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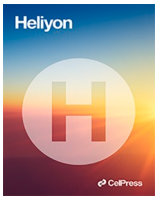

Research article

Genotypic variations in postfertility traits and yield components of mung bean (Vigna radiata (L.) R. Wilczek) germplasms in Chitwan, Nepal

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ABSTRACT

Assessment of economic traits of germplasms, which are associated with genetic variation, is vital for mung improvement. Therefore, by wielding the randomized complete block design with 3 replications, a probe analysis using multiple trait stability indexing and analysis of variance with Duncan's test at $p \leq 0.05$ is performed to compare the means of yield attributes. Moreover, simultaneous application of GA3 and NAA (50 mg/L each) was carried out at 30 DAS and at mid-flowering. Pondering not only factorial analysis but also correlation and path studies revealed that flower shedding before and 12 h after spraying is nearly detrimental to yield. In addition, yield/plant was positively ($p < 0.001$, $r = 0.67–0.96$) correlated with the harvesting index and test weight. 'Pratigya', demonstrating heightened sensitivity to environmental cues—unveils increased sensitivity—while 'VC3960A-88′ flourished with hormone-boosted pod formation. 'VC6368(46-40-3)' packed 11 pods/cluster, and 'CN95' thrived, excelling in abundant grains as well as clusters. Notably, 'VC6370-A′ topped yielder, whereas CN95 augmented an efficient harvest index of 0.48. Moreover, path analysis revealed that all postfertility traits are inherently associated with yield. By employing 17 % selection intensity, the MTSI unequivocally ascertained that not only 'VC6370A' but also 'CN95' are the ideal stable and prime performing genotypes for yield(3.04–2.8 tons/ha) as well as interactive traits, a marker for simultaneous selection, as well as improvement. The MTSI view of strengths and weaknesses harbingers that breeders need to focus on increasing the number of genotypes with the desired phenotypes—lower flower abscission, greater grain dimensions and pod setting, harvesting indices, and yields/ha.

1. Introduction

In the tropics and subtropics, mung bean is a legume crop that grows quickly (55–75 days) and pollinates itself [1,2]; it consists of 22 (diploid) chromosomes, except for the variety *V. reflexa pilosa*, which has 44 (tetraploid) chromosomes. Similarly, both the experimental variety *V. radiata* var. *radiata* (VC1973A) and its relatives have genome sizes of 475–579.35 million base pairs [3,4]. Mung beans, which constitute a low-cost nutrient reservoir enriched with 60–65 % carbohydrates, have a protein content that surpasses that of soy and kidney beans at 20.97–31.32 % compared with their 20–30 % range, and a modest 1–1.5 % fat content emerges as an exceptional source of iron and folate, as reviewed by Ref. [5–7]. In Nepal's Terai region, mung bean is widely grown, particularly

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in the eastern and central regions where irrigation is readily accessible. Similarly, the western terai and foothills account for the remaining 25 % of mung bean production. Approximately 12,000 ha are used for mung bean farming; however, the yield is 6500 tons, and the productivity is 600 kg/ha, implying a substantial yield gap compared with the global average of 2.8–3 tons/ha [8]. Additionally, mung bean production is beset by a combination of challenges—severe droughts, poor and inappropriate agricultural practices, and insufficient breeding efforts—to develop new mung bean varieties with preferable traits such as high yield, drought tolerance, and disease resistance. Therefore, these challenges significantly reduce not only yield stability but also the livelihoods of smallholder farmers.

Furthermore, the amount of grain that a green gram-type plant produces is influenced by myriad factors, including not only its genes and the environment in which it is grown but also how it is managed. Despite concerted efforts in crop improvement programs to optimize per-plant yield, a persistent disparity of 5–18 % exists between research trials and farmers' actual yields [9]. This disparity is attributable primarily to the decrease in yield stability. Consequently, bridging this gap necessitates research that harmonizes high-yield potential with enhanced stability. Unveiling a powerful tool for crop selection, this pioneering study utilizes phytohormone-responsive MTSI — as an example experiment at Chitwan — possessing a wide scope in resilient varieties selection of various crops to a wide range of agroclimatic conditions in the world, potentially increasing global food security. In addition, the MTSI offers a statistical tool for predicting the genetic value of genotypes. By concurrently evaluating multiple traits, selection indices dramatically improve the efficiency of identifying superior genotypes that more closely align with the ideal phenotype [10]. Specifying economic weights, variances, covariances, and vulnerability to multicollinearity limits the classic linear selection index [11]. Similarly, the stability index proposed by Ref. [12] allows for the selection of stable genotypes with favorable selection differentials for traits to increase and unfavorable selection differentials for traits to decrease. Moreover, the index technique used by Ref. [13], can also be used to assess both the strengths and the weaknesses of genotypes. This stability index is thus useful for simultaneously selecting for average performance and stability across an interactive myriad of traits.

Furthermore, Mung beans exhibit indeterminate pod maturity; they continue to produce flowers and pods throughout the growing season. To avoid pod loss, multiple harvests are needed, but phytohormones that regulate many aspects of plant growth and development can be used to improve postfertility traits, including pod and grain number, grain weight, and grain quality [14]. Nitrate reductase activity is increased by GA3, leading to increased protein content in cowpea, black cumin and mung bean [15]. Similarly, the exogenous application of phytohormones may affect *'FERONIA'*, a known flowering pathway gene that is a candidate quantitative trait locus (QTL) with the greatest effect on days to flowering [5]. Similarly, mung orthologs of two soybean flowering genes, E3 (phytochrome A) and J (early flowering 3), can be used to improve postfertility traits such as pod number, grain number, and grain

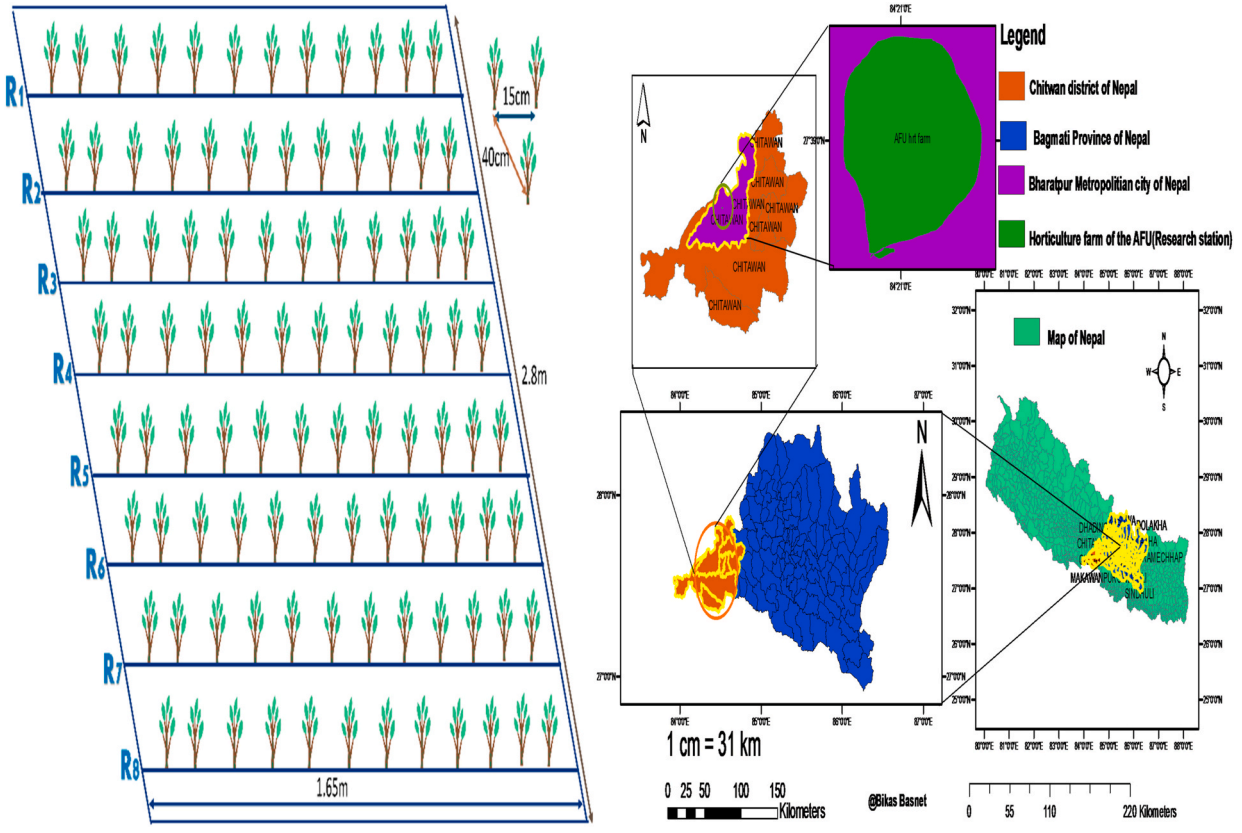

Fig. 1. Representation of the Experimental demo plot and GIS map of the Research site.

weight [16].

Although Mung has tremendous production potential in Nepal, flower shedding, sterility and poor grain setting in pods are overarching issues in farmers' fields. Exogenous application of phytohormones to horticultural crops has been documented in Nepal; after all, the use of standard research rates of plant growth-promoting substances in mung bean germplasm is unprecedented and underutilized in many developing countries. Similarly, asynchronous maturation of mung bean increased the influence of intricate genetic traits and varying environmental factors among the tested germplasms on yield. Identifying promising genotypes requires a comprehensive assessment of phenotypes. Unfortunately, contemporary crop selection paradigms and standardized bioregulation protocols remain conspicuously underutilized for discerning stable, high-performing genotypes. As a result, this study leveraged mean comparison techniques and linear mixed-model methodologies to pinpoint elite lines. This study seeks to identify elite mung bean genotypes with stable, high yields under foliar phytohormone treatment to improve grain and pod setting after flowering, considering that GA3 and NAA significantly affect not only fertility and yield improvement but also the selection of stable and high-performing genotypes through MTSI modeling, which is perceived as an alternate hypothesis.

2. Materials and methods

2.1. Source of mung bean germplasm, experimental site and design

Composed of thirteen exotic mung bean genotypes and three promising cultivars, the utilized germplasm was sourced primarily from Taiwan's Grain Legumes Research Program at NARC (Nepal Agricultural Research Council) in Khajura, Bake, Nepal, and detailed genotypic information is presented in Table S 1.

During the summer season, which spans from March 22 to June 7 at the Agriculture and Forestry University (AFU), Rampur, Agronomy Research Unit, the field experiment, which was designed via a randomized complete block design (RCBD) with a single factor, involved 16 different mung bean germplasm treatments that were replicated three times. Two blocks were established perpendicular to a fertility gradient within a single replication. Each individual plot, measuring 4.62 square meters with dimensions of 2.8 m by 1.65 m, contained seven rows, each with 11 plant spots (40 × 15-RR × PP), resulting in a total of 77 plant spots per plot Fig. 1. With dimensions of 27.9 m × 15.4 m, the entire research area underwent two rounds of harrowing and concurrent levelling to ensure uniformity. To prepare the field for sowing, fertilizers were applied as recommended, including 500 kg of farmyard manure (FYM) per hectare added three days prior and nitrogen, phosphorus, and potassium (N, P, K) at rates of 20:40:20 kg/ha applied 5 h before sowing. Furthermore, weeding was first conducted 15 days postsowing, followed by another before flowering commenced. In response to severe drought conditions, a single round of flooding irrigation was administered three days presowing, while irrigation was withheld during approximately 50 % of the flowering phase because rainfall occurred 53 days postsowing.

Seeds were sown on March 22 to obtain the optimal yield, as detailed by Ref. [17]. To achieve germination synchronization, the seeds subjected to hydropriming (100 g) were soaked in a water at a 1:1 weight-to-volume ratio for 6 h while maintaining a controlled temperature of 25 ± 1 °C, as described by Ref. [18].

2.2. Soil properties and observed traits

On the basis of the soil data from the experimental site, the soil is sandy loam with an acidic pH of 5.52 and has a medium organic matter content (3.42 %), medium total nitrogen content (0.20 %), medium total phosphorous content (10.5 ppm), and low total potassium content (5.5 ppm) Table 1.

2.3. Meteorological features of the study site

Weather parameters were recorded at the NMRP weather station in Rampur, Nepal, which is located approximately 500 m from the research site. A depiction of the weather pattern during the mung bean cultivation season is presented in Fig. 2.

Table 1
Methods for examining the soil properties at the research site.

S.N	Soil Property	Value/Rating	Method of Extraction
1	Sand%	49.3	The textural triangle of USDA
2	Slit%	34.9	The textural triangle of USDA
3	Clay%	15.8	The textural triangle of USDA
4	Textural Class	Sandy Loam	Determined by Marshall's triangular coordinates by USDA system
5	PH	5.52(Acidic Nature)	Digital pH Meter
6	Organic Carbon%	3.201	58 % of OM = Organic Carbon
7	Organic Matter	3.42(medium)	(1-S/B)0.6810 = 3.42 because this study has 11.6 and 23.4 value of S and B. (Walkley and Black method)
8	Total N%	0.20(Medium)	Micro-K-Jeldal Method
9	Total Phosphorous	10.5 ppm(medium)	Modified Olsen's Bicarbonate Method
10	Total Potassium	5.5 ppm(low)	Flame photometer method

2.4. Description of phytohormones and Stickers and their applications

Both enhancing Mung-Bean growth and yield through foliar spraying of 50 mg/L IAA or NAA +50 mg/L GA3 is the most recommended rate for sandy loam soil, as described by Refs. [14,19]. Phytohormones were applied following a standardized protocol. Gibberellic acid (GA3), Gib Max, a 20 % active ingredient powder from Vee Aar Industries (West Bengal, India), was used at a concentration of 50 mg/L. Alpha naphthaleneacetic acid (NAA), Plano-fix (Bayer Crops Science Limited, Mohali, Punjab), was applied at the same concentration via a battery-powered knapsack sprayer in a 4.5 % SL formulation. Half the prescribed phytohormone dose was foliar applied 30 days postsowing, with the remaining half applied during flowering (approximately day 54). A 1000-liter-per-hectare water mixture containing 0.5 ml/L Gorkha Sticker-More (Gorkha Agrochemical Pvt. Ltd.) was used for application and was conducted exclusively in the evenings to enhance efficacy. The grain dimensions were measured via a modern digital caliper for subsequent analysis.

2.5. Multiple traits correlation and yield calculation model

Pearson correlations were calculated between measurement means. The grain yield per hectare for each genotype was calculated from the net plot yield, taking into account the moisture content of the grain. The moisture content of the plots was measured via an automated moisture meter, and the final grain yield was adjusted to a moisture level of 10 % via the following formula [20].

$$Grain\ Yield\left(\frac{Kg}{ha}\right) = \frac{(100 - MC)*Plot\ Yield*1000(m^2)}{(100 - 10)*net\ plot\ area(m^2)} \ldots\ldots\ldots\ldots\ldots\ldots$$

The moisture content (MC) is expressed as a percentage of the weight of the grains. The straw yield was determined by subtracting the grain yield from the total biological yield (measured in kilograms per hectare). The collective yield of all plant materials is referred to as the biological yield, and the ratio of grain yield to biological yield is known as the harvest index, as defined by Ref. [21].

$$Harvesting\ Index = \frac{Econoic\ Yield\ (Grain\ Yield)}{Biological\ Yield(Grain\ Yield + Straw\ Yield)} \ldots\ldots\ldots\ldots\ldots\ldots$$

2.5.1. Multitrait genotype-ideotype distance index (MTGID)

Genotype selection in biological experiments is simplified by MTGID, developed by Olivoto and Nardino. The selection process for multiple traits is streamlined by MGIDI through the use of the distance between genotypes and an ideotype. Better outcomes are achieved with this straightforward solution [22].

$$\dot{\mathrm{MGIDI}}_i = \sqrt{\sum_{j=1}^{f} (Fij - Fj)^2} \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots$$

where $\dot{\mathrm{MGIDI}}_i$ represents the index of the multitrait genotype−ideotype distance for the ith genotype. F_{ij} represents the score assigned to a given genotype in relation to a specific factor, denoted by "i" for the ith genotype and "j" for the jth factor. The variables g and f correspond to the total number of genotypes and factors included in this analysis, and F_{ij} is the jth score of the ideotype.

The relative contribution of each factor to the MGIDI index for each genotype can be used to identify the strengths and weaknesses of those genotypes.

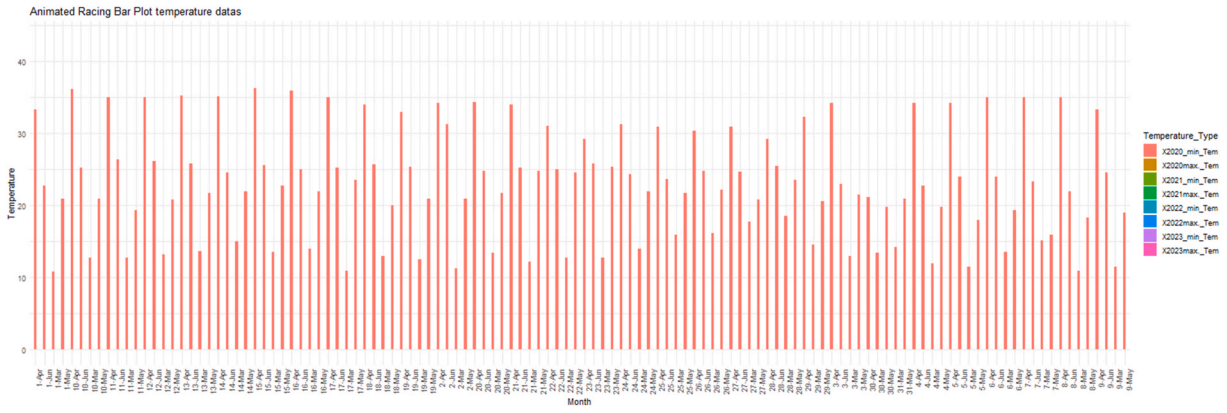

Fig. 2. Evaluating meteorological data of research stations from weather stations.

$$wij = \sqrt{\frac{D^2ij}{\sum_{j=1}^{f} D^2}}\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots$$

2.5.2. The traits were rescaled, factor analysis (FA) and spatial probability calculation were performed

This protocol is used for the identification of stable genotypes across traits and environments, as it considers multiple traits simultaneously and was devised by Refs. [23,24]. On the basis of these guidelines, this study used the following steps.

2.5.2.1. Rescaling the traits. Xij is considered a table consisting of i rows representing genotypes or treatments and j columns representing traits. To obtain the rescaled value for the ith row and jth column (rXij), the following formula is used:

$$rX_{ij} = \frac{Max_{nj} - Min_{nj}}{Max_{oj} - Min_{oj}} * \left(\varnothing_{ij} - Max_{oj}\right) + Max_{nj},$$

where Max_{nj} and Min_{nj} represent the updated maximum and minimum values for trait j following the rescaling process and where Max_{oj} and Min_{oj} represent the uppermost and lowermost limits of trait j, respectively.

2.5.2.2. Factor analysis. The following formula was used to express the factor analysis model:

$$X = \mu + LF + \varepsilon$$

X is the vector of measurements, μ is the vector of means, L is a matrix of loadings, F is a vector of common factors, and ε is the vector of unique factors. Varimax rotation criteria are used for analytic rotation and estimation of final loadings. Scores are obtained accordingly.

$$\mathrm{F} = \mathrm{Z}\left(\mathrm{A}^{\mathrm{T}}\mathrm{R}^{-1}\right)^{\mathrm{T}}\ldots\ldots\ldots\ldots$$

The matrix F contains the scores for factorial analysis, whereas Z is a matrix of standardized means that have been rescaled.

2.6. Statistical analysis

To assess the impact of foliar phytohormone application on mung bean cultivar yield and performance, an ANOVA was conducted, with data subsequently entered into Excel and analyzed via R version 4.3.1. Correlation analyses were then performed to examine the relationships among parameters at significance levels of 1 % and 5 %, followed by the application of Duncan's multiple range test (DMRT) [25] for mean separation. A suite of R packages, including "agricolae," "gvlma," and "metan," was employed to conduct statistical analyses encompassing normal distribution testing, correlation coefficient calculation, and genotype analysis under a randomized complete block design via the "gamem" function within "metan." Moreover, visualization of the results was accomplished

Table 2
Representation of flowering- and postflowering-associated traits with standard formulations of two phytohormones.

Genotypes	SPFDBAH	SPFDAAH	(Pod Length cm)	Pods/Cluster	Diameter of Grain (mm)
VC6368(46-40-3)	5.37	0.75	8.62	10.5[a]	3.60
NM-54	4.13	0.733	8.75	4.93	3.64
VC6370A	5.86	1.26[ab]	8.14	6.66	3.92[b]
VC1973A(SC)	6.13	0.80	7.99	7.60	4.06
VC6173C	5.20	0.53	6.98	6.71	3.75
CN95	6.40	0.80	9.20[a]	7.00	3.62
VC6848	5.33	0.86	8.16	5.46	3.86
PRATIGYA	8.13[a]	0.73	9.02[ab]	5.73	3.53
KPS-1	7.60	0.53	7.45	2.8	3.87
VC3890A	5.06	0.53	8.34	4.20	3.71
VC6173A	7.42	0.92	8.02	6.71	3.75
SAMRAT	6.53	0.46	7.43	3.60	3.67
PANT MUNG 2	7.60	0.60	8.16	4.20	3.59
MN92	7.466	1.0	8.84	5.26	3.73
VC6369	6.66	0.40	8.35	5.80	3.79
VC3960A-88	7.20	1.53[a]	9.04	7.80	3.96[a]
LSD(0.05)	0.33	0.94	0.135	0.675	0.03
SE_m	0.17	0.191	0.074	0.353	0.02
F-prob	<0.001	<0.01	<0.001	<0.05	<0.001
CV%	14.96	9.90	12.63	9.82	8.162

Note: Genotypes marked with superscripts represent the top performers for each measured variable according to the DMRT test.

through the utilization of the "ggplot," "circlize," and "reshape" packages, while treatment effects were determined via F test analysis.

3. Results

3.1. Analysis of variance (ANOVA) for mean performance evaluation and comparison of fertility- and yield-associated traits

The foliar application of plant growth promoters (PGPs) significantly reduced the flower drop of mung bean (*Vigna radiata*) ($p \leq 0.001$, 0.01, or 0.05), with a notable decrease observed 12 h postapplication when a combination of 25 mg/L alpha-naphthaleneacetic acid (NAA) and 25 mg/L gibberellic acid (GA3) was used, which is hypothesized to stimulate cell division and expansion within the ovary and other floral organs [10]. The cultivar Pratigya presented the highest flower drop incidence (8), followed by Pant mung 2, whereas NM54 presented the lowest flower drop incidence, likely attributed to its less responsive flowering behavior. VC6368 (46-40-3) displayed superior podding characteristics, with the highest number of pods per cluster despite an initial flower drop count of 5. A significant ($p < 0.01$) reduction in flower shedding after hormone application was observed, suggesting increased pollination and grain set, culminating in an average of 8 grains per pod. The ideal germplasms VC6370A and CN95 effectively controlled flower drop, resulting in elongated pods, increased pod numbers per cluster, and larger grain sizes. VC6370A presented the largest grain diameter (3.92 mm), closely followed by KPS1, while CN95 averaged 3.62 mm. The low coefficient of variation (CV) for posthormone flower drop (9.90 %) indicates consistent genotype responses to PGPs. Moreover, the 5 % decrease in CV for posthormone flower drop further highlights the efficacy of hormone treatment in reducing variability in flower shedding Table 2. Consequently, the observed reduction in variability is likely attributable to increased flower bud growth and development, decreased flower bud abortion, and increased flower bud resilience to environmental challenges, ultimately contributing to more consistent grain yields in mung bean production.

VC6370A, VC1973A-(SC), and VC6173A demonstrated significantly larger grain sizes, with VC6370A exhibiting the greatest grain area (21.96 mm^2), followed closely by VC1973A-(SC) and VC6173C (20.98 mm^2). Increased grain size is correlated with improved seed vigor and germination. While CN95 excelled in terms of the number of grains per pod (10 grains), MN95 presented a relatively high cluster count but relatively low number of grains per pod (7). The highly significant p values (F-prob <0.001) for all measured traits underscore the substantial genotypic variation and the critical role of genotype selection in mung bean breeding programs Fig. 3.

"VC6370A" and "VC3960A-88″ demonstrated superior grain yield potential because of their relatively high 100-grain weights. Both "VC6368(46-40-3)" and "VC1973A(SC)" offer elevated straw yields, benefiting livestock and soil health. Notably, "VC6370A" led in

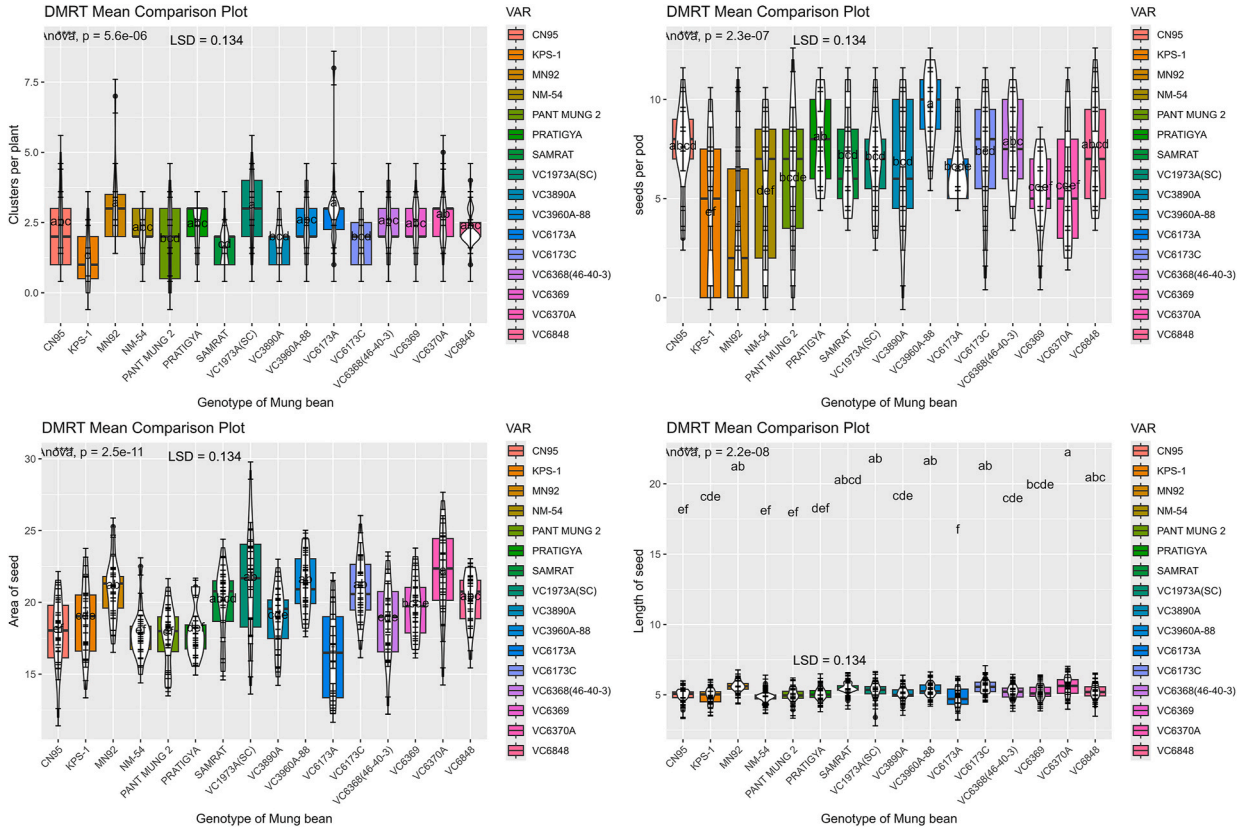

Fig. 3. Graphics depicting the: Area of the seed, Length of the seed, seeds per pod, Cluster/plant among tested germplasm.

terms of grain yield (3.04 ton/ha), followed by CN95 (2.84 ton/ha), indicating the potential to increase agricultural productivity and food security. Additionally, "VC3960A-88″ exhibits efficient resource utilization through its harvesting index Table 3.

3.2. Analysis of correlations and path coefficients among postfertilization quantitative traits

The correlation matrix, the pairwise relationships between variables, is computed via Pearson's correlation with listwise deletion for missing data. Each cell contains a correlation coefficient, which quantifies not only the strength but also the direction of the linear relationship between two variables, which is assessed for statistical significance (at the 0.05 or 0.001 level). Thus, more notable correlations were observed. The highest positive significant correlations were between the number of pods per cluster and the grain yield per hectare ($r = 0.96$, $p < 0.001$), followed by the grain yield per hectare and the harvesting index ($r = 0.95$, $p < 0.001$) and the straw yield and harvesting index ($r = 0.94$, $p < 0.001$). Interestingly, flower drop number, both before and after hormone application, was negatively correlated with the number of pod clusters ($r = -0.65$, $p < 0.05$ and $r = -0.65$, $p < 0.001$). These findings suggest that reducing flower abscission, particularly with hormonal assistance (bioregulation), can significantly increase pod development and consequently contribute to increased grain yield. Further examination revealed a positive correlation between the diameter and area of the grains ($r = 0.94$, $p < 0.001$), indicating that larger grains contribute directly to increased overall grain yield. The number of grains per pod was positively correlated with the grain yield per hectare ($r = 0.67$, $p < 0.05$). Additionally, 100-grain weight was negatively correlated with straw yield per hectare ($r = -0.80$, $p < 0.001$) and biological yield per hectare ($r = -0.63$, $p < 0.05$) Fig. 4.

All postfertility-linked traits strongly influence grain yield. However, the biological yield/ha is negatively influenced by the indirect effect, with a coefficient value of −1%. Moreover, pod/plant, cluster/plant, pod, and grain dimension associative traits are strongly associated with yield, with coefficient values greater than 0.80 Fig. 5.

3.3. Identification of ideal mung bean genotypes via the multitrait stability index (MTSI)

In terms of the genotypes VC6370A and CN95, superior performance in mung bean cultivation within the Chitwan region was evident on the basis of a comprehensive evaluation of key attributes. In terms of exceptional stability and adaptability across diverse conditions, these genotypes surpassed the overall mean for the majority of the examined traits, excluding SPFDAAH and NSPP. Notably, characterized by positive selection differences for most parameters, with the exception of SPFDAAH and NSPP, these genotypes presented a wide heritability range, culminating in perfect scores for HI, X100GSW, grain yield, and biological yield per hectare. While positive selection gains were observed across most studied parameters, with the most substantial increase observed in biological yield per hectare, negative gains were evident in NSPP and SPFDAAH.

3.3.1. Contribution factor ranks of the selected genotypes

For the traits FA1, FA3, and FA4, FA7 CN95 ranked first, whereas FA2, FA6 (prefertility traits) and FA9 ranked first for VC6370A across all analyzed attributes Tables 4 and 5. Consequently, the selected genotypes present greater genotypic stability than the original population does, which is crucial for genetic breeding efforts.

In this study, communalities for the postfertility-associated variables of mung bean indicate how much of the variance in each

Table 3
Evaluation of the yield-related characteristics and phytohormone Responsiveness of mung bean genotypes.

Genotypes	100 Grain weight(gm)	Straw Yield/ha(kg/ha)	Biological Yield kg/ha	Harvesting Index	Grain yield (Tons)/ha
VC6368(46-40-3)	5.15	3197	5779.60	0.45	2.58
NM-54	5.41	3154	5678.20	0.44	2.52
VC6370A	5.88[a]	3126	5610.36	0.44	3.04[a]
VC1973A(SC)	4.96	3207	5920.08	0.46	2.71
VC6173C	5.39	3056	5035.12	0.41	2.085
CN95	5.26	3293	6133.08	0.48[a]	2.84 [ab]
VC6848	5.80	3013	5385.60	0.44	2.37
PRATIGYA	5.46	3012	5322.534	0.43	2.31
KPS-1	6.66	2360	3494.18	0.32	1.134
VC3890A	6.21	3120	5578.330	0.44	2.45
VC6173A	4.87	3056	5545.172	0.45	2.48
SAMRAT	5.40	2120	3378.120	0.37	1.25
PANT MUNG 2	4.75	2930	5178.700	0.43	2.24
MN92	4.85	3186	5684.88	0.44	2.49
VC6369	5.36	2993	5805.60	0.46[b]	2.81
VC3960A-88	5.07	3267	6316.657	0.46[b]	2.83[ab]
LSD(0.05)	0.032	3.2	111.58	0.003	0.054
SE_m	0.002	1.24	54.97	0.0024	0.042
F-prob	<0.001	<0.001	<0.001	<0.001	<0.001
CV%	3.6	19.971	8.05	4.47	3.06

Note: Genotypes marked with superscripts represent the top performers for each measured variable according to the DMRT test.

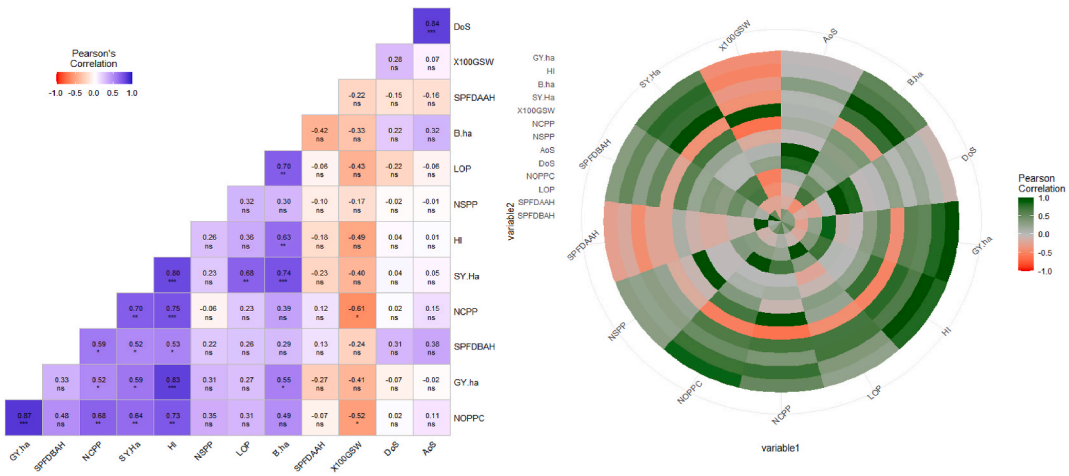

Fig. 4. Correlation Matrix Heatmap of the Post Fertility-Associated Traits of the Mung Bean Genotypes and Promising Cultivars. SPFDBAH & SPFDAAH: Sample plant flower drops before and after application of the hormone, LOP: Length of the Pod,NOPPC: pods/cluster, AoS&DoS: Area and diameter of seed, NCCP& NSPP:clusters/plant & Seeds/pod, GY.ha; B.ha; HI: Grain yield; Biological yield/ha & Harvesting index, X100GSW: 100grain test weight.

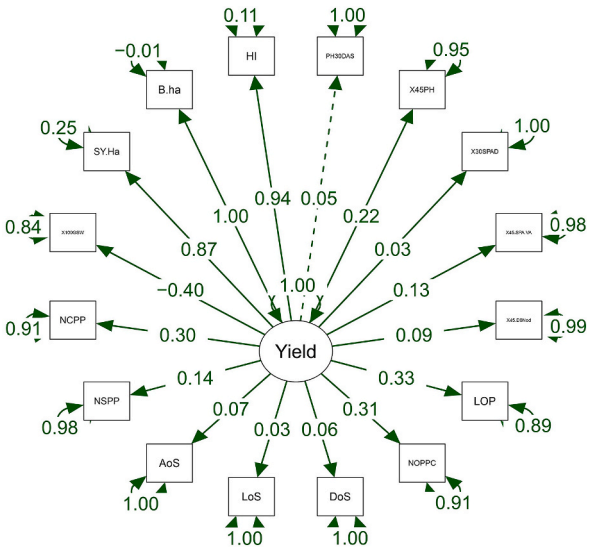

Fig. 5. Path coefficient analysis of the Yield attributing traits of the mung beans genotypes. Single arrow indicates the direct effect value and double arrow indicates the indirect effects variables.

Table 4
Representation of the contribution factor ranks of the selected genotypes. Exclusion of Genotypes FA5, FA6, FA7, and FA8 Due to Their Contribution to Prefertilization Traits (supp file).

FA1	FA2	FA3	FA4	FA5	FA6	FA7	FA8	FA9
CN95	VC6370A	CN95	CN95	CN95	VC6370A	CN95	VC6370A	VC6370A
VC6370A	CN95	VC6370A	VC6370A	VC6370A	CN95	VC6370A	CN95	CN95

variable is explained by the underlying factors. However, uniqueness indicates the degree to which an observed variable has unique variance that is not shared with other variables in the dataset. The uniqueness of the postfertility-associated variables of mung bean would indicate how much of the variance in each variable is not explained by the underlying factors. Therefore, the highest value (0.986) of communalities was expressed by biological yield/ha, followed by two traits (0.981) yield/ha and the harvesting index. The highest value of uniqueness is indicated by SPFDAAH, followed by the diameter of grains (DoS), as shown in Table 6.

Table 5
Summary of the estimation of the genetic parameters based on the multitrait selection index (MTSI) for fourteen postfertility-associated traits assessed in sixteen mung bean germplasms.

Variables	Factor	Xo	Xs	SD	SD%	h2	SG	SG%	sense
SPFDBAH	FA1	0.779	0.930	0.150	19.299	0.226	−0.034	−4.353	decrease
LOP	FA1	7.303	7.479	0.176	2.416	0.357	0.063	0.862	increase
NOPPC	FA1	5.750	5.794	0.044	0.765	0.157	0.007	0.120	increase
NCPP	FA1	2.283	2.467	0.183	8.027	0.361	0.066	2.901	increase
SY.Ha	FA1	2999.625	3210.077	210.452	7.016	1.000	210.386	7.014	increase
B.ha	FA1	10406.339	13229.841	2823.502	27.133	0.999	2821.425	27.113	increase
HI	FA1	0.697	0.750	0.052	7.519	1.000	0.052	7.516	increase
GY.ha	FA1	7.407	10.020	2.613	35.280	0.999	2.611	35.253	increase
DoS	FA2	3.738	3.767	0.030	0.790	0.424	0.013	0.335	increase
LoS	FA2	5.189	5.241	0.052	0.997	0.447	0.023	0.446	increase
AoS	FA2	19.428	19.856	0.428	2.203	0.536	0.229	1.181	increase
NSPP	FA3	6.500 >	6.477	−0.023	−0.349	0.413	−0.009	−0.144	increase
X100GSW	FA4	5.407	5.571	0.165	3.044	1.000	0.164	3.042	increase
SPFDAAH	FA9	3.188 >	3.107	−0.080	−2.522	0.271	−0.022	−0.683	decrease

Xo: overall mean of genotypes; Xs: mean of the selected genotypes; SD: selection differential; SG: selection gain or impact; h^2: heritability; SPFDBAH & SPFDAAH: sample plant flower drops before and after application of the hormone; LOP: Length of pod; NOPPC: pods/cluster; SY.ha: straw yield/ha; B. ha: Biological yield/ha; HI:harvest index; DoS,AoS& LoS: Diameter, area and Length of grain; NSPP: grain per pods; X100GSW:100 grain weight.

Table 6
Factor loading after varimax rotation, communalities, and uniqueness for postfertility-associated variables of mung bean.

Variables	FA1	FA2	FA3	FA4	FA9	Comm	Uniq(1-Co)
SPFDBAH	0.558	−0.397	0.038	0.058	0.302	0.886	0.114
SPFDAAH	−0.060	0.166	−0.234	0.014	0.793	0.843	0.157
LOP	0.639	0.197	−0.249	0.247	0.118	0.944	0.056
NOPPC	0.747	−0.116	−0.265	0.308	−0.228	0.885	0.115
DoS	0.126	−0.749	0.106	−0.291	0.071	0.857	0.143
LoS	−0.053	−0.849	0.084	0.286	−0.093	0.868	0.132
AoS	0.057	−0.926	0.122	0.036	−0.010	0.921	0.079
NSPP	0.200	0.000	−0.611	0.347	−0.240	0.866	0.134
NCPP	0.755	−0.196	0.041	0.363	0.106	0.888	0.112
X100GSW	−0.432	−0.180	0.000	−0.701	−0.184	0.887	0.113
SY.Ha	0.818	−0.127	−0.007	0.190	−0.096	0.950	0.050
B.ha	0.971	0.042	−0.021	0.038	−0.133	0.986	0.014
HI	0.961	0.073	0.025	0.101	−0.129	0.981	0.019
GY.ha	0.966	0.061	−0.022	0.018	−0.134	0.981	0.019

SPFDBAH& SPFDAAH: sample plant flower drops before and after application of the hormone; LOP:length of pod; NOPPC: no of pod per cluster; SY. ha: straw yield/ha; B.ha: Biological yield/ha; HI:harvest index; DoS,AoS& LoS: Diameter, area and Length of grain; NSPP: no of grain per pod; X100GSW:100 grain grain weight.

3.3.2. Assessment of genotype strengths and weaknesses for Post-fertility-associated traits

The factors that make up the MGIDI are divided into two categories: those that contribute more and those that contribute less. In the graphical representation, factors that contribute more to the MGIDI are closer to the center, whereas those that contribute less are closer to the edge. The dashed line shows what the MGIDI would be if all factors contributed equally Fig. 6. Radar plot analysis indicated that FA1, which encompasses the grain yield, biological yield, and harvesting index, minimally influenced the MGIDI of the high-performing genotypes VC6368 (46-40-3), VC1973A (SC), and CN95. Conversely, FA1 contributed more significantly to the MGIDI of the less productive genotypes KPS-1 and VC6173C. This pattern extended to other factors. The VC1973A(SC), CN95, VC6368 (46-40-3), VC3960A-88, and VC6173A genotypes excelled in terms of FA1 traits, suggesting optimal values for LOP, NOPPC, and NCPP. While FA2 minimally impacted VC6370A and MN92, indicating DoS, LoS, and AoS values superior to those of NM-54, 'SAMRAT' demonstrated dominance in FA3, reflecting a higher grain count per pod than VC6370A. VC6173C's prominent contribution to FA4 was linked to a lower 100-grain weight, in contrast with CN95. Finally, the minimal influence of FA9 on VC6370A and CN95 suggests a reduction in flower drop after hormone application, which is indicative of complete flowering and pollination. Table 6 presents data related to the traits of the selected genotypes in comparison with the overall mean traits of all the genotypes. This comprehensive approach helps to identify the best genotypes that can be used to breed mung bean varieties with high grain yields and other desirable characteristics.

4. Discussion

This study in Chitwan tested MTSI in mung bean genotypes and potentially other crops, aiming to identify stable and superior performers in diverse environments, such as rainfed conditions in Nepal. Mung bean genotypes identified through this heatmap can be

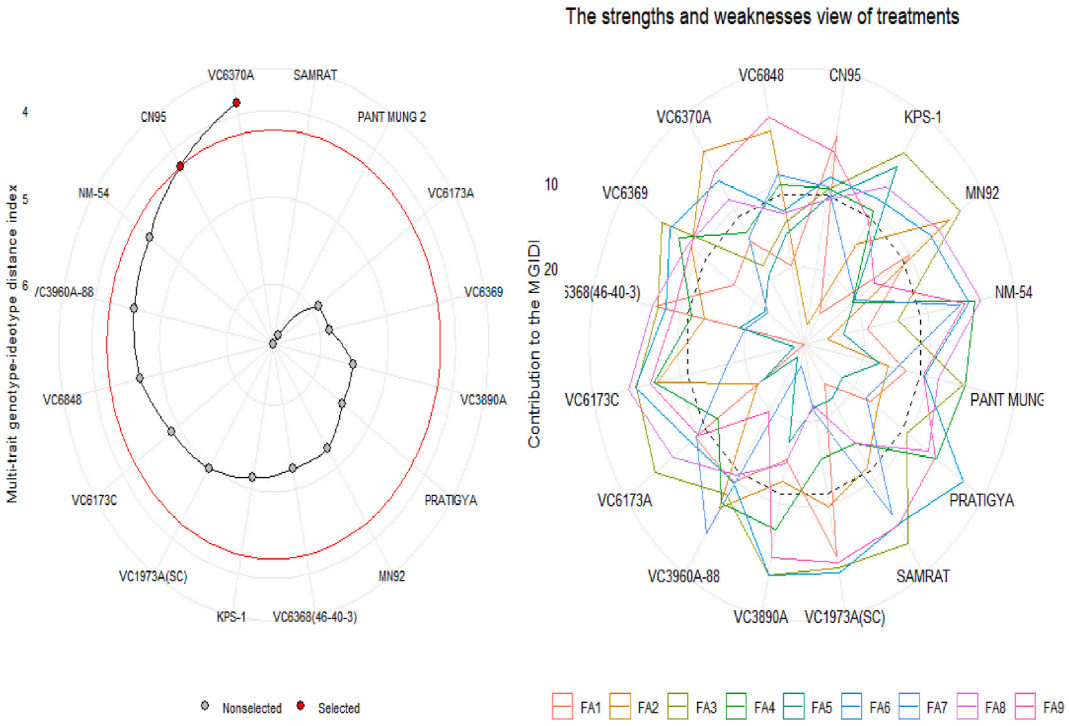

Fig. 6. Graphics depicting the selecte ideal and nonselected genotypes, and the strength and weakness of MTSI contributions to factor loading.

employed in breeding programs to develop superior varieties for rainfed environments [26]. The selected genotype 'VC6370A' had a higher genotypic rank than 'CN95' for FA2, FA6, FA8, and FA9, which are associated with flowering and postflowering traits. 'CN95' had a higher genotypic rank than 'VC6370A' for FA1, FA3, FA4, FA5, and FA7. This demonstrates the high reliability of the genotype ranking, as the same protocols were used to select Tahiti acid lime genotypes via Bayesian inference [27]. MTSI analysis revealed that the biological yield, grain yield, and harvesting index were the most stable traits, with factor loadings of 0.971, 0.966, and 0.961, respectively. The least stable trait was the diameter of the grain, with a factorial loading of 0.12. Sample plant flower drops after the application of hormone at an interval of 12 h had a negative factor loading of −0.06, indicating that they were unstable across environments. The highest factor loading for factor 1 was 0.197 for the length of the pod and grains/pod. All yield-related traits, such as the length of the pod, number of pods per cluster, number of clusters per plant, straw yield per ha, harvesting index, and grain yield, were distributed on factor 1. Factor 2 consisted of the diameter, length, and area of the grain, FA4, and FA9, which consisted of single traits such as 100 grain test weights and sample plant flower drops after the application of hormones. MTSI analysis suggests that breeders have concentrated on developing genotypes with desired yield-related traits. However, all fertility-related traits, with the exception of sample plant flower drops after the application of hormones, need to be increased. Thus, stable genotypes have improved morphological quantitative traits, such as clusters plant−1, pods cluster−1, grains pod−1, and branches plant−1 [11]. A separate study of white Guinea yam genotypes revealed that the FAI-BLUP index technique could be used to identify genotypes that could be used as parents to breed new varieties with improved agronomic traits and end-product quality [28]. A multienvironment trial of rapeseed revealed that the BLUP model could be used to select a single trait accurately. However, genotype recommendations on the basis of a single trait, such as the mean performance or stability, are incomplete and biased. Therefore, it is preferable to select genotypes on the basis of multiple traits [29]. Thus, the MTSI method is a statistical approach that uses structural equation modeling to rank genotypes on the basis of their similarity to an ideal genotype, using multitrait data without multicollinearity [30].

Investigating phytohormone impacts on various plant stages highlights the need for global dose optimization. The results of this study revealed a significant and noteworthy influence of exogenously applied phytohormones on flower shedding and postflowering traits, such as the number of clusters per plant, number of pods per cluster, pod length, number of grains per pod, grain dimensions, pod count, pod length, straw yield, harvest index, and overall grain yield, as depicted in Tables 2–4. The notable findings regarding the impact of phytohormones suggest that gibberellic acid (GA) may possess the capacity to intricately integrate with the flowering process. This integration appears to enable the fine-tuning of these responses, particularly when confronted with variable environmental factors in the field, such as fluctuations in moisture and temperature stress, as elucidated previously [31,32]. Similar outcomes were observed in a study where the combined foliar application of indole-3-acetic acid (IAA) and gibberellic acid (GA3) (referred to as IAA2 + GA2) had a notably robust effect on various yield attributes. This included a substantial increase of 66.0 % in the number of pods, a remarkable 142.0 % increase in the pod weight, and a noteworthy increase of 106.5 % in the grain yield compared with those of the control group [14]. In a separate investigation concerning soybean, the impact of 2,4-dichlorophenoxyacetic acid (2,4-DP) and benzyl aminopurine (BAP) on pod set and grain yield during reproductive stages indicated a significant improvement in 100-grain

weight. In particular, the application of 1 mM BAP resulted in a substantial increase to 22.3 g at the R1 stage [33]. Furthermore, an investigation of pigeon pea species demonstrated that foliar application of naphthalene acetic acid (NAA) had a marked effect on reducing flower drop per plant and enhancing yield-attributing traits. Notably, treatment with 80 ppm NAA exhibited superior efficacy to that of the other treatments and the control group [34]. An additional study on mung beans revealed that foliar application of gibberellic acid (GA3) at 200 ppm at 30 and 60 days after sowing (DAS) has the potential to promote growth and increase yield attributes and yield in mung beans [15]. In the context of the green gram (*Vigna radiata* L.), a study investigated the impact of post-flowering management via plant growth regulators, with a particular focus on auxin and zeatin. Among the various treatments, the application of a nanoemulsion of NAA at 30 ppm had the most favorable results, manifesting as a greater number of mature pods, increased grain yield, greater grain weight, and a lower percentage of flower shedding [35]. Similarly, a study focused on sesame (*Sesamum indicum* L. cv. Rama) evaluated the influence of plant growth regulators under moisture stress conditions. Notably, the application of 200 ppm of these regulators yielded remarkable results in terms of growth, morphophysiological characteristics, and grain yield [36]. Several genotypes, such as VC6370A, VC1973A-(SC), and VC6173A, present relatively large grain sizes; a rice seed gene called Big Grain1(*Bg1-D)* increases the flow of a plant hormone called auxin, leading to supersized rice grains [10], which indicates a chance to be orthologous to mung bean, indicating the scope of this study. These findings collectively underscore the significant influence of phytohormones and growth regulators on crop yield and associated attributes across various plant species, including mung beans, soybeans, pigeon peas, green grams, and sesame. This finding demonstrated a substantial degree of consistency with the original alternate hypothesis. To reinforce the effectiveness of phytohormone application in mung bean cultivation, additional research is needed to address study limitations, identify SNP markers associated with bioregulation, and confirm water stress resistance under field conditions.

5. Conclusion

By meticulously selecting economic traits such as grains per pod, clusters per plant, grain dimensions, hundred-grain weight, and harvesting index, which are strongly correlated with yield, mung bean breeding programs have the potential to significantly increase overall production. While a comprehensive analysis of variance unequivocally demonstrated significant genotypic variations across all measured traits, the concurrent foliar application of naphthalene acetic acid (NAA) and gibberellic acid (GA3), which were meticulously administered at a concentration of 50 mg/L, resulted in a marked increase in mung bean yield components, notably including pod number, length, and grain count—key determinants of overall yield variation. Genotypes, strategically selected through the MTSI technique, have emerged as promising progenitors for cultivating superior mung bean cultivars. Among these, VC1973A and CN95, distinguished by their exceptional stability and remarkable yield of 2.8 tons per hectare, warrant rigorous evaluation under diverse environmental conditions to ascertain their commercial viability.

CRediT authorship contribution statement

Bikas Basnet: Writing – review & editing, Writing – original draft, Visualization, Validation, Supervision, Software, Resources, Project administration, Methodology, Investigation, Funding acquisition, Formal analysis, Data curation, Conceptualization. **Umisha Upreti:** Writing – original draft, Investigation, Formal analysis. **Krishna Prasad Thapaliya:** Writing – original draft, Resources.

Data availability statement

Data that support the findings of this study are available from the corresponding author upon reasonable request.

Supplementary File Information

The genotypic information for this study is provided in the supplementary file of Table S 1. The significant correlation matrix values of the studied postfertility-related traits with the response of phytohormones are presented in Table S 2. The contribution factor ranks of selected and nonselected genotypes with their factorial analysis are presented in Table S 3. All the code associated with this study has been deposited in the GitHub repository of Bikas Basnet.

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Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.heliyon.2024.e39226.

References

[1] A. Ton, Multivariate analysis for agromorphological and cooking properties in chickpea (Cicer arietinum L.) germplasm, Turk. J. Agric. For. 47 (4) (2023) 590–601, https://doi.org/10.55730/1300-011X.3111.

[2] M.G. Azam, et al., 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) (2023), https://doi.org/10.3390/plants12101984.

[3] Y.J. Kang, et al., Genome sequence of mungbean and insights into evolution within Vigna species, Nat. Commun. 5 (2014), https://doi.org/10.1038/ncomms6443.

[4] C. Liu, et al., High-quality genome assembly and pangenome studies facilitate genetic discovery in mung bean and its improvement, Plant Commun 3 (6) (2022) 100352, https://doi.org/10.1016/j.xplc.2022.100352.

[5] K. Sandhu, A. Singh, Strategies for the utilization of the USDA mung bean germplasm collection for breeding outcomes, Crop Sci. 61 (1) (2021) 422–442, https://doi.org/10.1002/csc2.20322.

[6] Y.S. Zhu, et al., Mung bean proteins and peptides: nutritional, functional and bioactive properties, Food Nutr. Res. (2018) 1290, 10.29219%2Ffnr.v62.1290.

[7] M.G. Azam, et al., 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) (2023), https://doi.org/10.3390/plants12101984.

[8] Krishi. https://aitc.gov.np/uploads/documents/agriculture-diary-2081-file-2081-03-2pdf-6568-329-1719146649.pdf.

[9] K.P. Wilbois, J.E. Schmidt, Reframing the debate surrounding the yield gap between organic and conventional farming, Agronomy 9 (2) (2019) 1–16, https://doi.org/10.3390/agronomy9020082.

[10] K. Ezura, Y. Nomura, T. Ariizumi, Molecular, hormonal, and metabolic mechanisms of fruit set, the ovary-to-fruit transition, in horticultural crops, J. Exp. Bot. 74 (20) (2023) 6254–6268, https://doi.org/10.1093/jxb/erad214.

[11] N.K. Benakanahalli, et al., A framework for identification of stable genotypes basedon MTSI and MGDII indices: an example in guar (Cymopsis tetragonoloba L.), Agronomy 11 (6) (2021) 1221, https://doi.org/10.3390/agronomy11061221.

[12] D. Taleghani, A. Rajabi, A. Saremirad, P. Fasahat, Stability analysis and selection of sugar beet (Beta vulgaris L .) genotypes using AMMI , BLUP , GGE biplot and MTSI, Sci. Rep. (2023) 1–14, https://doi.org/10.1038/s41598-023-37217-7.

[13] S. Munda, M. Paw, S. Saikia, T. Begum, J. Baruah, M. Lal, Stability and selection of trait specific genotypes of Curcuma caesia Roxb.using AMMI, BLUP, GGE, WAAS and MTSI model over three years evaluation, J Appl Res Med Aromat Plants 32 (November 2022) (2023), https://doi.org/10.1016/j.jarmap.2022.100446.

[14] A. Parveen, et al., Effect of natural phytohormones on growth, nutritional status, and yield of mung bean (vigna radiata L.) and N availability in sandy-loam soil of sub-tropics, Soil Syst 7 (2) (2023) 1–17, https://doi.org/10.3390/soilsystems7020034.

[15] M.S. Islam, et al., Water relations and yield characteristics of mungbean as influenced by foliar application of gibberellic acid (GA3), Front Ecol Evol 11 (January) (2023), https://doi.org/10.3389/fevo.2023.1048768.

[16] J. Ha, et al., A near-complete genome sequence of mungbean (*Vigna radiata* L.) provides key insights into the modern breeding program, Plant Genome (2021) 143e20121.

[17] M.P. Neupane, H. Musalman, S.K. Sah, Influence of sowing date on phenology, biometric, and yield of mungbean (Vigna radiata) cultivars in chitwan, Nepal, International Journal of Agronomy 2023 (2023), https://doi.org/10.1155/2023/8927439.

[18] N. Shukla, H. Kuntal, A. Shanker, S.N. Sharma, Hydro-priming methods for initiation of metabolic process and synchronization of germination in mung bean (Vigna radiata L.) seeds, J Crop Sci Biotechnol 21 (2) (2018) 137–146, https://doi.org/10.1007/s12892-018-0017-0.

[19] M.F. El Karamany, M.S. Sadak, B.A. Bakry, Improving quality and quantity of mungbean plant via foliar application of plant growth regulators in sandy soil conditions, Bull. Natl. Res. Cent. 43 (1) (2019), https://doi.org/10.1186/s42269-019-0099-5.

[20] R. Bam, S.R. Mishra, S. Khanal, P. Ghimire, S. Bhattarai, Effect of biofertilizers and nutrient sources on the performance of mungbean at Rupandehi, Nepal, J Agric Food Res 10 (October) (2022) 100404, https://doi.org/10.1016/j.jafr.2022.100404.

[21] C.M. Donald, J. Hamblin, The biological yield and harvest index of cereals as agronomic and plant breeding criteria, Adv. Agron. 28 (C) (1976) 361–405, https://doi.org/10.1016/S0065-2113(08)60559-3.

[22] T. Olivoto, M. Nardino, Genetics and Population Analysis MGIDI : toward an Effective Multivariate Selection in Biological Experiments, vol. 37, 2021, pp. 1383–1389, https://doi.org/10.1093/bioinformatics/btaa981. December 2020.

[23] T. Olivoto, M.I. Diel, D. Schmidt, A.D. Lúcio, MGIDI: a powerful tool to analyze plant multivariate data, Plant Methods 18 (1) (2022) 1–13, https://doi.org/10.1186/s13007-022-00952-5.

[24] T. Olivoto, M. Nardino, Genetics and Population Analysis MGIDI : toward an Effective Multivariate Selection in Biological Experiments, vol. 37, 2021, pp. 1383–1389, https://doi.org/10.1093/bioinformatics/btaa981. December 2020.

[25] J. Hsu, Multiple Comparisons: Theory and Methods, CRC Press, 1996.

[26] T. Hussain, Z. Akram, G. Shabbir, A. Manaf, M. Ahmed, Saudi Journal of Biological Sciences Identification of Drought Tolerant Chickpea Genotypes through Multi Trait Stability Index, vol. 28, 2021, pp. 6818–6828.

[27] J. Santana, P. Coelho, R. Silva, Scientia Horticulturae Multitrait and multiharvest analyses for genetic assessment and selection of Tahiti acid lime genotypes through Bayesian inference Marco Ant o 290 (April) (2021).

[28] D. Genotypes, P.E. Norman, P.A. Agre, R. Asiedu, Multiple-Traits Selection in White Guinea Yam, 2022, pp. 1–15.

[29] Z. Li, W. Wu, Genotype Recommendations for High Performance and Stability Based on Multiple Traits Selection across a Multienvironment in Rapeseed, vol. 145, June 2022, 2023.

[30] L.G. Woyann, et al., Selection indexes based on linear-bilinear models applied to soybean breeding, Agron. J. 112 (1) (2020) 175–182.

[31] R. Castro-Camba, C. Sánchez, N. Vidal, J.M. Vielba, Plant development and crop yield: the role of gibberellins, Plants 11 (19) (2022), https://doi.org/10.3390/plants11192650.

[32] G.S.S. khattak, I. Saeed, T. Muhammad, Flowers' shedding under high temperature in mungbean (Vigna radiata (l.) Wilczek), Pak J Bot 41 (1) (2009) 35–39.

[33] Y. Cho, S.K. Suh, H.K. Park, A. Wood, Impact of 2,4-DP and BAP upon pod set and seed yield in soybean treated at reproductive stages, Plant Growth Regul. 36 (3) (2002) 215–221, https://doi.org/10.1023/A:1016590505449.

[34] K. Sharvani, V. Naik, M. Krishi Vidyapeeth, I.J. Deshmukh, S. V Kalyankar, J.D. Deshmukh, Effect of foliar spray of NAA (Naphthalene acaetic acid) on flower drop and seed yield of pigeonpea (Cajanus cajan (L.) Millsp.), ~ 1172 ~ The Pharma Innovation Journal 11 (1) (2022) 1172–1175.
[35] B.K. Priya, S. Panneerselvam, S. Marimuthu, K.S. Subramanian, A. Senthil, Post flowering management using plant growth regulators in greengram (Vigna radiata L.), Int J Plant Soil Sci 34 (24) (2022) 535–543, https://doi.org/10.9734/ijpss/2022/v34i242670.
[36] A.K. Garai, J.K. Datta, Influence of plant growth regulators on growth, morpho-physiological characters and yield of summer sesame (*Sesamum indicum* L. cv. Rama) under moisture stress, Acta Physiol. Plant. 21 (3) (1999) 277–281, https://doi.org/10.1007/s11738-999-0043-7.