LR-5264
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RESEARCH ARTICLE Legume Research- An International Journal

Morphological Characterization and Diversity Assessment of Mungbean [*Vigna radiata* (L.) Wilczek] Genotypes using DUS Descriptors as per PPV and FRA, 2001

Navreet Kaur Rai[1], Ravika[1], Rajesh Yadav[1], Amit, Karuna[1], Deepak Kaushik[1]

10.18805/LR-5264

ABSTRACT

Background: Variety characterization is the foremost important step that should be done by breeders to classify a variety into distinct groups. A significant technique for locating and assessing several genotypes for the registration, protection and production of seeds of superior quality is the Distinctness, Uniformity and Stability (DUS) characterization. Consequently, the current investigation aimed to use DUS descriptors to describe and assess the variance present in mungbean genotypes.

Methods: One hundred forty-two mungbean genotypes were examined using 21 agro-morphological qualitative DUS descriptors in a randomized block design with two replications across two seasons, *kharif* 2021 and *kharif* 2022.

Result: In the twenty-one DUS traits that were examined, four characters' plant growth habit, leaf shape, leaf size and seed size exhibited trimorphic variance. Three characters (plant habit, stem pubescence and pod pubescence) were found to be identical among all genotypes while fourteen characters displayed dimorphic variance. All of the mungbean genotypes displayed a significant degree of variance for all DUS characteristics. Based on the UPGMA method of clustering, the dendrogram classified all the one hundred forty-two genotypes into three major clusters. The presence of variation among the genotypes under study was demonstrated by the further classification of these primary clusters into five sub-clusters. The majority of the genotypes were found in cluster II (121 genotypes), which was followed by cluster I (18 genotypes) and cluster III (3 genotypes).

Key words: Dendrogram, Distinctness, Stability, Uniformity, UPGMA, Variance.

INTRODUCTION

Pulses have been a crucial component of India's subsistence agriculture since ancient times. Their natural ability to thrive in unfavourable climates is unmatched and their root nodules have the capacity to fix atmospheric nitrogen. They are among the nutritious foods recommended to address protein malnutrition and offer millions of people a means of nutritional security. Mungbean, often referred to as green gram, is one of the most common pulses growing in the Indian subcontinent. It is a short duration self-pollinated crop that thrives well in a broad range of environments owing to its short crop period. For the vegetarian Indian population, mungbean is regarded as a good source of easily digestible protein (240 g/kg), carbs and other micronutrients (Sheena *et al*., 2021). However, indeterminate plant growth, which necessitates numerous harvests, pod shattering at maturity and susceptibility to diseases and insect pests are the main obstacles to mungbean cultivation. The main issue with mungbean breeding programs is the lack of a broad genetic base and the absence of genotypes suitable for a variety of cropping scenarios. The evaluation and characterization of the available germplasm is an essential step in ensuring its optimal utilization and protection. Additionally, characterization facilitates the process of improving both quantitative and qualitative traits.

Evaluating common agro morphological parameters does not effectively classify genotypes into distinct clusters. According to the recommended practices outlined in the Protection of Plant Varieties and Farmers' Rights Act (PPV and FRA, 2001), Distinctness, Uniformity and Stability (DUS) characterization is essential for identification, the avoidance of duplication and accurate varietal registration. According to Janghel *et al.* (2020), DUS characterisation plays a significant role in the production and certification of high-quality seeds. The analysis of DUS descriptors is simple, inexpensive and requires no special laboratory techniques. Therefore, it is necessary to properly characterize and assess the variation present in mungbean genotypes in order to select suitable genotypes that can be marketed as a variety appropriate for a particular agro-climatic zone (Dhaliwal *et al*., 2020). In support of the aforementioned assertions, the present research had the objective to examine the DUS traits among elite mungbean genotypes.

[1]Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004, Haryana, India.

Corresponding Author: Ravika, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004, Haryana, India. Email: ravika.sheoran@hau.ac.in

How to cite this article: Rai, N.K., Ravika, Yadav, R., Amit, Karuna and Kaushik, D. (2024). Morphological Characterization and Diversity Assessment of Mungbean [*Vigna radiata* (L.) Wilczek] Genotypes using DUS Descriptors as per PPV and FRA, 2001. Legume Research. DOI: 10.18805/LR-5264

Submitted: 25-10-2023 **Accepted:** 21-12-2023 **Online**:07.02.2024

MATERIALS AND METHODS

The current study used 142 distinct genotypes of mungbean and was performed at the Pulses Research Area of the Department of Genetics and Plant Breeding, CCS HAU, Hisar, during the *kharif* 2021 and *kharif* 2022 seasons. Randomized block design (RBD) with two replications was used to grow different mungbean genotypes. Two rows of each genotype were grown, with 45 cm between-row distance and a 10 cm between-plant distance. Each DUS descriptor is studied in accordance with the recommendations of PPV and FRA (Anonymous, 2007). Twenty-one qualitative agro-morphological descriptors were investigated in mungbean genotypes at different stages of plant development.

Data on 21 qualitative DUS characters were used to analyse diversity using NTSYSpc version 2.02i (Rohlf, 1997). As per the method of Sneath and Sokal (1973), the ordinal scale of data of morphological characters was transformed into binary characters according to the variations present in each character. Method of Jaccard (1908) was used to carry out the cluster analysis based on the values of similarity coefficient. SAHN (Sequential Agglomerative Hierarchical Non-overlapping) clustering was used to make dendrogram based on similarity coefficient matrices obtained from the data using the UPGMA (Unweighted Pair Group Method with Arithmetic Averages).

RESULTS AND DISCUSSION

DUS-based variability analysis

In present study twenty-one qualitative DUS descriptors were utilized to describe one hundred forty-two elite mungbean genotypes at various growth stages. Significant differences were found between seventeen of the twenty-one distinct characters that were analysed, indicating that there is significant genetic variation that can be exploited and that these descriptors serve a purpose in determining the genotypes. Fig 1 represents the DUS descriptors that were used to classify all the genotypes into various categories along with their respective frequencies. DUS characterisation in mungbean was also used for identification and protection by (Sheena *et al*., 2021; Rahangdale *et al*., 2022; Joshi *et al*., 2022).

Hypocotyl pigmentation

Hypocotyl pigment is evaluated during the cotyledonary stage of mungbean plants and the pigment of the hypocotyl in mungbean is frequently regarded as a crucial morphological marker for identification and intellectual property rights protection. Out of the total of 142 genotypes examined in this study, 17 genotypes (12%) lacked anthocyanin pigmentation in the hypocotyl region and were found to be green in colour. The remaining 125 genotypes (88%) displayed anthocyanin pigmentation and were identified as purple in colour, indicating the considerable degree of variation across these genotypes for this trait.

Plant descriptors

Plant descriptors include plant growth habit and plant habit. At 50% flowering, the growth habit of the plant displayed great heterogeneity, with 15 genotypes (11%) being categorized as erect, 125 (88%) as semi-erect and 2 (1%) as spreading type. In general, erect-type plants are preferable because they receive more sunlight and have more effective food synthesis *via* their leaves, which promotes faster growth and development. Therefore, as the findings indicate, future mungbean breeding programs at Pulses Research Area, CCS HAU, Hisar, should include a greater proportion of erect type of germplasm. Due to the fact that all 142 genotypes displayed an inderminate type of growth, the plant habit was found to be monomorphic.

Stem descriptors

At the 50% flowering stage of the mungbean, stem colour and pubescence were observed. Only twenty-two of the 142 genotypes (15%) studied for stem colour displayed green stem colour, whereas, the remaining 120 genotypes (85%) had green colour with purple splashes. Therefore, a substantial amount of variability in stem colour was seen across all genotypes. Stem pubescence, however, was present in all genotypes and indicated that there was no variation, making it less useful descriptor for identifying and maintaining purity.

Leaf descriptors

During the 50% flowering stage of the mungbean, all of the leaf morphological characteristics, including leaf colour, shape, size, leaflet lobes, leaf vein colour and petiole colour were examined. Due to the fact that photosynthesis and transpiration occur mostly in the leaf, it is essential to consider the characteristics of the leaf when evaluating a crop plant's capacity to produce. All of the genotypes were divided into two groups based on leaf colour: green colour for 112 genotypes (79%) and dark green for the remaining 30 genotypes (21%). One hundred thirty-eight genotypes (97%) had ovate-shaped leaves, one genotype (1%) had lanceolate-shaped leaves and three genotypes (2%) had cuneate-shaped leaves, indicating a large trimorphic variance in leaf shape.

In terms of leaf size, fourteen genotypes (10%) had large leaves, one hundred fifteen genotypes (81%) had medium-sized leaves and thirteen genotypes (9%) had small leaves. Only three genotypes (2%) were found to have leaflet lobes in its leaves when the presence and absence of leaflet lobes were investigated; the remaining 139 genotypes (98%) had no leaflet lobes. Leaf vein colour displayed dimorphic variation, with veins of green colour present in seventeen genotypes (12%) and veins of purple colour present in 125 genotypes (88%). In terms of petiole color, sixteen genotypes (11%) had completely green petioles, whereas the remaining 126 genotypes (89%) had green petioles with purple splashes.

All of the leaf characteristics *viz*., foliage colour, leaf shape, leaf size and leaflet lobes-exhibited significant

variation and are helpful for characterizing plants, but because of their polygenic regulation, the impact of environmental influences cannot be completely eliminated.

Flower descriptors

In flower descriptors, flower colour was examined. Flower colour is utilized as a reliable morphological marker to differentiate mungbean genotypes. One hundred and

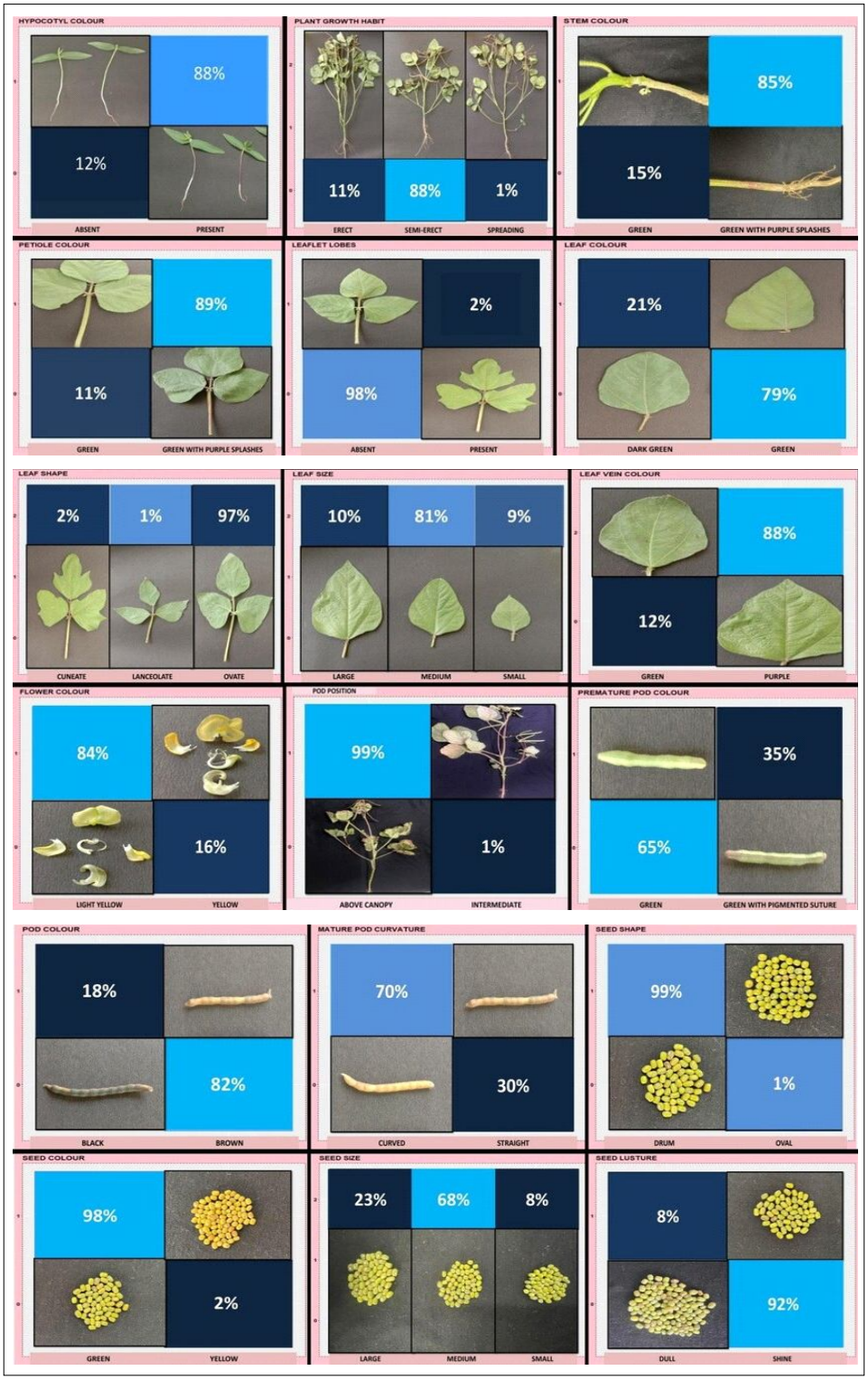

Fig 1: Presentation of variation found in DUS descriptors of mungbean.

Table 1: Scoring of 18 diverse DUS descriptors in mungbean genotypes.

Genotypes	Hypocotyl colour	Growth habit	Stem colour	Petiole colour	Leaf colour	Leaf size	Leaf shape	Leaflet lobes	Vein colour	Flower colour	Pre-mature pod colour	Pod position	Pod colour	Pod curvature	Seed colour	Seed lustre	Seed shape	Seed size
PM 1801	1	1	1	1	0	2	1	0	2	1	0	0	0	0	1	0	1	1
JLPM 707-27	1	0	1	1	0	2	1	0	2	0	1	0	0	0	1	1	1	1
ML 818	1	1	1	1	0	1	1	0	2	1	1	0	1	1	1	0	1	1
RMG-1148	1	1	0	1	0	1	1	0	0	1	0	0	0	1	1	0	1	0
IPM 02-3	1	1	1	1	1	1	1	0	2	0	0	0	1	1	1	0	1	1
IPM 1604-1	1	1	0	1	0	0	1	0	2	1	0	0	0	1	1	0	1	1
MH 1468	1	1	1	1	1	1	1	0	2	1	0	0	1	0	1	0	1	1
Pusa M 22-32	1	1	1	1	0	2	1	0	2	1	1	0	0	1	1	0	1	1
KM 2419	1	1	1	1	0	1	1	0	2	1	0	0	0	0	1	0	1	1
BCM 20-6	1	1	1	1	0	1	1	0	2	1	1	0	0	0	1	0	1	1
MML 2577	1	1	1	1	0	1	1	0	2	1	1	0	0	0	1	0	1	1
SVM 55	1	1	1	1	0	1	1	0	2	1	0	0	0	1	1	1	1	1
IPM 410-3	0	1	0	0	0	1	1	0	0	1	0	0	0	1	1	0	1	1
PMD-14	1	1	1	1	1	2	1	0	2	1	0	0	0	0	1	0	1	1
SVM 98	0	1	0	0	0	1	1	0	0	1	0	0	0	0	1	0	1	1
IPM 1704-14	1	1	1	1	0	1	1	0	2	1	0	0	0	0	1	0	1	1
PMS-12	1	1	1	1	0	2	1	0	2	1	0	0	0	0	1	0	1	1
TMB 230	1	1	1	1	0	1	1	0	2	1	0	0	0	1	1	1	1	1
IPM 604-16	1	1	1	1	0	1	1	0	2	1	0	0	0	0	1	0	1	2
MH 1871	0	1	1	1	0	1	1	0	2	0	0	0	0	0	1	0	1	2
IPM 205-7	1	1	1	1	0	0	1	0	2	1	0	0	1	0	1	0	1	1
Pusa BM 9	1	0	1	1	0	1	1	0	2	1	0	0	0	1	1	0	1	1
VGG 18-002	1	1	1	1	1	1	1	0	2	1	0	0	0	1	1	0	1	2
MH 421	0	1	0	0	0	2	1	0	0	0	0	0	1	0	1	0	1	1
IPMD 604-1-7	1	1	1	1	0	1	1	0	2	1	0	0	0	1	0	0	1	1
MML 2575	1	1	1	1	0	1	1	0	2	1	1	0	0	1	1	0	1	2
SKNM 1801	0	1	0	0	1	1	1	0	0	1	0	0	0	1	1	0	1	2
SML 832	1	1	1	1	0	1	1	0	2	0	0	0	1	1	1	0	1	2
DGGV 91	1	1	1	1	0	0	1	0	2	1	1	0	0	1	1	0	1	1
VGG 16-047	0	0	0	0	1	1	1	0	0	0	0	0	0	1	1	0	1	1
MH 1762	1	1	1	1	0	0	1	0	2	1	0	0	0	1	1	0	1	1
SML 1932	1	0	1	1	0	1	1	0	2	1	0	0	0	1	1	0	1	1
OBGG 108	1	1	1	1	0	1	1	0	2	1	0	0	0	1	1	0	1	1
VGG 17-043	1	1	1	1	0	1	1	0	2	1	0	0	0	1	1	0	1	1
PM 1602	1	1	1	1	0	1	1	0	2	1	0	0	0	1	1	0	1	1

Table 1: Continue...

Table 1: Continue...

Pant M 5	1	0	1	1	1	1	1	0	2	0	0	0	1	0	1	0	1	2
SML 1933	1	0	1	1	0	1	1	0	2	0	0	0	0	1	1	0	1	2
Pusa M 19111	1	1	1	1	0	1	1	0	2	0	0	0	0	0	1	0	1	2
MH 1703	1	1	1	1	0	1	1	0	2	1	0	0	1	0	1	0	1	2
MML 2560	1	1	1	1	0	1	1	0	2	0	1	0	0	1	1	0	1	2
Pusa M 1971	1	0	1	1	0	1	1	0	2	1	0	0	0	1	1	0	1	2
PM 1601	1	1	1	1	0	1	1	0	2	1	1	0	0	0	1	0	1	1
PM 1520	1	0	1	1	0	1	1	0	2	1	0	0	0	0	1	1	1	2
TCADM 20-5	1	1	1	1	0	1	1	0	2	1	0	0	0	1	1	1	1	1
IPMD 1604	1	1	1	1	0	1	1	0	2	1	0	0	0	1	1	0	1	1
IPM 1603-1	1	1	1	1	1	0	1	0	2	1	0	0	0	1	1	0	1	1
TBMB 117-5	1	1	1	1	0	0	1	0	2	1	0	0	0	1	1	0	1	1
Pusa M 2131	1	1	1	1	1	0	1	0	2	1	1	0	0	1	1	0	1	2
IPM 1103-1	1	1	1	1	0	1	1	0	2	1	1	0	0	1	1	0	1	1
TBMB 17-2	1	1	1	1	1	0	1	0	2	1	1	0	0	0	1	0	1	1
Pusa BM 16	1	1	1	1	0	1	1	0	2	1	0	0	0	1	1	0	1	1
PM 1605	1	1	1	1	0	1	1	0	2	1	0	0	0	1	1	0	1	1
IPMD 101-2	1	0	1	1	1	1	1	0	2	1	1	0	0	1	1	0	1	1
MML 2568	1	0	1	1	0	1	1	0	2	0	1	0	0	0	1	0	1	2
Pusa M 2132	1	1	1	1	1	1	1	0	2	1	1	0	0	1	1	0	1	2
MHBC 20-7	1	1	1	1	0	1	1	0	2	1	0	0	1	1	1	0	1	1
PM 504-20-27	1	2	1	1	0	1	1	0	2	0	1	0	1	1	1	0	1	1
PM 1624	1	0	1	1	1	2	1	0	2	1	1	0	0	1	1	0	1	1
MH 1830	1	1	1	1	0	1	1	0	2	1	1	0	0	1	1	0	1	2
IPM 1610-1	1	2	1	1	0	1	1	0	2	1	0	0	0	1	1	0	1	1
RMG 1132	1	1	1	1	0	1	1	0	2	1	0	0	1	1	1	0	1	1
RMG 1166	1	1	1	1	0	1	1	0	2	1	1	0	0	1	1	0	1	1
OBGG 105	1	1	1	1	0	1	1	0	2	1	0	0	1	0	1	0	1	2
MH 1890	1	1	1	1	0	1	1	0	2	1	0	0	0	1	1	0	1	1
ANDGG 1301	1	0	1	1	0	1	1	0	2	0	0	0	0	1	1	0	1	1
MML 2576	1	1	1	1	0	1	1	0	2	1	1	0	0	1	1	0	1	2
PMD-8	1	1	1	1	0	1	1	0	2	1	1	0	0	1	1	0	1	1
Pusa M 2141	1	1	1	1	0	1	1	0	2	1	0	0	0	1	1	0	1	2
OBGG 106	1	1	1	1	1	1	1	0	2	1	0	0	1	0	1	0	1	1
PMD-7	1	1	1	1	1	1	1	0	2	1	1	0	0	1	1	0	1	1
MH 1801	1	1	1	1	0	1	1	0	2	1	0	0	1	0	1	0	1	1
PMD-9	1	1	1	1	1	1	1	0	2	1	1	0	0	1	1	0	1	2

Table 1: Continue...

Table 1: Continue...

SKNM 1911	1	1	1	1	1	1	1	0	2	1	0	0	0	0	1	0	1	2
VGG 17-036	1	1	1	1	1	1	1	0	2	1	0	0	0	1	1	0	1	1
BDYR-1	1	1	1	1	0	1	1	0	2	1	0	0	0	1	1	0	1	1
COGG-8	1	1	1	1	0	1	1	0	2	1	0	0	0	0	1	1	1	1
Pusa 1072	1	1	1	1	0	1	1	0	2	1	0	0	0	1	1	0	1	1
COGG 1102	1	1	1	1	0	1	1	0	2	1	1	0	1	1	1	0	1	1
EC 30400	1	1	1	1	0	0	1	0	2	1	0	0	0	1	1	0	1	1
EC 251552	0	1	0	0	0	1	1	0	0	1	0	0	0	1	0	0	1	2
EC 399223	1	1	1	1	0	1	1	0	2	1	1	0	0	1	1	0	1	0
EC 393410	1	1	1	1	0	1	1	0	2	1	1	0	0	1	1	0	1	1
EC 470090	1	1	1	1	0	1	1	0	2	1	1	0	1	1	1	0	1	1
EC 581523	1	1	1	1	1	1	1	0	2	1	0	0	0	1	1	0	1	2
IPM 512-1	0	1	0	0	0	1	1	0	0	1	0	0	0	1	1	0	1	0
Ganga-8	1	1	1	1	0	2	1	0	2	0	0	1	0	1	1	0	1	1
HUM 16	1	1	1	1	1	1	1	0	2	0	0	0	1	0	1	0	1	1
IC 15276	1	1	1	1	0	1	2	1	2	1	1	0	0	1	1	0	1	2
IC 1031096	1	1	1	1	0	0	1	0	2	1	1	0	0	1	1	0	1	1
IPM 99-3	1	1	1	1	0	0	1	0	2	1	0	0	0	1	1	0	1	1
IPM 9901-8	1	1	1	1	0	1	1	0	2	1	0	0	0	1	1	0	1	1
Pusa 1701	1	1	1	1	0	1	1	0	2	1	1	0	0	1	1	0	1	1
IPM 2k 14-9	1	1	1	1	0	1	1	0	2	1	0	0	0	1	1	0	1	1
IPM 3072	1	1	1	1	0	1	1	0	2	1	1	0	0	1	1	0	1	1
2KM 101	0	1	0	0	0	1	1	0	0	1	1	0	0	1	1	1	1	1
2KM 111	1	1	1	1	0	1	1	0	2	1	0	0	0	1	1	0	1	1
KM 2328	1	1	1	1	0	1	1	0	2	1	0	0	0	0	1	0	1	2
LGG 460	1	0	1	1	1	1	1	0	2	0	0	0	0	1	1	0	1	1
M 395	1	1	1	1	1	2	1	0	2	1	1	0	0	0	1	0	1	2
COGG 13-19	1	1	1	1	0	1	1	0	2	1	1	0	0	1	1	0	1	1
ML 194	0	1	0	0	0	1	1	0	0	1	0	0	0	1	1	0	1	0
ML 778	1	1	1	1	0	1	1	0	2	1	0	0	0	1	1	0	1	1
COGG 13-14	1	1	1	1	1	2	1	0	2	1	0	0	0	0	1	0	1	1
NVL 638	1	1	1	1	0	1	1	0	2	1	1	0	0	1	1	0	1	1
NDMZ-13-11	1	1	1	1	0	1	1	0	2	1	1	0	1	1	1	0	1	1
NDMZ-15-2	1	1	1	1	0	1	1	0	2	1	1	0	0	1	1	0	1	1
NDMZ 215-1	1	1	1	1	0	1	1	0	2	1	0	0	0	1	1	0	1	0
NBPGR 150	1	1	1	1	0	1	1	0	2	1	1	0	1	1	1	0	1	1
OUM 11-5	1	1	1	1	0	0	1	0	2	0	0	0	0	0	1	0	1	1

Table 1: Continue...

Table 1: Continue...

	0=A 1=P	0=E	1=ES	2=DS	0=G 1=PG	0=G 1=PG	0=G 1=GD	0=S 1=M	2=L	0=NL 1=O	2=C	0=A 1=P	0=G 1=PG	2=P	0=Y 1=NL	0=G 1=CG	0=CA 1=I	2=SN	0=B 1=B	0=S 1=C	0=Y 1=G	0=NS 1=D	0=VO 1=D	0=S 1=M	2=L
PBM-14	1	1	1	1	1	0	0	1	1	1	1	0	2	1	1	0	0	0	0	1	1	0	1	0	0
PDM 96-262	1	1	1	1	0	0	1	1	1	1	1	0	2	1	1	1	0	0	0	1	1	0	1	1	2
PLM 24	1	1	1	1	0	0	2	1	1	1	1	0	2	1	1	0	0	0	0	1	1	0	1	1	1
Pusa 105	1	1	1	1	0	0	1	1	1	1	1	0	2	0	1	0	0	0	0	1	1	0	1	1	2
Pusa 0871	1	1	1	1	0	0	1	1	1	1	1	0	2	1	1	1	0	0	0	1	1	0	1	1	1
T-44	1	1	1	1	0	0	1	1	1	1	1	0	2	1	1	1	0	0	0	1	1	0	1	1	0
RMG 991	1	1	1	1	0	0	1	1	1	1	1	0	2	0	0	0	0	0	0	1	1	0	1	1	1
SML 1455	1	1	1	1	0	0	1	1	1	1	1	0	2	0	0	0	0	0	0	1	1	0	1	1	2
SMH 95-1	1	1	1	1	0	0	1	1	1	1	1	0	2	1	1	1	0	0	1	1	1	1	1	1	1
SMH 99-1	1	1	1	1	0	0	1	1	1	1	1	0	2	1	1	0	0	0	0	1	1	1	1	1	1
Sona Mung-1	0	1	0	0	0	0	0	0	1	0	0	0	0	1	1	0	0	0	0	1	0	1	1	0	0
SVM 6111	0	1	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	1	0	1	2	2
TRCM 2014-2	1	1	1	1	0	0	1	1	1	0	0	0	2	1	1	0	0	0	0	1	1	0	1	1	1
VGG ru-2	1	1	1	1	1	0	1	1	2	1	0	0	2	1	1	0	0	0	0	1	1	0	1	1	1
WBM-031	0	1	0	0	0	0	0	1	1	0	0	0	0	1	1	0	0	0	0	1	1	0	1	1	0
VGG 16-036	0	1	0	0	0	0	0	1	1	0	0	0	0	1	1	0	0	0	0	1	1	0	0	1	0
TBM 37	1	1	1	1	0	0	0	1	1	0	0	0	2	1	1	0	1	0	1	0	1	0	0	0	1
VGG 18-021	1	0	1	1	1	1	1	1	2	1	1	0	2	1	1	0	0	0	1	1	1	0	1	1	1
IPM 1205-2	1	1	1	1	0	0	1	1	1	0	0	0	2	1	1	1	0	0	0	1	1	0	1	0	0
VMK 18-02	1	1	1	1	1	1	1	1	1	0	0	0	2	1	1	1	0	0	0	1	1	0	1	1	1
KM 2421	0	1	0	0	0	0	1	1	1	0	0	0	0	1	1	0	0	0	0	1	1	0	1	1	1
MHBC 20-14	1	1	1	1	0	0	1	1	1	0	0	0	2	0	0	0	0	0	0	1	1	0	1	2	2
RMG 1169	1	1	1	1	0	0	1	1	1	0	0	0	2	1	1	1	0	0	0	1	1	0	1	1	1
MH 18-181	1	0	1	1	1	1	1	1	1	0	0	0	2	1	1	0	0	0	1	1	1	0	1	1	0
Pusa M 41	1	1	1	1	0	0	1	1	1	0	0	0	2	1	1	1	0	0	0	1	1	0	1	1	1
MHBC 20-8	1	1	1	1	0	0	1	1	1	0	0	0	2	1	1	1	0	0	0	1	0	0	1	1	1
MML 2579	1	1	1	1	1	1	1	1	1	0	0	0	2	1	1	1	0	0	1	1	1	0	1	1	1
SKNM 2006	0	1	0	0	0	0	1	1	1	0	0	0	0	1	1	0	0	0	0	1	1	0	1	1	1
IPMD 1202-1	1	1	1	1	0	0	1	1	1	0	0	0	2	0	0	0	0	0	0	1	1	0	1	1	1
Pusa M 42	1	1	1	1	1	1	2	1	1	0	0	0	2	1	1	0	0	0	1	0	1	0	1	1	1
MGG 499	0	1	0	0	0	0	2	1	1	0	0	0	0	1	1	0	0	0	0	0	1	1	1	1	1
MH 18-189	1	1	1	1	0	0	1	1	1	0	0	0	2	1	1	0	0	0	0	0	1	0	1	1	1
VGG 17-106	1	1	1	1	1	1	2	1	1	0	0	0	2	1	1	0	0	0	0	1	1	0	1	1	1

[A= Absent; P= Present; E= Erect; SE= Semi-Erect; Sp= Spreading; G= Green; GP= Green with purple splashes; DG= Dark green; S= Small; M= Medium; L= Large; Ln= Lanceolate; O= Ovate; C= Cuneate; Pr= Purple; Y= Yellow; LY= Light Yellow; GC= Green with colored suture; AC= Above canopy; I= Intermediate; NS= Not seen; B= Brown; Bl= Black; St= Straight; Cu= Curved; Sh= Shine; Dl= Dull; Ov= Oval; D= Drum].

nineteen genotypes (84%) with light yellow flowers and twenty-three (16%) with yellow flowers were identified in this study.

Pod descriptors

Pod descriptors in mungbean are key yield-attributing parameters for genotype identification. With the exception of pod pubescence, all pod features showed significant variation. Ninety-two genotypes (65%) had green premature pod colour and fifty genotypes (35%) had green pods with pigmented sutures. There was presence of pod pubescence in all genotypes. Pod position was found above canopy in 141 genotypes (99%) and only single genotype (1%) had pods at intermediate position.

The colour of mature pods in mungbean is another helpful morphological marker that may be used to monitor a mixture of different varieties during the maturity stage of quality seed production. Significant variation in pod colour was discovered in the current material, comprising 26 genotypes (18%) with black mature pods and 116 genotypes (82%) with brown mature pods. In 42 genotypes (30%), the mature pod's curvature was straight while in 100 genotypes (70%), it was curved. For pod characters, Kaur *et al.* (2017) and Chakraborty *et al.* (2022) found similar results.

Seed descriptors

The acceptance of premium genotypes by consumers and the negotiation of their prices depend on a number of mungbean seed descriptors (Pratap *et al*., 2018). In general, oval seeds with a bright green colour and medium size are favoured. All of the seed-related characteristics, including seed colour, seed shape, seed size and seed lustre, were noted in this study after harvest. In terms of seed colour, there are two categories: yellow and green, comprising three (2%) and 139 genotypes (98%), respectively. Only one genotype (1%) was discovered to have an oval seed shape, while the majority of genotypes (99%) had drum-shaped seeds. Thirty-three genotypes (23%) had large seeds, compared to 97 genotypes (69%) with medium-sized seeds and 12 genotypes (8%) with small seeds. Twelve genotypes (8%) with dull seeds lacked seed lustre, but the remaining 130 genotypes (92%) possessed shining seeds.

As a result, all of the seed features demonstrated the presence of variation among all of the genotypes investigated and some of these genotypes may be used in future mungbean breeding programs to produce more consumer-oriented genotypes with favourable seed qualities at premium pricing in the market. The significance of seed features in the characterization of mungbean genotypes was also explored by (Yadav *et al.,* 2020 and Chakraborty *et al.,* (2022).

Diversity analysis using DUS descriptors

Cluster analysis was carried out using the UPGMA (Unweighted Pair Group Method Using Arithmetic Averages) method of clustering. The binary scoring of eighteen DUS descriptors showing variation is shown in

Table 2: Classification of genotypes based on the clusters from UPGMA dendrogram using DUS descriptors.

Cluster	Number of genotypes	Name of genotypes
I	18	SKNM 2006, KM 2421, VGG 16-036, ML 194, IPM 512-1, IPM 410-3, MGG 499, WBM-031, COGG-8, 2KM 101, SVM 98, RMG-1148, EC 251552, SKNM 1801, SVM 6111, VGG 16-047, MH 421, Sona Mung-1
II	121	PM 1801, JLPM 707-27, ML 818, IPM 02-3, IPM 1604-1, MH 1468, Pusa M 22-32, KM 2419, BCM 20-6, MML 2577, SVM 55, PMD-14, IPM 1704-14, PMS-12, TMB 230, IPM 604-16, MH1871, Virat (IPM 205-7), Pusa BM 9, VGG 18-002, IPMD 604-1-7, MML 2575, SML 832, DGGV 91, MH 1762, SML 1932, OBGG 108, VGG 17-043, PM 1602, Pant M 5, SML 1933, Pusa M 19111, MH 1703, MML 2560, Pusa M 1971, PM 1601, IPM 410-3, PM 1520, TCADM 20-5, IPMD 1604, IPM 1603-1, TBMB 117-5, Pusa M 2131, IPM 1103-1, TBMB 17-2, Pusa BM 16, PM 1605, IPMD 101-2, MML 2568, Pusa M 2132, MHBC 20-7, PM 504-20-27, PM 1624, MH 1830, IPM 1610-1, RMG 1132, RMG 1166, OBGG 105, MH 1890 andGG 1301, MML 2576, PMD-8, Pusa M 2141, OBGG 106, PMD-7, MH 1801, PMD-9, SKNM 1911, VGG 17-036, BDYR-1, Pusa 1072, COGG 1102, EC 30400, EC 399223, EC 393410, EC 470090, EC 581523, Ganga-8, HUM 16, IC 1031096, IPM 99-3, IPM 9901-8, Pusa 1701, IPM 2k 14-9, IPM 3072, 2KM 111, KM 2328, LGG 460, M 395, COGG 13-19, ML 778, COGG 13-14, NVL 638, NDMZ-13-11, NDMZ-15-2, NDMZ 215-1, NBPGR 150, OUM 11-5, PBM-14, PDM 96-262, PLM 24, Pusa 105, Pusa 0871, T-44, RMG 991, SML 1455, SMH 95-1, SMH 99-1, TRCM 2014-2, TBM 37, IPM 1205-2, VMK 18-02, MHBC 20-14, RMG 1169, MH 18-181, Pusa M 41, MHBC 20-8, MML 2579, IPMD 1202-1, Pusa M 42, MH 18-189, VGG 17-106
III	3	IC 15276, VGG ru-2, VGG 18-021
Total	142	

Table 1. According to the dendrogram, all one hundred forty-two mungbean genotypes were grouped into three major clusters (Table 2). Cluster II was the largest cluster with 121 genotypes subdivided into many subclusters. Second largest cluster was cluster I (18) followed by cluster III (3). The study was in accordance with Waniale *et al.* (2014) who classified 35 genotypes into five clusters. Sunayana *et al.* (2017) also classified sixty genotypes into nine distinct groups using UPGMA method of clustering.

CONCLUSION

All of the genotypes examined in the current study showed a substantial amount of variation based on several DUS descriptors. Four characters displayed trimorphic grouping and three of the characters lacked variation. The remaining fourteen traits showed dimorphic groupings of all genotypes. Overall, the current DUS characterization of mungbean genotypes can be utilized as a reference in future breeding programs to recognize and categorize distinct genotypes into different groups for particular traits. The current study also emphasizes the significance of introducing new germplasm for the expansion of the genetic base and permits the simple registration of new cultivars with these different traits under PPVFRA. UPGMA clustering-based diversity analysis revealed that genotypes can be grouped together based on their differences in qualitative traits and suggested utilizing these genotypes for the selection of diverse parents in the mungbean hybridization program for improved heterotic response. Breeders will get benefit from this categorization of varieties into different clusters since, cluster analysis is a valuable method for determining variability and identifying potential varieties which can be used in future breeding programmes.

Conflict of interest

The authors have no conflicts of interest to declare. All co-authors have seen and agree with the contents of the manuscript and there is no financial interest to report.

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