



Integrating Multivariate Analysis to Evaluate Trait Performance and Genetic Variability in Mung Bean Lines

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10.18805/LRF-915

ABSTRACT

Background: Mung bean is an alternative legume crop cultivated globally, with increasing consumption in recent years. To meet this demand, high-yielding and agronomically superior cultivars must be developed.

Methods: Selection breeding was applied to lines collected from various regions of Türkiye starting in 2015, resulting in the development of 25 pure lines by 2020. In 2022, these lines were evaluated alongside two registered varieties.

Result: Among phenological traits, the shortest flowering time was recorded in line 07G01-17. Early pod setting was observed in the Partow cultivar and line 50N01-16, while the shortest vegetative period was noted in line 27S08-1. Regarding agronomic traits, the tallest plant height was observed in line 07A05-3 and the highest first pod height in line 07G05-5. The highest number of seeds per plant and yield per plant were obtained from line 46G01-2. The most seeds per pod were recorded in line 07G05-5, followed by 07G01-17. The highest grain yield was obtained from line 33M02-17. According to multivariate analysis and the MGIDI index, line 46G01 showed superior performance, while some lines such as 70S01-9 showed promise for early maturity. These results highlight valuable material for future mung bean breeding.

Key words: MGIDI, Multivariate analysis, Mungbean, Pure line breeding, Yield.

INTRODUCTION

Mung bean [*Vigna radiata* (L.) Wilczek] is an important warm-season legume widely cultivated across Asia, Africa and parts of Europe. Its global demand has risen steadily due to its short growth cycle, high protein content and broad use in food and feed systems (Azam *et al.*, 2023).

Mungbean is an important legume crop for the world. It is a short duration grain legume crop grown primarily for their dry seeds. It contains about 25 per cent protein, which is nearly three times than that of cereals (Basnet *et al.*, 2014).

The total cultivation area of mung bean in the world is approximately 7.3 million hectares, with an average yield of 721 kg ha⁻¹, resulting in a total production of 5.3 million tons. India and Myanmar contribute 30% to this production (Nair and Schreinemachers, 2020). As a result of surveys with farmers in Turkey, it was determined that mung beans are cultivated in Mersin, Karaman, Konya, Adıyaman and Nevşehir provinces and offered to the domestic market. Although mung bean is cultivated in such a large area within the borders of our country, it is not included in TUIK records. It is thought that these mung bean data are collected under the title of beans as in FAO. During the survey trips, it was stated that the lines used were not registered varieties, that they had been using them for many years and that they had grown the seeds themselves (Karaman and Kaya, 2020). In addition, it was determined that mung bean cultivation in our country contributed 790.6 thousand TL to our economy by exporting 68.3 tons in 2020 (Turkish Statistical Institute, 2020).

Phenological development and yield performance in mung bean are strongly influenced by regional and environmental conditions. Although mung bean is generally

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How to cite this article: Karaman, R., Nawaz, H., Türkay, C., Akgün, I. and Kaya, M. (2026). Integrating Multivariate Analysis to Evaluate Trait Performance and Genetic Variability in Mung Bean Lines. *Legume Research*. 1-11. doi: 10.18805/LRF-915.

Submitted: 20-11-2025 **Accepted:** 16-01-2026 **Online:** 03-02-2026

classified as a short-day species, recent studies show that photoperiod sensitivity varies substantially among genotypes, with some lines exhibiting partial or complete photoperiod insensitivity (Singh *et al.* 2021). On long days, flowering is prolonged and ripening may be delayed. Most of the world production is obtained from species grown in regions with 600-1000 mm rainfall (semi-arid, semi-humid). In our country, agronomic studies on mung bean are limited and there are no registered varieties available to date. Especially Pakistan, India, USA, Japan, Taiwan, Japan, Taiwan and Australia have focused on the breeding of this plant and even a research institute (Australian Mungbean Association) was established in Australia on mungbean breeding and cultivation. According to the Asian Vegetable Research and Development Center (AVRDC), 44 mung beans have been officially characterized and given species accession numbers in our country since 1984. In fact, three mung bean materials collected from Hakkari-

Üzümcü village in our country were reported to be wild mung bean by USDA (Schafleitner *et al.* 2015).

Despite the growing importance of mung bean as a nutritious and climate resilient crop, its production in Türkiye remains limited by the lack of high-yielding, early maturing and locally adapted cultivars. Existing varieties often exhibit insufficient yield potential, unstable agronomic performance and poor adaptation to regional environmental conditions. These limitations hinder efforts to expand mung bean cultivation and meet the increasing domestic and global demand. Therefore, identifying and developing superior genotypes with improved phenological and agronomic traits has become a critical necessity for strengthening mung bean production in Türkiye.

Although several studies have evaluated mung bean germplasm globally, comprehensive assessments of newly developed Turkish lines are scarce. In Türkiye, no recent research has combined phenological and agronomic evaluation with multivariate selection tools such as the MGIDI index to identify superior genotypes for breeding. Additionally, the performance of the 25 pure lines developed through selection breeding since 2015 has not yet been systematically compared with registered cultivars under local growing conditions. This gap limits the availability of evidence-based recommendations for varietal improvement and future breeding programs.

This study was conducted to: (i) Evaluate the phenological and agronomic performance of 25 newly developed mung bean pure lines alongside two registered cultivars, (ii) Identify superior genotypes based on yield-related and morphological traits using multivariate analysis and the MGIDI index, (iii) Support future mung bean breeding efforts by selecting lines with desirable traits such as early maturity, high seed production and improved plant architecture.

MATERIALS AND METHODS

Experimental site

The experiment was conducted in research and experimental farm of the Isparta University of Applied Sciences, Isparta Türkiye. Isparta is in the transition zone between the Mediterranean and continental climate zones.

Plant material collection

Mung bean materials were collected across Turkey in 2015 with support from local authorities and coded by province. From 91 collected lines, 50 were selected and tested in 2017–2018 using an Augmented design with 5 replications. Based on two years of data, 660 single plants were chosen from 20 populations in 2019 through pure line selection, leading to 250 pure lines in 2020 (Fig 1). From these, 25 promising lines were selected (Fig 2) for evaluation in 2022 for yield- and quality-related traits, alongside two registered control varieties (Partow and Jade AU).

Planting and maintenance of the experiment

The superior lines used in the trial were planted in 3 replications according to the randomized completely block design (RCBD). In the experiment, sowing was carried out in hand-dug rows with a plot size of 6 × 3m. Sowing was done on May 10, 2022. Fertilizer was applied with the calculation of 30 kg N and 60 kg P₂O₅ ha⁻¹. During the

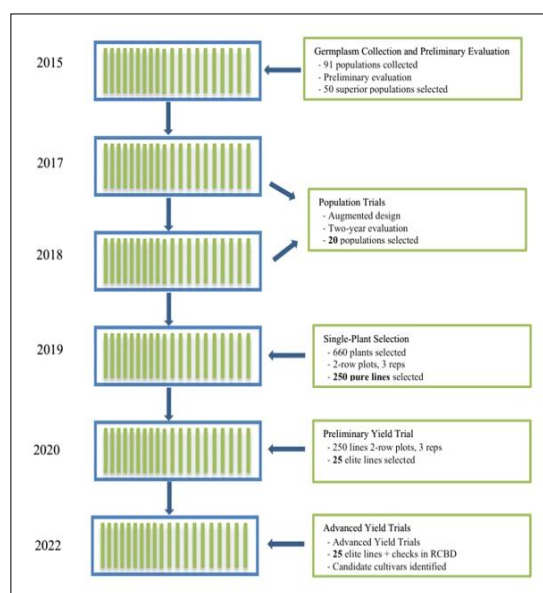


Fig 1: Flowchart/schematic of selection steps (2015-2022).

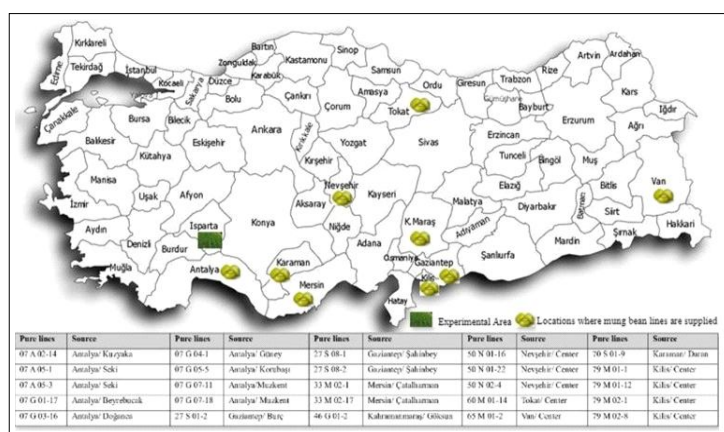


Fig 2: Source map of pure lines across Turkey.

vegetation period, drip irrigation was applied 1-2 times a week according to the water needs of the plants. For the control of weeds, pre-emergence herbicide was applied after sowing the weeds were removed with hand and machine hoeing. Since ripening dates varied among lines, harvesting was generally carried out between August 15 and October 15. Harvesting was done by excluding the first and last rows of the plants in the plot and the 50 cm from the beginning and end of the rows at both ends of the plot and observations were made on 10 randomly selected plants in single plant evaluations.

Examined features in the experiment

Data was recorded on phenological characteristics (flowering time, 50% pod setting time, vegetation duration) and agronomic characteristics (plant height, first pod height, pods plant⁻¹, seeds plant⁻¹, seeds pod⁻¹, yield per plant (g) and grain yield (kg ha⁻¹).

Climatic and soil characteristics of the study site

The climatic data for the year in which the study was conducted (2022) and for many years are given in Fig 3. Soil samples taken from different parts of the experimental area at 0-30 cm depth were analyzed and the data on soil properties. According to the results of the analysis, the soil texture of the test area is clayey-loamy, slightly alkaline reaction (pH value 7.7), salt content (EC) 322 (µS/cm) and is in the slightly saline group. It is rich in lime content (28.7%) and poor in organic matter content (1.54%).

Multitrait genotype-ideotype distance index (MGIDI)

The multi-trait index based on factor analysis and genotype-ideotype distance (MGIDI) proposed by (Olivoto and Nardino, 2021) was used to select the novel donors with high performing lines. The MGIDI was computed as follows: $MGIDI_i^{0.5}$

$$MGIDI_i = \sum_{j=1}^f [(y_{ij} - \bar{y}_j)^2]^{0.5} \quad \dots 1$$

Where,

$MGIDI_i$ = Distance index of multi-trait genotype-ideotype for the i^{th} genotype.

y_{ij} = Score of the i^{th} genotype in the j^{th} factor $i = 1, 2, \dots, g$; $j = 1, 2, \dots, f$.

g and f = Number of genotypes and factors, respectively.

$\bar{y}_j$ = Ideotype's j^{th} score.

The proportion of the MGIDI index of the i^{th} row/genotype/treatment explained by the j^{th} factor (ω_{ij}) is used to show the strengths and weaknesses of genotypes/treatments and is computed as:

$$\omega_{ij} = \frac{\sqrt{D_{ij}^2}}{\sum_{j=1}^f \sqrt{D_{ij}^2}} \quad \dots 2$$

Statistical analysis

The analysis of variance of the data was carried out in MINITAB 17 package program in accordance with the randomized complete block experimental design and the

differences between the lines were determined using Tukey multiple comparison test ($P < 0.05$). Prior to analysis, the assumptions of normality and homogeneity of variances were evaluated using the Shapiro Wilk and Levene's tests, respectively. The data met the assumptions required for analysis of variance (ANOVA). Principal component analysis, cluster analyses and MGIDI were determined in the R program (version 4.1.2).

RESULTS AND DISCUSSION

Days to flowering

Mung bean is one of the warm climate legumes, it requires cool air and low humidity during the flowering period. The flowering time of the pure lines obtained by pure line selection of mung bean lines obtained from Turkey are presented in Table 1. The flowering period of 25 pure lines and registered mung bean cultivars varied between 70.0 and 89.0 days. Among the pure lines, the shortest flowering time was 70.0 days in line 07G01-17 and the longest flowering time was 88.7 days in line 70S01-9. The latest flowering was determined in Jade-AU variety (89.0 days) among the lines and varieties used in the study. The average flowering time of the lines and cultivars was determined as 80.2 days and 19 of the 25 mung bean lines flowered in less than this period (Table 1). This shows that there are promising lines for the variety among the existing lines.

Previous multi-environment studies have demonstrated that flowering time in mung bean is highly influenced by both genetic background and environmental conditions. For example, Çancı and Toker (2005) observed a wide range of 20-76 days under the Mediterranean climate of Antalya, with a high heritability estimate (88%), indicating strong genetic control of this trait. Similarly, Karaman and Kaya (2020) reported flowering times of 83.4-120.4 days in 2017 and 84-120 days under the conditions of Isparta, further supporting the presence of substantial genetic variability across environments.

The variation observed in our study is consistent with these findings and highlights the responsiveness of mung bean genotypes to environmental stimuli. Importantly, the documented high heritability suggests that flowering time can be effectively manipulated through selection, making it a valuable trait for breeding programs. Early or optimally timed flowering is particularly advantageous when developing high yielding recombinant lines adapted to contrasting environments.

50% Pod formation

In breeding studies of legume crops, traits such as earliness, flowering time, pod tying time and vegetation duration are positively correlated with seed emergence time. In the present study, pod setting time of different mung bean pure lines and cultivars varied between 80.0 - 103.0 days (Table 1). The earliest pod setting was determined in Partow cultivar with line 50N01-16, followed by lines 27S08-1 (82 days), 27S08-2 (85 days), 79M01-1 (85 days), 79M02-1 (85 days) and 79M02-8 (85 days). Jade-AU, another

registered variety, had a later pod setting time (except 70S01-9) than the lines obtained from our country. The latest pod setting time was determined in line 70S01-9.

The mean pod setting time of the evaluated lines varied significantly. This variability is consistent with reports showing that pod-setting time in mung bean is shaped by

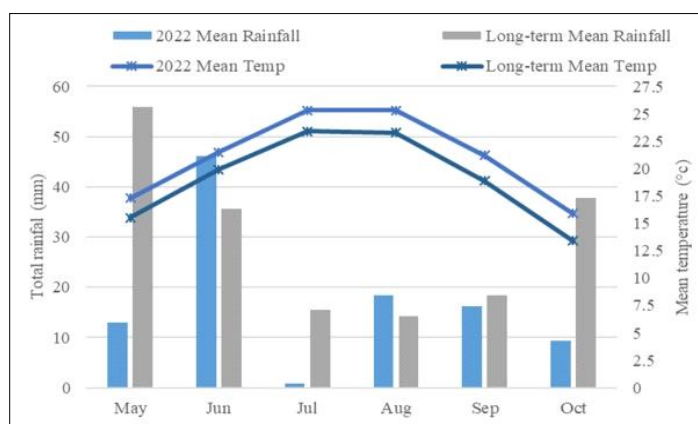


Fig 3: Climatic data of Isparta province for the year the research was conducted and for many years.

Table 1: Mean values of days to flowering, 50% pod formation, vegetation duration, plant height, first pod height and pods plant⁻¹ of mung bean lines and varieties.

Line / Variety	Days to flowering	50% pod formation	Vegetation duration	Plant height (cm)	First pod height (cm)
07A02-14	84.0ab	90.00bc	149.00cd	68.08a-c	32.67b-e
07A05-1	84.0ab	90.00bc	150.00bc	66.40bc	31.19c-e
07A05-3	80.3 bc	90.00bc	150.00bc	73.92a	42.40a
07G01-17	70.0e	87.00cd	153.00a	66.15bc	34.95b
07G03-16	80.0b-d	90.00bc	131.00f	66.47bc	34.04bc
07G04-1	84.0ab	90.00bc	131.00f	61.23cd	33.30b-d
07G05-5	80.0b-d	87.00cd	152.00ab	72.69ab	45.20a
07G07-11	80.0b-d	87.00cd	137.00e	40.58h-k	20.11g-i
07G07-18	80.0b-d	87.00cd	137.00e	46.42f-i	17.20 i-l
27S01-2	88.0a	87.33b-d	151.00a-c	65.12c	31.55c-e
27S08-1	77.0cd	82.00de	120.00g	36.17kl	21.20gh
27S08-2	77.0cd	85.00c-e	122.00g	35.26kl	19.98g-i
33M02-1	80.0b-d	87.00cd	132.00f	37.22j-l	21.28g
33M02-17	80.0b-d	87.00cd	132.00f	44.10g-j	16.87j-l
46G01-2	80.0b-d	90.00bc	151.00a-c	41.54g-k	14.83kl
50N01-16	75.0de	80.00e	147.00d	45.72f-i	16.08j-l
50N01-22	78.0cd	90.00bc	131.00f	37.39j-l	14.21l
50N02-4	80.0b-d	87.00cd	135.00e	44.77g-i	17.74i-k
60M01-14	77.0cd	87.00cd	150.00bc	42.23g-k	15.76j-l
65M01-2	80.0b-d	87.33b-d	151.00a-c	45.16g-i	18.06ij
70S01-9	88.7a	103.00a	151.00a-c	52.56ef	30.67de
79M01-1	77.0cd	85.00c-e	122.00g	46.49f-h	18.38g-j
79M01-12	77.0cd	87.00cd	137.00e	37.31j-l	16.80j-l
79M02-1	77.0cd	85.00c-e	131.00f	32.46l	18.23h-j
79M02-8	77.0cd	85.00c-e	131.00f	39.42i-l	16.89j-l
Jade AU	89.0a	93.00b	153.00a	48.25fg	26.51f
Partow	85.0ab	80.00e	153.00a	56.33de	29.70e
Mean	80.2	87.52	140.37	49.98	24.29
F-Value	20.16**	16.39**	499.49**	493.96**	259.43**
CV	4.59	4.59	0.61	4.40	3.94

**: $P \leq 0.01$, ¹The difference between the values shown with different letters is significant at $P \leq 0.01$ level.

both genotype and environmental conditions (Begum *et al.* 2013). Reproductive traits such as flowering and pod initiation are known to respond strongly to temperature, moisture and humidity (Akbar *et al.* 2020) and previous studies have recorded first pod-setting times ranging from 47 to 68 days (Pekşen *et al.* 2015). The variation observed in our study indicates a useful level of genetic diversity, suggesting that earlier pod-setting lines may serve as promising parents for developing high-yielding recombinants and for selection in multi-environment breeding programs.

Vegetation duration

The vegetation period of mung bean varieties and pure lines varied between 120.0-153.0 days. The earliest vegetation period was completed by 27S08-1 line and the latest by 07G01-17 line. 28S08-1 line was in the same statistical group with 28S08-2 (122 days) and 79M01-1 (122 days) lines. The average vegetation period of the varieties and lines was determined as 140.4 days and 14 lines completed their vegetation before this period.

Registered varieties reached maturity later than the lines obtained from Turkey (except 07G01-17 line) under Isparta conditions (Table 1). According to the results, it can be stated that especially the climate and soil conditions of the region where mung bean is grown affect the vegetation period considerably. At the same time, (Sohail *et al.* 2016) found that vegetation duration was significantly and positively correlated with plant height ($r=0.62$). In the literature studies, it was determined that the vegetation period of mung bean varied between 59-162 days (Begum *et al.* 2013; Mehandi *et al.* 2013; Tajoddin *et al.* 2014; Ahmad *et al.* 2014).

Plant height

Plant height is one of the most important components that play a significant role on plant yield. In this study, plant height of mung bean lines and varieties varied between 32.5-73.9 cm. The maximum plant height was found in 07A05-3 line and there was no statistical difference with 07G05-5 (72.7 cm) and 07A02-14 (68.1 cm) lines. The shortest

Table 2: Mean values of pods plant⁻¹, seeds plant⁻¹, seeds pod⁻¹, yield plant⁻¹ (g) and grain yield of mung bean lines and varieties.

Line / Variety	Pods plant ⁻¹	Seeds plant ⁻¹	Seeds pod ⁻¹	Yield plant ⁻¹ (g)	Grain yield (kg ha ⁻¹)
07A02-14	32.00g	331.95ef	10.29a-g	21.17ab	2283.6b-d
07A05-1	21.67j	244.41k	11.22ab	15.33d-h	2371.3bc
07A05-3	28.12h	305.64h	11.01a-c	15.41d-h	1838.7f-i
07G01-17	26.00hi	301.68h	11.46a	18.12b-d	1706.6h-k
07G03-16	21.46j	234.87kl	10.97a-d	11.66i-l	1584.10kl
07G04-1	20.26jk	205.79m	10.34a-f	11.16j-l	1646.3j-l
07G05-5	28.29h	320.95fg	11.48a	16.57c-f	1766.3g-j
07G07-11	34.88d-f	334.59e	9.95a-h	16.00c-g	1897.1fg
07G07-18	41.44c	358.55d	8.88e-i	16.36c-f	2232.7cd
27S01-2	20.63jk	224.02l	11.01a-c	12.59h-k	2005.9ef
27S08-1	16.58lm	154.95o	9.47b-i	8.57lm	1177.4no
27S08-2	20.30jk	199.25m	9.49b-i	11.42i-l	1358.4m
33M02-1	17.61lm	183.00n	10.35a-e	7.81m	1327.3mn
33M02-17	33.67	299.35h	8.80e-i	14.53e-i	2571.0a
46G01-2	57.43a	534.37a	9.21d-i	23.70a	2226.3cd
50N01-16	33.87e-g	258.05j	7.71i	14.23e-j	1876.7f-h
50N01-22	35.83de	309.77gh	8.48hi	13.75f-j	1698.3i-k
50N02-4	32.92fg	277.57i	8.56f-i	13.12g-k	1922.5fg
60M01-14	37.04d	302.39h	8.04i	16.93c-f	2203.9cd
65M01-2	39.52c	328.83ef	8.54g-i	19.15bc	2409.2ab
70S01-9	37.10d	375.29c	10.02a-h	18.50b-d	2148.4d-e
79M01-1	46.38b	389.18b	9.30c-i	17.01c-e	2328.0bc
79M01-12	35.85de	326.20ef	9.10e-i	14.21e-j	1858.9f-i
79M02-1	18.56kl	165.82o	8.44hi	10.43k-m	1026.2o
79M02-8	39.73c	326.59ef	8.46hi	20.28b	2229.4cd
Jade AU	16.19m	155.13o	9.20d-i	11.15j-l	1477.8lm
Partow	24.31i	209.97m	8.61e-i	14.01e-j	1708.6h-k
Mean	30.28	283.64	9.57	14.93	1884.5
F-Value	597.90**	1392.27**	11.76**	42.96**	163.24*
CV	2.31	1.38	5.88	6.72	2.87

**: $P \leq 0.01$, *The difference between the values shown with different letters is significant at $P \leq 0.01$ level.

plant height was determined in 79M02-1 line and this line was in the same statistical group with 27S08-2 (35.3 cm), 27S08-1 (36.2 cm), 33M02-1 (37.2 cm), 79M01-12 (37.3 cm), 50N01-22 (37.4 cm), 79M02-8 (39.4 cm). The overall average plant height of pure lines and cultivars was 49.98 cm and 9 pure lines and Partow cultivar were above this average (Table 1). Literature reports indicate that mung bean plant height commonly ranges from 24 to 70 cm (Gul *et al.*, 2008; Begum *et al.* 2013; Tajoddin *et al.* 2014; Khan *et al.*, 2017), reflecting substantial genetic variability across environments. The broad range observed in our study further supports this variability and suggests strong genotype $\times$ environment responsiveness. Importantly, several lines combined desirable yield performance with contrasting growth habits either tall plants with longer vegetation periods or short plants with earlier maturity. Such diverse yet productive phenotypes represent valuable genetic resources for breeding.

First pod height

The highest first pod height of mung bean lines and varieties was determined in line 07G05-5 with 45.2 cm and there was no statistical difference between it and line 07A05-3 with 42.4 cm. The shortest first pod height was determined in line 50N01-22 with 14.2 cm. The general average of the first pod height of pure lines and varieties was determined as 24.3 cm and 9 pure lines and two varieties were above this average (Table 1). In the study, it was determined that the lines with maximum plant height (07A05-3 73.9 cm; 07G05-5 72.7 cm) also had higher first pod height. (Pekşen *et al.*, 2015) reported a negative and significant correlation between first pod height and harvest index and grain yield. They reported that there were significant increases in the number of inflorescences, plant height and first pod height with the prolongation of the first flowering and pod setting period. In addition, Akgunduz, (2016) reported that lines with higher plant height also had higher first pod height.

Pods plant⁻¹

In this study, the number of pods per plant of mung bean lines and varieties varied between 16.2-57.4. The highest number of pods was determined in 46G01-2 line and the lowest in Jade-AU variety. The average number of pods of lines and cultivars was 30.3 pods. In terms of the number of pods, the lines were significantly higher than the registered varieties and significant variations were found among the lines (Table 2). The number of pods per plant is a key determinant of yield in legumes (Vega *et al.* 2001) and its strong positive association with grain yield in mung bean has been well documented (Khattak *et al.* 2002). Previous studies report pod numbers ranging from 7 to 25 per plant (Akbay *et al.* 2020; Gölğül *et al.* 2023), indicating considerable genetic and environmental influence on this trait. The variation observed among the lines in our study similarly reflects both genotype-dependent differences and field-related factors such as plant density. Lines that consistently produce higher pod numbers represent

valuable material for breeding, particularly when integrated into multi-environment evaluations and multi-trait selection frameworks like MGIDI to identify high-yielding recombinant genotypes.

Grains plant⁻¹

In this study, significant ($P \leq 0.01$) differences were found between grains plant⁻¹ of the lines and varieties and the averages of the seeds plant⁻¹ (Table 2). The number of seeds plant⁻¹ of the lines and cultivars varied between 154.95-534.37. The highest seeds plant⁻¹ was determined in line 46G01-2. The lowest seeds plant⁻¹ was determined in line 27S08-1, while there was no statistical difference between line 79M02-1 and Jade AU variety. The average grains plant⁻¹ of the lines and varieties was 283.64. Grain number is closely related to the number of pods in the plant and generally increase the number of grains in the plant. (Garje *et al.* 2014) reported a significant and positive correlation between the grains plant⁻¹ and the number of pods plant⁻¹, grains pod⁻¹ ($r=0.53$) and grain yield plant⁻¹ in mung bean.

The averages of the seed pod⁻¹ of mung bean lines and varieties are given in Table 2. The seed pod⁻¹ of the lines and varieties varied between 7.71-11.48, the average was 9.57. The highest seed pod⁻¹ among the lines and varieties was determined in line 07G05-5, followed by 07G01-17 (11.46) and 07A05-1 (11.22). Seeds per pod is a critical yield determining trait in mung bean and previous studies have shown a significant positive association between seeds pod⁻¹, pods plant⁻¹ and final grain yield (Çancı and Toker 2014). In our study, seeds pod⁻¹ varied markedly among the evaluated lines, indicating substantial genetic variability. Notably, several lines produced more seeds per pod than the registered control varieties, suggesting the presence of superior genetic combinations.

Yield plant⁻¹

The mean yield plant⁻¹ of mung bean lines and varieties are given in Table 2. Statistically ($P \leq 0.01$) significant differences were found between the yield plant⁻¹ of the lines and varieties. Yield plant⁻¹ varied between 7.81-23.70 (g plant⁻¹). The highest yield plant⁻¹ was determined in line 46G01-2 and was statistically in the same group with line 07A02-14. The lowest yield plant⁻¹ was determined in line 33M02-1. The average yield plant⁻¹ of the lines and varieties was 14.93 g plant⁻¹. Yield plant⁻¹ is a trait that directly affects grain yield and is one of the most important selection criteria in breeding studies.

Plant height, pods plant⁻¹ and grains plant⁻¹ are known to be positively associated with yield plant⁻¹ in mung bean (Pekşen and Gülümser, 2005). Ahmad *et al.* (2014) reported a mean yield of 13.76 g plant⁻¹ and noted that yield plant⁻¹ had relatively low heritability (0.42), indicating strong environmental influence. Previous research also shows wide variation in yield plant⁻¹, ranging from 2.58-5.77 g (Gul *et al.* 2008), 6.78-11.57 g (Mondal *et al.* 2012), 21.87-45.35 g (Begum *et al.* 2013) and 24.19-29.42 g (Tajoddin *et al.* 2014),

highlighting substantial genetic diversity across studies. In our study, yield plant⁻¹ similarly differed among the lines, reflecting both genetic variation and sensitivity to environmental conditions during the growing period. Such variability reinforces the importance of multi-environment evaluation and multi-trait selection frameworks when identifying stable, high-yielding genotypes for breeding programs.

Grain yield

Significant differences were found between the grain yield of the lines and varieties used in the study and the averages of grain yield are presented in Table 2. Grain yield varied between 1026.2-2571.0 kg ha⁻¹. The highest grain yield was determined in line 33M02-17 and there was no statistical difference with line 65M01-2 (2409.2 kg ha⁻¹). The lowest grain yield was determined in line 79 M 02-1. The average grain yield of lines and varieties was 1884.5 kg ha⁻¹. This situation shows that these lines are superior in terms of yield and it can be stated that these lines with high grain yield should be taken into consideration during selection.

Grain yield in mung bean is strongly influenced by climatic, edaphic and genetic factors. Previous studies

have reported highly variable yields, ranging from 500 to 4500 kg ha⁻¹ (Toker *et al.* 2002; Çancı and Toker 2005; Gul *et al.* 2008; Sohail *et al.* 2016), demonstrating substantial genotype × environment interaction for this trait (Sharma *et al.* 2022). The variation observed in our study is consistent with this broad yield range and further supports the conclusion that both genetic differences among lines and environmental conditions play crucial roles in determining grain yield.

Principal component analysis (PCA)

Principal component analysis (PCA) signifies the importance of the major contributor to the total variation at each axis of distinction (Sharma *et al.*, 1998). The results of PCA explained the genetic diversity of the 25 lines and two varieties under study. Three principal components (PC1 to PC3) were extracted from the original data accounting for more than 82% of the total variation. Suggesting these three principal component scores might be used to review the original variables in any further analysis. Correspondingly, Pandiyan *et al.* (2012) showed that 63.79% variation was justified by the first 3 principal components for 18 quantitative and 37 qualitative characters of 646

Table 3: The eigen value, per cent variance and percent cumulative variance for three principal components (PCs) and factor loading between PCs and traits studied in mungbean.

	Eigen value	% Var. Exp.	Cum.Var. Exp.	Examined traits with loading factor									
				DF	PF	VD	PH	FPH	PPP	SPP	SP	YPP	GY
PC1	3.68	36.88	36.88	0.02	0.01	0.05	0.02	0.18	0.94	0.84	0.20	0.75	0.64
PC2	3.41	34.19	71.07	0.30	0.33	0.49	0.78	0.70	0.00	0.04	0.52	0.13	0.09
PC3	1.15	11.54	82.62	0.52	0.35	0.00	0.09	0.06	0.00	0.01	0.06	0.03	0.00

Where DF: Days to flowering, PF: Days to pod formation, VD: Vegetation duration, PH: Plant height, FPH: First pod height, PPP: Pods per plant, SPP: Seeds per plant, SP: Seed per pod, YPP: Yield per plant, GY: Grain yield.

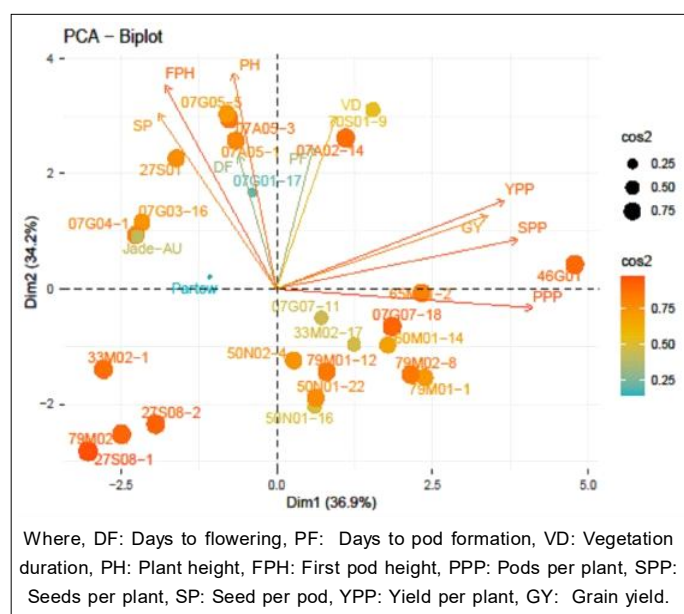


Fig 4: Distribution of mung bean lines according to PC1 and PC2 axes.

mungbean accessions subjected to multivariate analysis. Out of total principal components maintained PC1, PC2 and PC3 with values 36.88%, 34.19% and 11.54% (Table 3 and Fig 4) respectively were contributed more to the total variation. (Chahal *et al.* 2002) proposed that attributes with lower absolute value closer to zero influence the clustering less than those with largest absolute value closer to unity within the first principal component. In crop breeding programmes, PCA are very useful in identifying the phenotypic characteristics that contribute higher genetic variations among the genotypes studied, as well as in selecting potential parents for crossing to improve the desired characters for productivity in quantity and quality (Abna *et al.* 2012; Basnet *et al.* 2014).

The first principal component (PC1) accounted for the largest share of variation (36.88%) and was dominated by pods plant⁻¹, seeds plant⁻¹ and yield plant⁻¹. These traits are key yield determinants in mung bean, indicating that PC1 captures variation directly related to reproductive efficiency and overall yield potential. The clustering of these traits within a single component suggests that genotypes combining higher pod and seed numbers tend to express superior yield performance. Similar patterns were reported by Mehandi *et al.* (2015), who also found that the primary component in mung bean largely reflects yield-related variability, supporting the consistency of these associations across environments and genetic backgrounds.

PC2 explained an additional 34.19% of total variability and was strongly influenced by plant height, first pod height and seeds pod⁻¹. This component reflects differences in plant architecture and pod placement traits known to interact with environmental conditions and to influence harvestability and light interception. The substantial contribution of PC2 highlights the presence of meaningful architectural diversity among the lines.

Together, PC1 and PC2 summarize major axes of genetic variation and show that yield components and plant architecture jointly structure diversity in the evaluated material. These results underscore the importance of multi-trait selection approaches. Integrating PCA-derived trait patterns with tools such as MGIDI can improve the identification of genotypes with balanced ideotypes, supporting the development of high-yielding recombinant lines adapted to diverse environments.

Heat map analysis

Heat map is a two-dimensional data visualization approach that reveals the data in rows and columns in a data matrix together with the hierarchical clustering structure (Barua *et al.* 2022). The heat map of 2 varieties and 25 mung bean

Table 4: Predicted genetic gain for the effective traits in the MGIDI index of lines.

Factor	Variables	Sense	h ²	Selection gain (%)
FA ₁	PPP	Increase	0.983	22.7
FA ₁	SPP	Increase	0.989	29.8
FA ₁	YPP	Increase	0.942	29.4
FA ₁	GY	Increase	0.990	19.1
FA ₂	VD	Increase	0.998	9.00
FA ₂	PH	Increase	0.952	11.9
FA ₂	FPH	Increase	0.990	12.7
FA ₂	SP	Increase	0.874	4.76
FA ₃	DF	Increase	0.950	4.48
FA ₃	PF	Increase	0.939	5.52

Where, PPP: Pods per plant, SPP: Seeds per plant; YPP: Per plant, GY: Grain yield, VD: Vegetation duration, PH: Plant height, FPH: First pod height, SP: Seed per pod, DF: Days to flowering, PF: Days to pod formation.

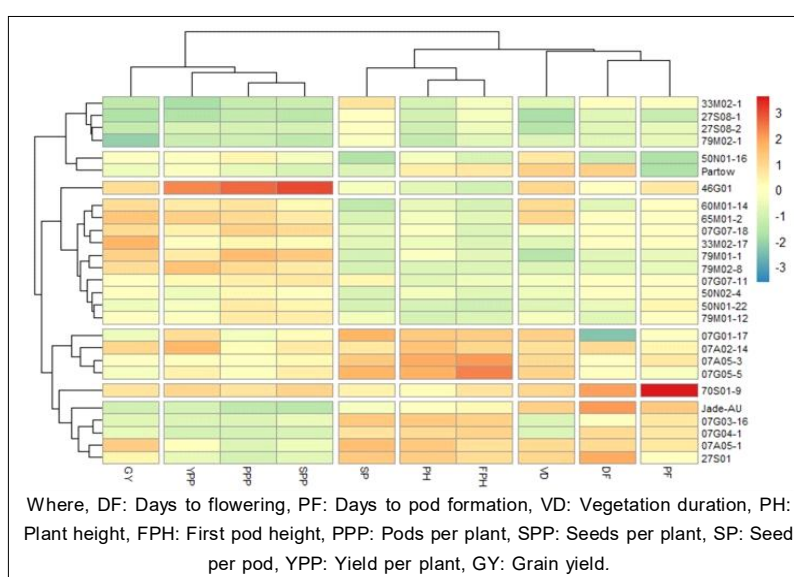


Fig 5: Heat map analysis of the examined traits.

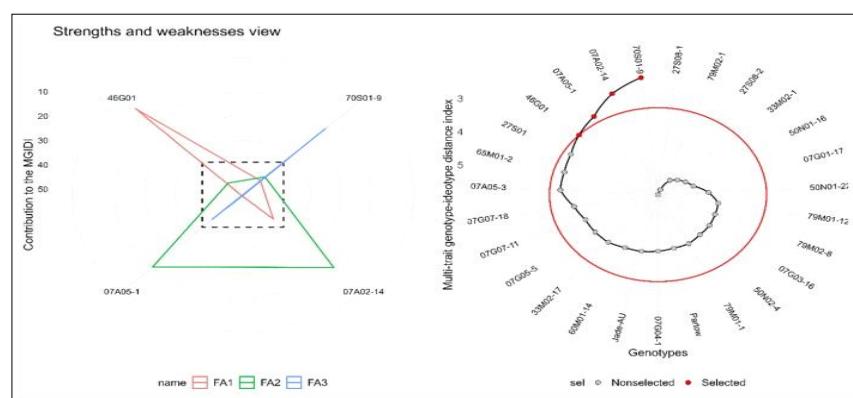


Fig 6: Strength and weaknesses of the lines and ranking of lines based on MGIDI index.

lines and 10 traits examined in the study according to the clustering analysis shown in Fig 5. There are two dendrograms in the heat map; one reflects the lines (rows) and the other reflects the traits (columns) that trigger color distribution (Barua *et al.* 2022). In the dendrogram formed as a result of clustering analysis, lines were divided into seven groups depending on the traits examined. In these groups, Group 4 had the highest number of lines with 10 lines, followed by Groups 7, while group 1 and 5 had the same number of lines (5). Similarly, Group 2 had only two lines while group three and 6 had the least number of member with 1 lines.

The lines selected by the multitrait genotype-ideotype distance index (MGIDI) were 46G01, 07A05-1, 07A02-14 and 70S01-9 (Fig 6). G13, G04 and G19 were very close to the cut-off point for index three (the red line that indicates the number of lines selected according to the selection pressure), which indicates that these lines have exciting features. Thus, further attention should be paid to the investigation of lines that are extremely close to the cut-off point.

Fig 6 shows the strengths and weaknesses of the lines showed that the first factor FA1 had a higher contribution to the MGIDI of 46G01, suggesting that this genotype performs poorly for the rest of parameters. On the other hand, FA1 had the smallest contribution to lines 07A05-1, 07A02-14 and 70S01-9, indicating these lines were the best-performing among the selected ones for the FA1 traits. FA2 had greater contributions to the MGIDI of 07A05-1 and 07A02-14 and smaller contributions to lines 46G01 and 70S01-9, resulting in these lines having strengths related to FA1 and FA3. Likewise, the contribution of FA3 was higher for the genotype 70S01-9 including the traits DF and PF.

In view of the traits of PPP and YPP and GY in FA1, positive gains are desired, so this lines (46G01) have higher contribution to these traits in comparison to others. In addition to the DF and PF traits in FA3, these lines were shown to have a shorter time to flowering and pod formation. Similarly, the lines 07A05-1 and 07A02-14 were observed to be in the same category (Table 4) as FA2 with superiority in phenological parameters (VD, PH, FPH, SP). these findings are in lined with those of (Pour-Aboghadareh *et al.*, 2021; Al-Ashkar *et al.*, 2023; Gogoi

et al., 2024). Based on multivariate and MGIDI analysis the desired features of mung bean lines can be obtained from line 46G01 for better yield, while early maturity performance based line suggested as 70S01-9.

CONCLUSION

This study revealed substantial genetic variability among the evaluated mung bean lines, demonstrating that the population contains valuable diversity for improving key phenological and morphological traits. The integration of multi-trait selection through the MGIDI index provided a clearer distinction of ideotype-aligned genotypes, highlighting its usefulness as a modern selection tool for mung bean improvement. Importantly, the identification of lines such as 46G01 and 70S01-9, which combined desirable reproductive traits with favorable maturity characteristics, underscores the potential of this germplasm for developing high-yielding and well-adapted recombinant lines. Overall, the study contributes novel insight into trait-based selection strategies in mung bean and provides a set of promising parental candidates for future breeding programs.

ACKNOWLEDGEMENT

We are thankful to Scientific Research Projects Coordination of Isparta University of Applied Science Türkiye for supporting this project (2021-ILK1-0156).

Disclaimers

The authors declare that the views expressed in this article are their own and do not necessarily represent those of their affiliated institutions.

Conflict of interest

The authors have no relevant financial or non-financial interests to disclose.

REFERENCES

- Abna, F., Golam F., Bhassu, S. (2012). Estimation of genetic diversity of mungbean (*Vigna radiata* L.) in Malaysian tropical environment. *African Journal of Microbiology Research*. 6: 1770-1775. doi:10.5897/AJMR11.1133.

- Ahmad, H., Rauf, B., Rafiq, S., Mohsin, M., Shahbaz, A.U., Sajjad, M. (2014). Genetic variability for yield contributing traits in mung bean (*Vigna radiata*, L.). *Journal of Global Innovations in Agricultural Sciences*. **2**: 52-54.
- Akbay, F., Uslu, O.S., Erol, A. (2020). The effect of different planting times on the agronomic characteristics and forage quality of mung bean [*Vigna radiata* (L.) Wilczek]. *Turkish Journal of Agriculture - Food Science and Technology*. **8**: 1160-1165. doi: 10.24925/turjaf.v8i5.1160-1165.3335.
- Akgunduz, M. (2016). Determination of drought sensitivities of mung bean (*Vigna radiata* L.) genotypes. *Ondokuz Mayıs University, Institute of Science and Technology*, p. 96.
- Al-Ashkar, I., Sallam, M., Almutairi, K.F., Shady, M., Ibrahim, A., Alghamdi, S.S. (2023). Detection of high-performance wheat genotypes and genetic stability to determine complex interplay between genotypes and environments. *Agronomy*. **13**: 585. doi: 10.3390/agronomy13020585.
- Azam, M.G., Hossain, M.A., Sarker, U., Alam, A.M., Nair, R.M., Roychowdhury, R., Ercisli, S., Golokhvast, K.S. (2023). Genetic analyses of mungbean [*Vigna radiata* (L.) Wilczek] breeding traits for selecting superior genotype(s) using multivariate and multi-traits indexing approaches. *Plants*. **12**(10): 1984. doi:10.3390/plants12101984
- Barua, H., Saha, S.R., Ivy, N.A., Rasul, G., Islam, A.A. (2022). Genetic divergence of guava (*Psidium guajava* L.) genotypes in Bangladesh. *SAARC Journal of Agriculture*. **20**: 15-28. doi: 10.3329/sja.v20i1.60618.
- Basnet, K.M., Adhikari, N.R., Pandey, M.P. (2014). Multivariate analysis among the Nepalese and exotic mungbean [*Vigna radiata* (L.) Wilczek] genotypes based on quality parameters. *Universal Journal of Agricultural Research*. **2**: 147-155. doi: 10.13189/ujar.2014.020502.
- Begum, S., Noor, M., Rahman, H., Hassan, G., Durrishahwar, Ullah, H., Ali, F. (2013). Heritability estimates and correlations among flowering and yield related traits in mungbean genotypes. *British Journal of Applied Science and Technology*. **3**: 472-481. doi: 10.9734/BJAST/2014/2588.
- Chahal, P.P.K., Chahal, V.P.S. (2002). Influence of hydrogen uptake positive strain of rhizobium, meloidogyne incognita and *Fusarium oxysporum* on ureide content and growth characters of *Vigna radiata*. *Significance*. **3**: 2-3.
- Çancı, H. and Toker, C. (2014). Yield components in mung bean [*Vigna radiata* (L.) Wilczek]. *Turkish Journal of Field Crops*. **19**: 258-261. doi: 10.17557/tjfc.79162.
- Çancı, H. Toker, C. (2005). The broad-sense heritability for yield and yield components in mung bean (*Vigna radiata* (L.) Wilczek). In *GAP IV Agriculture Congress*, Sanliurfa, Türkiye, pp. 21-23.
- Garje, U.A., Bhailume, M.S., Nagawade, D.R., Parhe, S.D. (2014). Genetic association and path coefficient analysis in green gram [*Vigna radiata* (L.) Wilczek]. *Journal of Food Legumes*. **27**: 151-154.
- Gogoi, L.R., Behera, P.P., Borah, N., Sarma, R.N. (2024). Genetic variability and correlation studies for yield and yield attributing traits in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Research*. **47**(11): 1851-1857. doi: 10.18805/LR-5241.
- Gölgül, I., Kimak, H., Ali, I.H. (2023). Yield components and crop water stress index (CWSI) of mung bean grown under deficit irrigations. *Gesunde Pflanzen*. **75**: 271-281. doi: 10.1007/s10343-022-00698-z.
- Gul, R., Khan, H., Mairaj, G., Ali, S. (2008). Correlation study on morphological and yield parameters of mung bean (*Vigna radiata*). *Sarhad Journal of Agriculture*. **24**: 37-42.
- Karaman, R., Kaya, M. (2020). Characterization of mung bean (*Vigna radiata* L.) genotypes in terms of phenological traits under Isparta conditions. *Turkish Journal of Agriculture - Food Science and Technology*. **8**: 2307-2312.
- Khan, F.U., Khan, M., Hassan, M., Gul, R. (2017). Genotypic differences among mung bean (*Vigna radiata* L.) genotypes for yield and associated traits. *International Journal of Applied Agricultural Sciences*. **3**: 47-50. doi: 10.11648/j.ijaas.20170302.13.
- Khattak, G.S., Haq, M.A., Ashraf, M., Hassan, S. (2002). Yield and yield components at various flower flushes in mungbean [*Vigna radiata* (L.) Wilczek]. *Breeding Science*. **52**(1): 61-63. doi: https://doi.org/10.1270/jsbbs.52.61.
- Mehandi, S., Singh, C.M., Kushwaha, V.K. (2013). Estimates of genetic variability and heritability for yield and yield component traits in mungbean [*Vigna radiata* (L.) Wilczek]. *Bioscan*. **8**: 1481-1484.
- Mehandi, S., Singh, I.P., Bohra, A., Singh, C.M. (2015). Multivariate analysis in green gram (*Vigna radiata* L.). *Legume Research*. doi: 10.18805/lr.v38i6.6720.
- Mondal, M.M.A., Puteh, A.B., Malek, M.A., Ismail, M.R., Rafii, M.Y., Latif, M.A. (2012). Seed yield of mungbean [*Vigna radiata* (L.) Wilczek] in relation to growth and developmental aspects. *The Scientific World Journal*. 425168. doi: 10.1100/2012/425168.
- Nair, R., Schreinemachers, P. (2020). Global status and economic importance of mungbean. *The mungbean genome* (pp. 1-8). Springer International Publishing. doi: 10.1007/978-3-030-20008-41.
- Olivoto, T., Nardino, M. (2021). MGIDI: Toward an effective multivariate selection in biological experiments. *Bioinformatics*. **37**: 1383-1389. doi: 10.1101/2020.07.23.217778.
- Pandiyan, M., Senthil, N., Packiaraj, D., Gupta, S., Nadarajan, N., Pandian, R.T., Jagadeesh, S. (2012). Characterisation and evaluation of 646 greengram (*Vigna radiata*) genotypes for constituting core collection. *Wudpecker Journal of Agricultural Research*. **1**(8): 294-301.
- Pekşen, E., Gulumser, A. (2005). Relationships and path analysis between yield and yield components in some bean (*Phaseolus vulgaris* L.) genotypes. *Anatolian Journal of Agricultural Sciences*. **20**: 82-87.
- Pekşen, E., Toker, C., Ceylan, F., Aziz, T., Farooq, M. (2015). Determination of promising high yielded mungbean (*Vigna radiata* L.) genotypes under middle black sea region of Turkey. *Anatolian Journal of Agricultural Sciences*. **30**: 169-175. doi: 10.7161/anajas.2015.30.2.169-175.
- Pour-Aboughadreh, A., Sanjani, S., Nikkhah-Chamanabad, H., Mehrvar, M.R., Asadi, A., Amini, A. (2021). Identification of salt-tolerant barley genotypes using multiple-traits index and yield performance at the early growth and maturity stages. *Bulletin of the National Research Centre*. **45**: 1-16. doi: 10.1186/s42269-021-00576-0.
- Schafleitner, R., Nair, R.M., Rathore, A., Wang, Y.W., Lin, C.Y., Chu, S.H., Ebert, A.W. (2015). The AVRDC-the world vegetable center mungbean (*Vigna radiata*) core and mini core collections. *BMC genomics*. **16**(1): 344.

- Sharma, N. (2022). Photosynthetic efficiency and yield stability in mungbean genotypes under diverse environments. *Legume Research*. **45(1)**: 50-60. doi: 10.18805/LR-4344.
- Sharma, R.K., Pavel, M., Leen, T.K. (1998). Multistream video fusion using local principal components analysis. *Infrared Technology and Applications*. **3436**: 717-725.
- Singh, C., Choudhary, S., Singh, V., Singh, R. (2021). Photoperiod sensitivity and flowering behavior in mungbean (*Vigna radiata* L.) under varying environmental conditions. *Legume Research*. **44(5)**: 547-553. doi: 10.18805/LR-4365.
- Sohail, A., Gul, R., Ahmed, S. (2016). Genetic variability and trait association for morphological and yield parameters of mungbean (*Vigna radiata* L.). *Pure and Applied Biology*. **5**: 622.
- Tajoddin, M., Manohar, S., Lalitha, J. (2014). Agronomic characteristics and seed yield of mung bean cultivars differing in seed color using organic and conventional farming in Indian subtropical region. *Asian Australasian Journal of Plant Science and Biotechnology*. **6**: 38-40.
- Toker, C., Canci, H.M., Hag, A., Cagırgan, D. (2002). Determination of agronomic, morphological and phenological characteristics of mung bean (*Vigna radiata* L.) genotypes grown in the Western Mediterranean Region of Turkey. *Turkish Journal of Field Crops*. 78-83.
- Turkish Statistical Institute (TSI) (2020). <https://www.tuik.gov.tr/> (Accessed January 01, 2020).
- Vega, C.R. andrade, F.H., Sadras, V.O., Uhart, S.A., Valentinuz, O.R. (2001). Seed number as a function of growth: A comparative study in soybean, sunflower and maize. *Crop Science*. **41**: 748-754. doi: 10.2135/cropsci2001.413748x.