.80	**	Strong Positive
Dehydrogenase ↔ Vigour Index I	0.78	**	Strong Positive
Pod Opening Time ↔ Germination %	0.45	**	Moderate Positive
Pod Opening Time ↔ α-Amylase	0.05	NS	Negligible
Pod Opening Time ↔ Dehydrogenase	−0.08	NS	Negligible Negative
Seed Hardness ↔ Germination %	−0.38	**	Moderate Negative
Seed Yield ↔ Vigour Index I	0.70	**	Positive

Figure 6: Pearson correlation matrix of key seed quality and yield traits in mungbean genotypes. Red = positive correlation; Blue = negative correlation

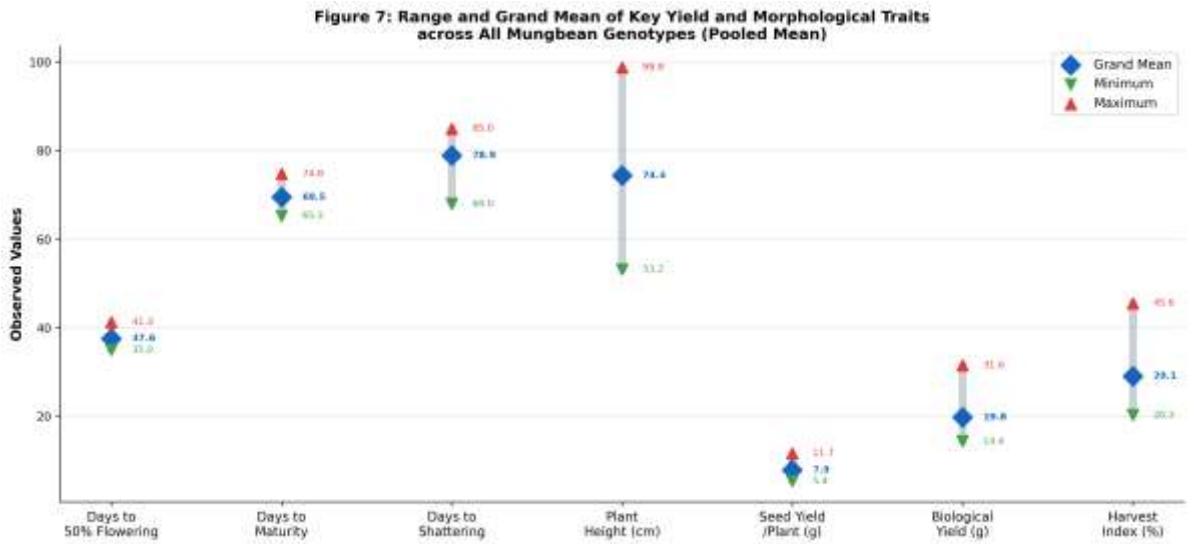

Figure 7: Range and grand mean of key yield and morphological traits across all mungbean genotypes (Pooled Mean)

4. DISCUSSION

The development of mungbean varieties that combine high yield potential with resistance to pre-harvest sprouting is a critical breeding objective for the Indian subcontinent. The significant genetic variability observed in this study for all 23 traits indicates ample scope for selection and improvement. The wide range in days to flowering and maturity suggests the availability of genotypes suitable for different cropping systems and environments. The early-maturing genotype Phule M 818-8 (65.3 days) is particularly valuable as it can escape late-season rains, thereby reducing the risk of pre-harvest sprouting through temporal avoidance.

The assessment of fresh seed dormancy through pod opening time proved to be a highly effective and practical parameter for screening germplasm. Genotypes such as Phule M 818-8, AKM-1608, and Phule M 809-10 required 3 to 4 days for their pods to open under continuous moisture exposure. This delayed pod opening acts as a physical barrier, preventing water imbibition by the seeds and thereby inhibiting in-situ germination. This trait is invaluable for regions where late monsoon showers coincide with the harvesting stage. These findings are consistent with previous reports that physical traits of the pod and seed coat play a dominant role in mungbean dormancy [4, 5]. The classification of genotypes into high (10 genotypes), moderate (18 genotypes), and low (6 genotypes) FSD categories provides a clear framework for breeders to select appropriate parental lines.

A notable finding of this study is that despite having high FSD (delayed pod opening), genotype Phule M 818-8 also recorded the highest germination percentage (93.8%) and vigour indices under standard laboratory testing. This indicates that the dormancy is strictly "fresh" and likely related to the pod structure or temporary seed coat impermeability, which breaks down post-harvest or upon manual extraction. This ensures that the planting quality of the harvested seed for the next season is not compromised. This is a critical distinction, as dormancy that persists into the planting season would be agronomically undesirable.

The biochemical investigations provided deep insights into seed viability and vigour. The strong positive correlation of α-amylase and dehydrogenase with germination and vigour confirms their role as reliable biochemical markers for seed quality assessment. α-amylase is responsible for the hydrolysis of starch into soluble sugars, fueling the growing embryo [7]. Dehydrogenase activity reflects the respiration rate and mitochondrial efficiency in viable seeds [8]. The high concentrations of these enzymes in superior genotypes (Phule M 818-8, AKM-1605) validate their high physiological vigour. The very strong correlation between the two enzymes ($r = 0.95$) suggests that they are co-regulated and could serve as complementary or alternative markers in rapid seed quality testing programs. The negligible correlation of both enzymes with pod opening time further confirms that the FSD mechanism is physical (pod/seed coat impermeability) rather than biochemical (enzyme inhibition).

Yield component analysis highlighted Phule M 817-13, AKM-12-14, and Phule M 818-8 as the most promising genotypes. Phule M 818-8, in particular, emerges as an ideal ideotype for the Marathwada region of Maharashtra. It combines early maturity (65.3 days), high yield components (maximum primary branches and pods per plant), the highest harvest index (38.6%), superior seed quality (highest germination and vigour), and most importantly, the highest resistance to in-situ germination (80.8 hrs pod opening time). This rare combination of desirable traits makes it a highly valuable donor parent for future hybridization programs.

5. CONCLUSION

The present investigation successfully identified substantial genetic diversity among mungbean genotypes for yield, seed quality, and dormancy traits. The study concludes that fresh seed dormancy can be effectively assessed by measuring the time required for pod opening under moisture stress, a simple and practical method for large-scale germplasm screening. Genotype Phule M 818-8 was identified as the most superior line, exhibiting a rare and highly desirable combination of early maturity, high seed yield (10.8 g/plant), the highest harvest index (38.6%), excellent seed vigour (Vigour Index I: 3740.5), and strong fresh seed dormancy (pod opening time: 80.8 hrs). Genotypes AKM-1608, Phule M 809-10, and AKM-1609 also demonstrated high FSD and are recommended as donor parents for pre-harvest sprouting resistance. Furthermore, the activities of α-amylase and dehydrogenase enzymes serve as robust biochemical indicators of seed germination capacity and vigour, and their strong mutual correlation ($r = 0.95$) suggests that either enzyme can be used as a rapid screening tool for seed quality. The promising genotypes identified in this study hold immense potential for utilization in hybridization programs aimed at developing high-yielding, weather-resilient mungbean varieties for rainfed environments.

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REFERENCES

[1] Kamleshwar, S., Yadav, S. K., and Pandey, P. (2014). Nutritional and dietary value of Mung bean (Vigna radiata L.). Journal of Legume Research, 37(3), 250–255.

[2] Ram Nair, R. (2019). Global mungbean production and trade: Current status and future prospects. Agricultural Economics, 45(2), 112–118.

[3] Rahim, M. A., Mia, A. A., Mahmud, F., Zeba, N., and Afrin, K. S. (2010). Genetic variability, character association and genetic divergence in mungbean (Vigna radiata L. Wilczek). Plant Omics Journal, 3(1), 1–6.

[4] Ahmad, S., Shahzad, M. A., Saleem, M., and Cheema, M. A. (2014). Pre-harvest sprouting in crops: Mechanism and management. Acta Physiologiae Plantarum, 36(5), 1105–1115.

[5] Durga, K. K., and Kumar, C. V. S. (1997). Pre-harvest sprouting in mungbean and its management. Legume Research, 20(3), 145–150.

[6] Wareing, P. F. (1963). The germination of seeds. Advances in Botanical Research, 1, 195–227.

[7] Bernfeld, P. (1955). Amylases, alpha and beta. Methods in Enzymology, 1, 149–158.

[8] Thimaya, V. K. (1990). Dehydrogenase activity as an indicator of seed viability. Journal of Seed Technology, 14(2), 88–95.

[9] ISTA (1999). International rules for seed testing. Seed Science and Technology, 27 (Supplement), 1–333.

[10] Panse, V. G., and Sukhatme, P. V. (1989). Statistical Methods for Agricultural Workers (4th ed.). Indian Council of

Agricultural Research, New Delhi.
[11] Mehandi, S., Singh, I. P., Bohra, A., and Singh, C. M. (2019). Genetic diversity and population structure analysis in mungbean (Vigna radiata L.) genotypes. Legume Research, 42(1), 1–8.
[12] Souframanien, J., and Gopala Krishna, T. (2004). A critical evaluation of genetic similarity among accessions of black gram (Vigna mungo) using RAPD and ISSR markers. Euphytica, 135(3), 331–339.
[13] Singh, R., and Ahlawat, I. P. S. (2005). Pre-harvest sprouting in grain legumes and its impact on seed quality. Seed Science and Technology, 33(1), 45–52.
[14] Copeland, L. O. (1976). Principles of Seed Science and Technology. Burgess Publishing Company, Minneapolis, USA.
[15] ISTA (1976). Seed vigour testing seminar. International Seed Testing Association, Zurich, Switzerland.
[16] Lenka, D., and Mishra, B. (1973). Path coefficient analysis of yield in rice varieties. Indian Journal of Agricultural Sciences, 43(4), 376–379.
[17] Saleem, M., Haris, W. A. A., and Malik, M. A. (1998). Nutritional composition of mungbean genotypes. Pakistan Journal of Agricultural Sciences, 35(1), 25–28.
[18] Thirumaran, A. S., and Seralathan, M. A. (1988). Utilization of cowpea. In: Cowpea Research, Production and Utilization. John Wiley and Sons, New York.
[19] Jadhav, R. A. (2019). Genetic variability and character association studies in mungbean. Ph.D. Thesis, VNMKV, Parbhani.
[20] Autade, A. D. (2018). Biochemical studies in mungbean. Ph.D. Thesis, VNMKV, Parbhani.