DUS Trait Evaluation in Urdbean Genotypes: Implications for Breeding through Morphological Markers

---

ABSTRACT

Urdbean (*Vigna mungo* L. Hepper) is most prevalent types out of pluses crops. In this research, comprehensive evaluation of 96 Urdbean (*Vigna mungo* L. Hepper) genotypes, which included two check varieties, to assess genetic variation across 21 distinct morphological traits. The present investigation was conducted in Randomized complete block design at JNKVV, Jabalpur (Madhya Pradesh). The observations were taken at various stages of the plant's development. Determine the important morphological traits using PPV&FRA descriptors. These characteristics encompass a broad spectrum, including hypocotyl anthocyanin coloration, timing of flowering, growth and habit of the plant, stem color and pubescence, leaf shape, foliage and vein color, leaf pubescence, petiole color, pod characteristics (including green color intensity in immature pods and pubescence, peduncle length, pod length and color, plant height, and several seed traits (color, shape, luster, and size). Our analysis revealed substantial variability in 19 morphological traits out of the 21 traits evaluated under Distinctness, Uniformity, and Stability (DUS) traits. However, there is no significant variation was detected in the traits of anthocyanin pigment and plant habit while in remaining 19 traits significant variation was observed. As a result, these traits have a distinct morphological identity that will make identification easier. For simple visibility of varietal associated traits during maintenance and resistance breeding programs, this attributes might be taken into consideration in the development of the urdbean variety.

Keywords: Morphological trait diversity; urdbean breeding; DUS trait evaluation.

1. INTRODUCTION

Urdbean, scientifically named *Vignamungo* L. Hepper, is classified within the Angiosperms phylum, under the sub-phylum Dicotyledones, Lignosae division, and the Leguminaceae family (Jayamaniet al., 2014). The genus Vigna (Leguminosae) consists of seven subgenera and has about 150 species (Rajasekhar & Lal,2020).This legume, known by various regional names such as Biri, Urd, Urad, Urid, Mash, and Mungo, originated from Vignamungo var. silvestris.It has a chromosome count of 2n=22 and an estimated genome size of 574 Mbp (Jegadeesan et al., 2021). Renowned for its adaptability, Urdbean is cultivated across diverse agroecological conditions, making it a versatile crop in both arid and humid environments. As a self-pollinated, diploid grain legume, it is a significant agricultural staple, particularly in Asian countries, cultivated primarily during the kharif and rabi seasons.

Pulses are an excellent option for dietary protein (Dar et al., 2024).Nutritionally, Urdbean is a powerhouse, offering a high protein content ranging from 20.8 to 30.5%, and carbohydrates between 56.5 to 63.7% (Jayamani,2014). Its protein content is notably higher than cereals, providing about 26% protein, which is almost three times more. Additionally, it is a valuable source of phosphoric acid and calcium. Its

---

cultivation plays a crucial role in enhancing soil nitrogen content, contributing to soil fertility, especially in the traditional farming regions of Southern Asia, including India, Afghanistan, Pakistan, Myanmar, and Bangladesh.

Morphological characterization of urdbean genotypes is essential for their protection under Plant Variety Protection (PVP) legislation because varietal testing of (DUS) Distinctness Uniformity and Stability (DUS) are the basis for granting protection of new variety under PPV and FR Act 2001. DUS is very essential to distinguish genotypes on the basis of their morphology, it provides unique identity to genotypes, makes easy for the breeders to select superior types of genotypes based on their morphology.Characteristics such as lanceolate leaf shape and pubescence degree play a significant role in indicating environmental adaptability and stress resistance (IBPGR, 1985). Keeping this in view ninety-six genotypes including two checks were characterized for 21 DUS descriptors (PPV and FR, 2007).

2. MATERIALS AND METHODS

The experimental material used in present study comprised of ninety six genotypes of urdbean including two check varieties TJU 130 and TJU 339 collected from JNKVV, Jabalpur and PAU, Punjab. The present experiment was conducted in Randomized Complete Block Design with two replications in kharif 2023 with row to row distance 30 cm. and plant to plant distance 15 cm. The full package of practices, recommended for urdbean cultivation in Madhya Pradesh was strictly adopted for optimum crop growth. The agronomical operations were timely carried out. Five competitive plants were randomly tagged in each genotype, in each replication for recording observations for analyzing traits like anthocyanin colour at cotyledon stage, nine specific traits at 50% flowering, pod characteristics at green pod stage, and seed attributes including color, lustre, shape, and size at maturity. This study provided detailed insights into the agro-morphological and seed trait diversity of urdbean genotypes, enhancing their characterization and classification, as depicted in Fig.1.

3. RESULTS AND DISCUSSION

Morphological characterization is the initial step in describing and classifying the item being investigated. Characteristics are employed to assess the criteria for distinction, uniformity, and stability. A thorough comprehension of the physical characteristics is essential for identifying, selecting, and transferring advantageous genes, as well as for designing new populations. This is a fundamental requirement of the genetic improvement program. Employing standardized descriptors to characterize the attributes of a crop species is advantageous for enhancing the utilization and preservation of germplasm. A study was done to categorize 96 Urdbean genotypes based on their Urdbean morphological characteristics. An effort was made to categorize the Urdbean genotypes and identify them based on their distinct characteristics, due to the significant diversity in qualitative attributes. The 96 genotypes can be differentiated from one another based on morphological variations, for 21 DUS traits as mention in Table 2.

3.1 Anthocyanin Pigmentation

The presence of anthocyanin pigmentation in the hypocotyl serves as a valuable morphological indicator in genetic research and cultivar identification. The genotypes are classified according to the presence or absence of hypocotyl anthocyanin coloring. All ninety-six genotypes have anthocyanin pigment (Dhanraj et al., 2024) found similar morphological differences across the genotypes in Urdbean as seen in Table 2 and inFig. 2(a) shows presence or absence of anthocyanin pigment.

3.2 Flower Character

Flower characteristics, including the timing of flowering, were observed in 50% of the plants that had at least one flower at the open stage as shown in Table 2. The genotypes were classified into three distinct categories early, intermediate and late flowering. A total of 72 genotypes had early flowering (less than 40 days), whereas 24 genotypes exhibited intermediate flowering (40-50 days) as determined by their flowering time. No genotype exhibiting late flowering was identified. Early maturing genotypes are highly significant because they can mitigate the negative impacts of terminal heat stress and ultimately rains during harvest as well as early maturing genotypes suited for rice fallow system in Madhya Pradesh.

Table 1. List of genotypes

S. no.	Genotypes	S. no.	Genotypes	S. no.	Genotypes	S. no.	Genotype
1	JU-3	25	TJU 4	49	KUG 1152	73	KUG 1137
2	PDU-1	26	TJU 22	50	KUG 1153	74	KUG 1138
3	TJU45-1	27	TJU 67	51	KUG 1154	75	KUG 1140
4	TU-98-14	28	TJU 24	52	KUG 1155	76	KUG 1141
5	TJU 139	29	TJU 339 (CHECK)	53	KUG 1156	77	KUG 1139
6	TJU 328	30	TJU 130 (CHECK)	54	KUG 1157	78	KUG 1162
7	TJU 213	31	TJU 231	55	KUG 1158	79	KUG 1163
8	TAU 2	32	TJU 48	56	KUG 1159	80	KUG 1164
9	TJU 18	33	TJU 273	57	KUG 1160	81	KUG 1165
10	INDIRA URD 1	34	TJU 111	58	KUG 1121	82	KUG 1167
11	TJU 42	35	TJU 41-1	59	KUG 1122	83	KUG 1168
12	PU 19	36	TJU 84	60	KUG 1123	84	KUG 1169
13	TJU 134	37	PU 35	61	KUG 1124	85	KUG 1170
14	TU 94-2	38	KUG 1149	62	KUG 1125	86	KUG 1171
15	TJU 55	39	MASH 114	63	KUG 1126	87	KUG 1173
16	TJU 24-10	40	MASH 479	64	KUG 1127	88	KUG 1174
17	TJU 41-2	41	MASH1137	65	KUG 1129	89	KUG 1175
18	T 9	42	MASH1008	66	KUG 1130	90	KUG 1176
19	TJU 103	43	KUG 1142	67	KUG 1131	91	KUG 1177
20	TJU 62	44	KUG 1145	68	KUG 1132	92	KUG 1178
21	LBG 20	45	KUG 1146	69	KUG 1133	93	KUG 1179
22	TJU 262	46	KUG 1147	70	KUG 1134	94	KUG 1180
23	URDI LOCAL	47	KUG 1148	71	KUG 1135	95	KUG 1181
24	IPU 2-43	48	KUG 1151	72	KUG 1136	96	MASH 338

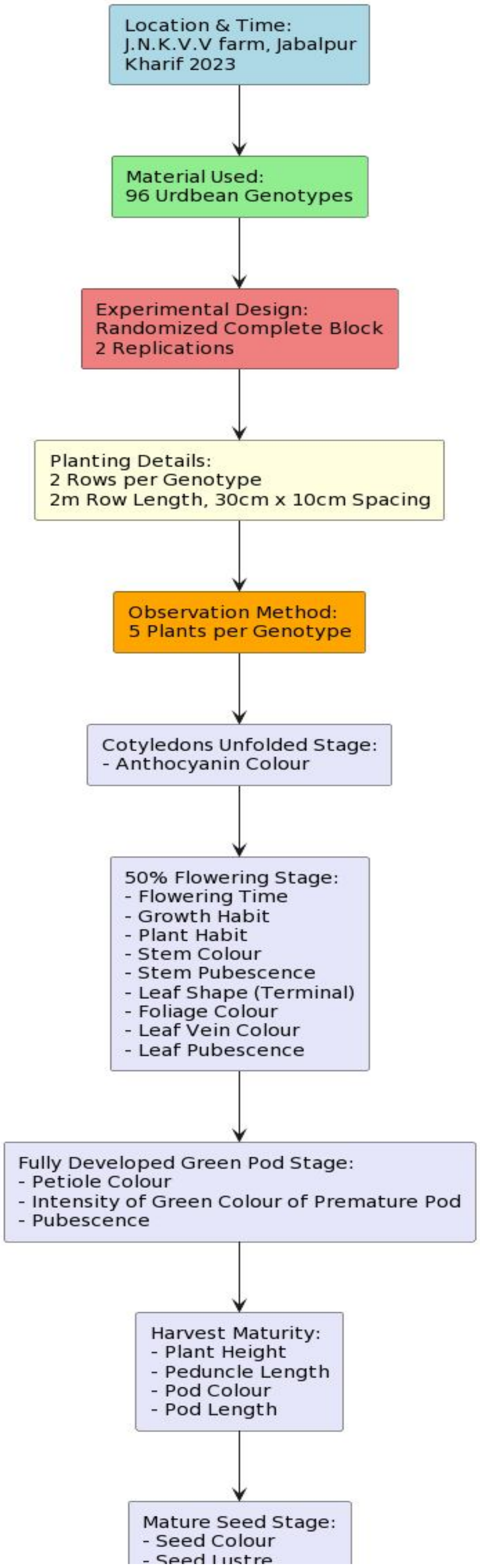


Fig. 1. A Methodological overview from planting to trait analysis

Table 2. Comprehensive morphological characterization according to DUS guidelines

S. NO	Characteristics	Stages of Observation	Expression / States	Note/ Score	Genotype frequency	Percentage contribution	Name of genotype
1	Hypocotyl: Anthcyanincolouration	Cotyledon unfolded	Absent	1	0	0	Nil
			Present	9	100	100	All genotypes
2	Time of flowering	50% plants with at least one open flower	Early (<40 days)	3	72	75	JU3,PDU1,TJU451,TU9814,TJU328,TJU2410,T9,TJU262,IPU243,TJU4,TJU22,TJU67,TJU339(CHECK),TJU130(CHECK),TJU(231),TJU48,TJU273,TJU84,PU35,KUG1149,MASH479,KUG1135,MASH1008,KUG1142,KUG1145,KUG1146,KUG1147,KUG1148,KUG1151,KUG1152,KUG1153,KUG1154,KUG1155,KUG1156,KUG1157,KUG1158,KUG1159,KUG1160,KUG1121,KUG1122,KUG1123,KUG1124,KUG1125,KUG1126,KUG1127,KUG1129,KUG1130,KUG1131,KUG1132,KUG1133,KUG1134,KUG1135,KUG1136,KUG1137,KUG1138,KUG1140,KUG1141,KUG1139,KUG1162,KG1163,KUG1164,KUG1165,KUG1167,KUG1168,KUG1169,KUG1170,KUG1171,KUG1173,KUG1174,KUG1175,KUG1176,KUG1177,KUG1178,KUG1179,KUG1180,KUG1181,MASH338.
			Medium (40-50 Days)	5	24	25	TJU-139, TJU 213, TAU 2, TJU 18, INDIRA URD 1, TJU 42, PU 19, TJU134, TU942, TJU55, TJU412, TJU103, TJU62,LBG20,URDILOCAL,TJU24,TJU111,TJU411,PU35,KUG1149,MASH114,MASH479, MASH1137,KUG1153,
			Late (>50 days)	7	0	0	NIL
3	Plant: Growth habit	50% flowering	Erect	3	4	4.16	TJU41-2,TJU62,KUG1148,KUG1153
			Semi -erect	5	29	30.20	JU-3, PDU-1, TJU45-1, TU-98-14,TAU-2,INDIRA URD-1, PU 19, TJU 134, TU 94-2, TU 94-2, TJU 55 T9,TJU103,LBG20,TJU262,TJU 4, TJU 22, TJU 67,TJU,130,KUG1149,MASH1137,MASH1008,KUG1151,KUC1130,KUG1131,KUG1138,KUG1171,KUG1175,KUG1178,KUG1181
			Spreading	7	63	65.62	TJU 139, TJU 328, TJU 213, TJU 18, TJU 42, TJU 24-10, URDI LOCAL,IPU 2-43,TJU 24,TJU 339 (CHECK),TJU 231,TJU 48,TJU 273,TJU 111,TJU41-1, TJU 84, PU 35, MASH 114, MASH 479, KUG 1135, KUG 1136, KUG 1137,MASH 479, KUG 1154, KUG 1155,KUG 1156, KUG 1157, KUG 1158, KUG 1124, KUG 1125, KUG 1126, KUG 1127, KUG 1129, KUG 1159, KUG 1160, KUG 1121, KUG 1122, KUG 1123, KUG 1142, KUG 1145, KUG 1146, KUG 1147, KUG 1152, KUG 1132, KUG 1133, KUG 1134, KUG 1140, KUG 1141, KUG 1139, KUG 1162, KUG 1163, KUG 1164, KUG 1165, KUG 1167, KUG 1168, KUG 1169, KUG 1170, KUG 1173, KUG 1174, KUG 1176,KUG 1177, KUG 1179, KUG 1180, MASH 338
4	Plant : Habit	50% flowering	Determinate	1	0	0	NIL
			Indeterminate	3	100	100	All genotypes
5	Stem: Colour	50% flowering	Green	1	1	1.04	MASH 338
			Green with purple splahes	2	21	21.87	TU-98-14, TJU 328, TJU 22, TJU 67, TJU 339 (CHECK), TJU 111, TJU 41-1, MASH 114, MASH 1008, KUG 1142, KUG 1145, KUG 1148, KUG1153, KUG 1158, KUG 1122, KUG 1123, KUG 1124, KUG 1139, KUG 1175, KUG 1176, KUG 1181
			Purple with green splashes	3	74	77.08	JU-3, PDU-1, TJU45-1, TJU 213, TJU 139, TJU 24-10, TJU 41-2, T 9, TJU 103, TJU 62, LBG 20, TJU 262, URDI LOCAL, IPU 2-43, TJU 4, TAU 218, INDIRA URD 1, TJU 42, PU 19, TJU 134, TU 94-, TJU 5, TJU 2, TJU 130 (CHECK), TJU 231, TJU 48, TJU 27, TJU 8, PU 3, KUG 1149, MASH 479, MASH 113, KUG 1146, KUG 1147, KUG 1151, KUG 1152, KUG 1154, KUG 1157, KUG 1156, KUG 1155, KUG 1159, KUG 1160, KUG 1121, KUG 1125, KUG 1126, KUG 1127, KUG 1129, KUG 1130, KUG 1131, KUG 1132, KUG 1133, KUG 1134, KUG 1141, KUG 1162, KUG 1135, KUG 1136, KUG 1137, KUG 1138, KUG 1140, KUG 1171, KUG 1173, KUG 1174, KUG 1163, KUG 1164, KUG 1165, KUG 1167,

S. NO	Characteristics	Stages of Observation	Expression / States	Note/ Score	Genotype frequency	Percentage contribution	Name of genotype
							KUG 1168, KUG 1169, KUG 1170, KUG 1177, KUG 1178, KUG 1179, KUG 1180
			Purple	4	0	0	NIL
6	Stem: Pubescence	50% flowering	Absent	1	2	2.08	URDI LOCAL, KUG 1130
			Present	9	94	97.91	JU-3, PDU-1, TJU45-1, TU-98-14, TJU 139,TJU 328, TJU 213, TAU 2, TJU 18, INDIRA URD 1, TJU 42, PU 19, TJU 134, TU 94-2, TJU 55, TJU 22, TJU 67, TJU 24, TJU 339 (CHECK), TJU 130 (CHECK), MASH 1137, MASH 1008, KUG 1142, KUG 1145, KUG 1146, KUG 1159, KUG 1160, KUG 1121, KUG 1122, KUG 1123, KUG 1135, KUG 1136, KUG 1137, KUG 1138, KUG 1140, KUG 1171, KUG 1173, KUG 1174, KUG 1175, KUG 1176, TJU 24-10, TJU 41-2, T 9, TJU 103, TJU 62, LBG 20, TJU 262, IPU 2-43, TJU 4, TJU 231, TJU 48, TJU 273, TJU 111, TJU 41-1, TJU 84, PU 35, KUG 1149, MASH 114, MASH 479, KUG 1147, KUG 1148, KUG 1151, KUG 1152, KUG 1153, KUG 1154, KUG 1155, KUG 1156, KUG 1157, KUG 1158, KUG 1124, KUG 1125, KUG 1126, KUG 1127, KUG 1129, KUG 1131,KUG 1132, KUG 1133, KUG 1134, KUG 1141, KUG 1139, KUG 1162, KUG 1163, KUG 1164, KUG 1165, KUG 1167, KUG 1168, KUG 1169, KUG 1170, KUG 1177, KUG 1178, KUG 1179, KUG 1180, KUG 1181, MASH 338
7	Leaf(termial): Shape	50% flowering	Deltoid	1	19	19.76	TJU 55, TJU 24, IPU 2-43, TJU 231, PU 35, MASH 479, KUG 1154, KUG 1122, KUG 1123, KUG 1125, KUG 1126, KUG 1132, KUG 1135, KUG 1138, KUG 1140, KUG 1162, TU-98-14, TJU 18, KUG 1134
			Ovate	2	31	32.29	JU-3, TJU45-1, TJU 139, TJU 213, TJU 328, URDI LOCAL, TJU 42, PU 19, TJU 134, TJU 41-2, T 9, LBG 20, TJU 67, TJU 339 (CHECK), TJU 273, TJU 41-1, TJU 84, MASH 114, MASH 1137, KUG 1145, KUG 1153, KUG 1155, KUG 1158, KUG 1131, KUG 1136, KUG 1141, KUG 1139, KUG 1164, KUG 1165, KUG 1173, KUG 1177
			Lanceolate	3	33	34.37	TJU 22, TJU 24-10, PDU-1, TAU 2, INDIRA URD 1, TU 94-2, TJU 103, TJU 62, TJU 262, TJU 4, TJU 130 (CHECK), TJU 48, TJU 111, KUG 1149, KUG 1142, KUG 1146, KUG 1147, KUG 1148, KUG 1151, KUG 1152, KUG 1155, KUG 1157, KUG 1159, KUG 1160, KUG 1121, KUG 1127, KUG 1129, KUG 1130, KUG 1137, KUG 1163, KUG 1171, KUG 1180, KUG 1181
			Cuneate	4	13	13.54	KUG 1133,KUG 1167,KUG 1168,KUG 1169,KUG 1170,KUG 1174,KUG 1175 ,KUG 1176,KUG 1178,KUG 1179,MASH 338
8	Foliage colour	50% flowering	Green	1	9	9.37	TU-98-14,TJU 328,TAU 2,MASH1008,KUG 1160,KUG 1174,KUG 1176,KUG 1177,KUG 1178
			Dark green	2	87	90.62	T 9,TJU 103,TJU 62,LBG 20,TJU 262,URDILOCAL,IPU 2-43,TJU 4,TJU 22,TJU 67,TJU 24,TJU 339 (CHECK),TJU 130 (CHECK),TJU 24-10,TJU 41-2,JU-3,PDU-1,TJU45-1,TJU 139,TJU 213,TJU 18,INDIRA URD 1,TJU 42,PU 19,TJU 134,TU 94-2,TJU 55,TJU 231,TJU 48,TJU 273,TJU 111,TJU 41-1,TJU 84,PU 35,KUG 1149,MASH 114,MASH 479,MASH1137,KUG 1142,KUG 1145,KUG 1146,KUG 1147,KUG 1148,KUG 1151,KUG 1152,KUG 1153,KUG 1154,KUG 1155,KUG 1156,KUG 1157,KUG 1158,KUG 1159,KUG 1121,KUG 1122,KUG 1123,KUG 1124,KUG 1125,KUG 1126,KUG 1127,KUG 1129,KUG 1130,KUG 1131,KUG 1132,KUG 1133,KUG 1134,KUG 1135,KUG 1136,KUG 1137,KUG 1138,KUG 1140,KUG 1141,KUG 1139,KUG 1162,KUG 1163,KUG 1164,KUG 1165,KUG 1167,KUG 1168,KUG 1169,KUG 1170,KUG 1171,KUG 1173,KUG 1175,KUG 1179,KUG 1180,KUG 1181,MASH 338
9	Leaf : Vein colour	50% flowering	Green	1	82	85.41	JU-3,PDU-1,TU-98-14,TJU 139,TJU 328,TJU 213,TAU 2,TJU 18,TJU 42,PU 19,TJU 134,TU 94-2,TJU 55,TJU 24-10,,TJU 41-2,T 9,TJU 62,LBG 20,TJU 262,TJU 22,TJU 67,TJU 24,TJU 339 (CHECK),TJU 130 (CHECK),TJU 231,TJU 48,TJU 273,TJU 111,TJU 411,TJU,84,PU35,KUG1149,MASH114,MASH479,MASH1137,MASH1008,KUG 1142,KUG 1145,KUG 1146,KUG 1147,KUG 1148,KUG 1151,KUG 1153,KUG 1154,KUG 1155,KUG 1157,KUG 1158,KUG 1159,KUG 1160,KUG 1122,KUG 1126,KUG 1127,KUG 1129,KUG 1130,KUG 1131,KUG 1132,KUG 1133,KUG 1135,KUG 1136,KUG 1137,KUG 1138,KUG

S. NO	Characteristics	Stages of Observation	Expression / States	Note/ Score	Genotype frequency	Percentage contribution	Name of genotype
							1140,KUG 1141,KUG 1139,KUG 1162,KUG 1163,KUG 1164,KUG 1165,KUG 1167,KUG 1168,KUG 1169,KUG 1170,KUG 1171,KUG 1173,KUG 1174,KUG 1175,KUG 1176,KUG 1177,KUG 1178,KUG 1180,KUG 1181,MASH 338
			Purple	2	14	14.58	TJU45-1,INDIRA URD 1,TJU 103,URDILOCAL,IPU 2-43,TJU 4,KUG 1152,KUG 1156,KUG 1121,KUG 1123,KUG 1124,KUG 1125,KUG 1134,KUG 1179
10	Leaf : Pubescence	50% flowering	Absent	1	2	2.08	URDI LOCAL, KUG1130
			Present	9	94	97.91	JU-3,PDU-1,TJU45-1,TU-98-14,TJU 139,TJU 328,TJU 213,TAU 2,TJU 18,INDIRA URD 1,TJU 42,PU 19,TJU 134,TU 94-2,TJU 55,TJU 24-10,TJU 41-2,T 9,TJU 103,TJU 62,LBG 20,TJU 262,URDILOCAL,IPU 2-43,TJU 4,TJU 22,TJU 67,TJU 24,TJU 339 (CHECK),TJU 130 (CHECK),TJU 231,TJU 48,TJU 273,TJU 111,TJU 411,TJU84,PU35,KUG1149,MASH114,MASH479,MASH1137,MASH1008,KUG 1142,KUG 1145,KUG 1146,KUG 1147,KUG 1148,KUG 1151,KUG 1152,KUG 1153,KUG 1154,KUG 1155,KUG 1156,KUG 1157,KUG 1158,KUG 1159,KUG 1160,KUG 1121,KUG 1122,KUG 1123,KUG 1124,KUG 1125,KUG 1126,KUG 1127,KUG 1129,KUG 1130,KUG 1131,KUG 1132,KUG 1133,KUG 1134,KUG 1135,KUG 1136,KUG 1137,KUG 1138,KUG 1140,KUG 1141,KUG 1139,KUG 1162,KUG 1163,KUG 1164,KUG 1165,KUG 1167,KUG 1168,KUG 1169,KUG 1170,KUG 1171,KUG 1173,KUG 1174,KUG 1175,KUG 1176,KUG 1177,KUG 1178,KUG 1179,KUG 1180,KUG 1181,MASH 338
11	Petiole: Colour	Fully Developed green pods	Green	1	3	3.12	TJU130(Check),KUG1122,MASH338
			Green with Purple splashes	2	72	75	PDU-1,TJU45-1,TU-98-14,TJU 139,TJU 328,TJU 213,TAU 2,TJU 18,TJU 42,PU 19,TU 94-2,TJU 24-10,TJU 41-2,T 9,TJU 103,TJU 62,LBG 20,TJU 262,URDI,LOCAL,TJU4,TJU67,TJU24,TJU,339(CHECK),,TJU 231,TJU 48,TJU 273,TJU 111,TJU 41-1,PU 35,KUG 1149,MASH 114,MASH1137,MASH1008,KUG 1142,KUG 1145,KUG 1146,KUG 1147,KUG 1148,KUG 1151,KUG 1153,KUG 1155,KUG 1156,KUG 1157,KUG 1158,KUG 1159,KUG 1160,KUG ,KUG 1123,KUG 1124,KUG 1126,KUG 1127,KUG 1129,KUG 1130,KUG 1131,KUG 1132,KUG 1133,KUG 1134,KUG 1137,KUG 1138,KUG 1162,KUG 1163,KUG 1164,KUG 1167,KUG 1168,KUG 1169,KUG 1171,KUG 1173,KUG 1174,KUG 1176,KUG 1177,KUG 1178,KUG 1179,KUG 1181,
			Purple	3	21	21.87	JU3,INDIRA URD 1,TJU134,TJU55,IPU2-43, TJU 22, TJU 84, MASH 479, KUG1152, KUG 1154, KUG 1121, KUG1135,KUG1136,KUG1140,KUG1141,KUG1139,KUG1165,KUG1170,KUG1175,KUG1180,
12	Pod intensity of green colour of premature pods	Fully Developed green pods	Yellowish green	3	33	34.37	JU-3,PDU-1,TJU 139,TJU 328,TAU 2,TJU 18,PU 19,TJU 134,TU 94-2,TJU 55,TJU 24-10,TJU 41-2,T 9,LBG 20,TJU 262,URDI LOCAL,TJU 4,TJU 22,TJU 67,TJU 24,TJU 130 (CHECK),TJU 231,TJU 48,TJU 273,TJU 111,TJU 41-1,TJU 84,MASH1137,KUG 1163,KUG 1165,KUG 1171,KUG 1174, KUG 1175
			Green	5	35	36.45	TJU45-1,TU-98-14,TJU 213,TJU 42,TJU 103,TJU 62,IPU 2-43,TJU 339, (CHECK,PU 35,KUG 1149,MASH 114,MASH 479,MASH1008,KUG 1142,KUG 1145,KUG 1146,KUG 1154,KUG 1155,KUG 1156,KUG 1158,KUG 1159,KUG 1122,KUG 1123,KUG 1124,KUG 1126,KUG 1129,KUG 1133,KUG 1164,KUG 1167,KUG 1168,KUG 1176,KUG 1177,KUG 1178,KUG 1179,KUG 1181
			Dark green	7	28	29.16	INDIRA URD 1,KUG 1147,KUG 1148,KUG 1151,KUG 1152,KUG 1153, KUG 1157,KUG 1160,KUG 1121,KUG 1125,KUG 1127,KUG 1130, KUG 1131,KUG 1132,KUG 1134,KUG 1135,KUG 1136,KUG 1137,KUG 1138,KUG 1140,KUG 1141,KUG 1139,KUG 1162,KUG 1169,KUG 1170,KUG 1173,KUG 1180,MASH 338
13	Pod : Pubescence	Fully Developed green pods	Absent	1	15	15.62	TJU 45-1,TJU 328,INDIRA URD 1,TJU 55,T 9,TJU 62,LBG 20,IPU 2-43,KUG 1147,KUG 1129,KUG 1130,KUG 1131,KUG 1121,KUG 1133,KUG 1136
			Present	9	81	84.37	JU-3,PDU-1,TU-98-14,TJU 139,TJU 213,TAU 2,TJU 18,TJU 42,PU 19,TJU 134,TU 94-2,TJU 24-10,TJU 41-2,TJU 103,TJU 262,URDI LOCAL,TJU 4,TJU 22,TJU 67,TJU 24,TJU

S. NO	Characteristics	Stages of Observation	Expression / States	Note/ Score	Genotype frequency	Percentage contribution	Name of genotype
							339 (CHECK),TJU 130 (CHECK),TJU 231,TJU 48,TJU 273,TJU 111,TJU 41-1,TJU 84,PU 35,KUG1149, MASH114,MASH,479,MASH1137,MASH1008,KUG 1142,KUG 1145,KUG 1146,KUG 1148,KUG 1151,KUG 1152,KUG 1153,KUG 1154,KUG 1155,KUG 1156,KUG 1157,KUG 1158,KUG 1159,KUG 1160,KUG 1122,KUG 1123,KUG 1124,KUG 1125,KUG 1126,KUG 1127,KUG 1132,KUG 1134,KUG 1135,KUG 1137,KUG 1138,KUG 1140,KUG 1141,KUG 1139,KUG 1162,KUG 1163,KUG 1164,KUG 1165,KUG 1167,KUG 1168,KUG 1169,KUG 1170,KUG 1171,KUG 1173,KUG 1174,KUG 1175,KUG 1176,KUG 1177,KUG 1178,KUG 1179,KUG 1180,KUG 1181,MASH 338
14	Peduncle : Length	Harvest maturity	short (<5cm)	3	62	64.58	PDU-1,TJU 45-1,TU-98-14,TJU 139,TJU 328,TJU 213,TJU 42,PU 19,TJU 55,TJU 41-2,T 9,TJU 103,TJU 62,URDI LOCAL,IPU 2-43,TJU 22,TJU 231,MASH 114,MASH1137,KUG 1142,KUG 1146,KUG 1148,KUG 1151,KUG 1152,KUG 1154,KUG 1155,KUG 1156,KUG 1157,KUG 1159,KUG 1121,KUG 1124,KUG 1125,KUG 1127,KUG 1132,KUG 1133,KUG 1134,KUG 1135,KUG 1136,KUG 1137,KUG 1138,KUG 1140,KUG 1141,KUG 1139,KUG 1162,KUG 1163,KUG 1164,KUG 1165,KUG 1167,KUG 1168,KUG 1169,KUG 1170,KUG 1171,KUG 1173,KUG 1174,KUG 1175,KUG 1176,KUG 1177,KUG 1178,KUG 1179,KUG 1180,KUG 1181
			Medium (5-10 cm)	5	32	33.33	JU-3,TAU 2,TJU 18,TJU 134,TU 94-2,TJU 24-10,LBG 20,TJU 262 TJU 4,TJU 67,TJU 24,TJU 130 (CHECK),TJU 48,TJU 273,TJU 111, TJU 41-1,TJU 84,PU 35,KUG 1149,MASH 479,MASH1008,KUG 1145,KUG 1147,KUG 1153,KUG 1158,KUG 1160,KUG 1122,KUG 1123,KUG 1126,KUG 1129,KUG 1131,MASH 338
			Long(>10cm)	7	2	2.08	INDIRA URD 1, TJU 339 (CHECK)
15	pod: length	Harvest maturity	small (<5cm)	3	89	92.7	JU-3,PDU-1,TJU 45-1,TU-98-14,TJU 139,TJU 328,TJU 213,TAU 2,TJU 18,INDIRA URD 1,TJU 42,PU 19,TJU 134,TU 94-2,TJU 55,TJU 24-10,TJU 41-2,T 9,TJU 103,TJU 62,LBG 20,TJU 262,URDILOCAL,IPU 2-43,TJU 4,TJU 22,TJU 67,TJU 24,TJU 130 (CHECK),TJU 231,TJU 48,TJU 273,TJU 111,TJU 41-1,PU 35,KUG 1149,MASH 114,MASH 479,MASH1137,MASH1008,KUG 1142,KUG 1145,KUG 1146,KUG 1147,KUG 1148,KUG 1152,KUG 1153,KUG 1154,KUG 1155,KUG 1156,KUG 1157,KUG 1158,KUG 1159,KUG 1160,KUG 1121,KUG 1123,KUG 1124,KUG 1125,KUG 1126,KUG 1127,KUG 1130,KUG 1131,KUG 1132,KUG 1133,KUG 1134,KUG 1135,KUG 1136,KUG 1137,KUG 1138,KUG 1140,KUG 1141,KUG 1139,KUG 1162,KUG 1163,KUG 1164,KUG 1165,KUG 1167,KUG 1168,KUG 1169,KUG 1170,KUG 1171,KUG 1173,KUG 1174,KUG 1175,KUG 1176,KUG 1178,KUG 1179,KUG 1180,MASH 338
			Medium (5-7cm)	5	7	7.29	TJU 339 (CHECK), TJU 84,KUG 1151,KUG 1122,KUG 1129,KUG 1177,KUG 1181
			long(>10 cm)	7	0	0	NIL
16	Pod: Colour of mature pod	Harvest maturity	buff (off white)	1	2	2.08	KUG 1179, KUG 1180
			brown	2	12	12.5	JU-3,PDU-1,TU-98-14,PU 19,TJU 134,TJU 41-2,TJU 84,PU 35, KUG 1159,KUG 1160,KUG 1168,KUG 1174
			black	3	82	85.41	TJU 45-1,TJU 139,TJU 328,TJU 213,TAU 2,TJU 18,INDIRA URD 1 TJU 42,TU 94-2,TJU 55,TJU 24-10,T 9,TJU 103,TJU 62,LBG 20,TJU 262,URDI LOCAL,IPU 2-43,TJU 4,TJU 22,TJU 67,TJU 24,TJU 339 (CHECK),TJU 130 (CHECK),TJU 231,TJU 48,TJU 273,TJU 111,TJU 41-1,KUG 1149,MASH 114,MASH 479,MASH1137,MASH1008, KUG 1142,KUG 1145,KUG 1146,KUG 1124,KUG 1125,KUG 1126,KUG 1127,KUG 1129,KUG 1130,KUG 1131,KUG 1132,KUG 1133,KUG 1134,KUG 1135,KUG 1136,KUG 1137,KUG 1138,KUG 1140,KUG 1147,KUG 1148,KUG 1151,KUG 1152,KUG 1153,KUG 1154,KUG 1155,KUG 1156,KUG 1157,KUG 1158,KUG 1121,KUG

S. NO	Characteristics	Stages of Observation	Expression / States	Note/ Score	Genotype frequency	Percentage contribution	Name of genotype
							1122,KUG 1123,KUG 1141,KUG 1139,KUG 1162,KUG 1163,KUG 1164,KUG 1165,KUG 1167,KUG 1169,KUG 1170,KUG 1171,KUG 1175,KUG 1176,KUG 1177,KUG 1178,KUG 1181,MASH 338
17	Plant: height	Harvest maturity	short(<45cm)	3	95	98.95	KUG 1141,KUG 1139,KUG 1162,KUG 1163,KUG 1164,KUG 1165,KUG 1167,KUG 1168,KUG 1169,KUG 1170,KUG 1171,KUG 1173,KUG 1174,KUG 1175,KUG 1176,JU-3,PDU-1,TJU 45-1,TU-98-14,TJU 139,TJU 328,TJU 213,TAU 2,TJU 18,INDIRA URD 1,TJU 42,PU 19,TJU 134,TU 94-2,TJU 55,TJU 24-10,TJU 41-2,T 9,TJU 103,TJU 62,LBG 20,TJU 262,URDILOCAL,IPU 2-43,TJU 4,TJU 22,TJU 67,TJU 339 (CHECK),TJU 130 (CHECK),TJU 231,TJU 48,TJU 273,TJU 111,TJU 41-1,TJU 84,PU 35,KUG 1149,MASH 114,MASH 479,MASH1137,MASH1008,KUG 1142,KUG 1145,KUG 1146,KUG 1147,KUG 1148,KUG 1151,KUG 1152,KUG 1153,KUG 1154,KUG 1155,KUG 1156,KUG 1157,KUG 1158,KUG 1159,KUG 1160,KUG 1121,KUG 1122,KUG 1123,KUG 1124,KUG 1125,KUG 1126,KUG 1127,KUG 1129,KUG 1130,KUG 1131,KUG 1132,KUG 1133,KUG 1134,KUG 1135,KUG 1136,KUG 1137,KUG 1138,KUG 1140,KUG 1177,KUG 1178,KUG 1179,KUG 1180,KUG 1181,MASH 338
			medium (45-60cm)	5	1	1.04	TJU 24
			long (>60cm)	7	0	0	NIL
18	seed: colour	mature seeds	green	1	1	1.04	URDILOCAL
			greenish brown	2	2	2.08	PDU-1, TJU 67
			brown	3	0	0	NIL
			black	4	93	96.87	JU-3,TJU 45-1,TU-98-14,TJU 139,TJU 328,TJU 213,TAU 2, TJU 18,INDIRA URD 1,TJU 42,PU 19,TJU 134,TU 94-2,TJU 55,TJU 24-10,TJU 41-2,T 9,TJU 103,TJU 62,LBG 20,TJU 262,IPU 2-43,TJU 4,TJU 22,TJU 24,TJU 339 (CHECK),TJU 130 (CHECK),TJU 48,TJU 273,TJU 111,TJU 41-1,TJU 84,PU 35,KUG 1149,MASH 114,MASH 479, MASH1137, MASH1008,KUG 1142,KUG 1145,KUG 1146,TJU 231,KUG 1147,KUG 1148,KUG 1151,KUG 1152,KUG 1153,KUG 1154,KUG 1155,KUG 1156,KUG 1157,KUG 1158,KUG 1159,KUG 1160,KUG 1121,KUG 1122,KUG 1123,KUG 1124,KUG 1125,KUG 1126,KUG 1127,KUG 1129,KUG 1130,KUG 1132,KUG 1133,KUG 1134,KUG 1135,KUG 1136,KUG 1137,KUG 1138,KUG 1140,KUG 1141,KUG 1139,KUG 1162,KUG 1163,KUG 1164,KUG 1165,KUG 1167,KUG 1168,KUG 1169,KUG 1170,KUG 1171,KUG 1173,KUG 1174,KUG 1175,KUG 1176,KUG 1177,KUG 1178,KUG 1179,KUG 1180,KUG 1181,MASH 338
			mottled	5	0	0	NIL
19	seed: lusture	mature seeds	shiny	1	2	2.08	LBG 20,KUG 1132
			dull	2	94	97.91	JU-3,PDU-1,TJU 45-1,TU-98-14,TJU 139,TJU 328,TJU 213,TAU 2,TJU 18,INDIRA URD 1,TJU 42,PU 19,TJU 134,TU 94-2,TJU 55,TJU 24-10,TJU 41-2,T 9,TJU 103,TJU 62,TJU 262,URDILOCAL,IPU 2-43,TJU 4,TJU 22,TJU 67,TJU 24,TJU 339, (CHECK),TJU 130 (CHECK),TJU 231,TJU 48,TJU 273,TJU 111,TJU 41-1,TJU 84,PU 35,KUG 1149,MASH 114,MASH 479,MASH1137,MASH1008,KUG 1142,KUG 1145,KUG 1146,KUG 1147,KUG 1148,KUG 1151,KUG 1152,KUG 1153,KUG 1154,KUG 1155,KUG 1156,KUG 1157,KUG 1158,KUG 1159,KUG 1160,KUG 1121,KUG 1122,KUG 1123,KUG 1124,KUG 1125,KUG 1126,KUG 1127,KUG 1129,KUG 1130,KUG 1131,KUG 1133,KUG 1134,KUG 1135,KUG 1136,KUG 1137,KUG 1138,KUG 1140,KUG 1141,KUG 1139,KUG 1162,KUG 1163,KUG 1164,KUG 1165,KUG 1167,KUG 1168,KUG 1169,KUG 1170,KUG 1171,KUG 1173,KUG 1174,KUG 1175,KUG 1176,KUG 1177,KUG 1178,KUG 1179,KUG 1180,KUG 1181,MASH 338
20	seed: shape	mature seeds	globose	1	3	3.12	TU-98-14,PU 19,TJU 24

S. NO	Characteristics	Stages of Observation	Expression / States	Note/ Score	Genotype frequency	Percentage contribution	Name of genotype
			oval	2	93	96.87	JU-3,PDU-1,TJU 45-1,TJU 139,TJU 328,TJU 213,TAU 2,TJU 18,INDIRA URD 1,TJU 42,TJU 134,TU 94-2,TJU 55,TJU 24-10,TJU 41-2,T 9,TJU 103,TJU 62,LBG 20,TJU 262,URDILOCAL,IPU 2-43,TJU 4,TJU 22,TJU 67,TJU 339 (CHECK),TJU 130 (CHECK),TJU 231,TJU 48,TJU 273,TJU 111,TJU 41-1,TJU 84,PU 35,KUG 1149,MASH 114,MASH 479,MASH1137,MASH1008,KUG 1142,KUG 1145,KUG 1146,KUG 1147,KUG 1148,KUG 1151,KUG 1152,KUG 1153,KUG 1154,KUG 1155,KUG 1156,KUG 1157,KUG 1158,KUG 1159,KUG 1160,KUG 1121,KUG 1122,KUG 1123,KUG 1124,KUG 1125,KUG 1126,KUG 1127,KUG 1129,KUG 1130,KUG 1131,KUG 1132,KUG 1133,KUG 1134,KUG 1135,KUG 1136,KUG 1137,KUG 1138,KUG 1140,KUG 1141,KUG 1139,KUG 1162,KUG 1163,KUG 1164,KUG 1165,KUG 1167,KUG 1168,KUG 1169,KUG 1170,KUG 1171,KUG 1173,KUG 1174,KUG 1175,KUG 1176,KUG 1177,KUG 1178,KUG 1179,KUG 1180,KUG 1181,MASH 338
			drum shaped	3	0	0	NIL
21	seed: size(weight of 100 seeds)	mature seeds	small (<3g)	3	1	1.04	KUG 1135
			medium (3-5g)	5	78	81.25	TJU 45-1,TU-98-1,TJU 139,TJU 328,TJU 213,TJU 18,INDIRA URD 1,PU 19,TJU 134,TU 94-2,TJU 55,TJU 24-10,TJU 41-2,T 9,TJU 103,TJU 62,LBG 20,TJU 262,URDILOCAL,IPU 2-43,TJU 4,TJU 22,TJU 339 (CHECK),TJU 130 (CHECK),TJU 231,TJU 48,TJU 273,PU 35,KUG 1149,MASH1137,MASH1008,KUG 1142,KUG 1145,KUG 1146,KUG 1147,KUG 1148,KUG 1153,KUG 1154,KUG 1155,KUG 1156,KUG 1157,KUG 1159,KUG 1160,KUG 1121,KUG 1122,KUG 1123,KUG 1124,KUG 1125,KUG 1126,KUG 1127,KUG 1129,KUG 1130,KUG 1132,KUG 1133,KUG 1134,KUG 1136,KUG 1137,KUG 1138,KUG 1140,KUG 1141,KUG 1139,KUG 1162,KUG 1163,KUG 1164,KUG 1167,KUG 1169,KUG 1170,KUG 1171,KUG 1173,KUG 1174,KUG 1175,KUG 1176,KUG 1177,KUG 1178,KUG 1179,KUG 1180,KUG 1181,MASH 338
			large (>5g)	7	17	17.7	JU-3,PDU-1,TAU 2,TJU 42,TJU 67,TJU 24,TJU 111,TJU 41-1,TJU 84,MASH 114,MASH 479,KUG 1151,KUG 1152,KUG 1158,KUG 1131,KUG 1165,KUG 1168

(a)Anthocyanin pigment

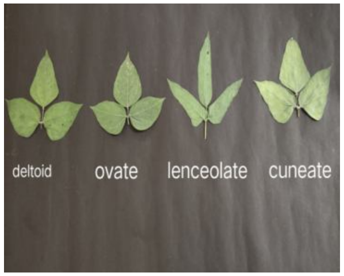
(b)Petiolecolour

(c)Growth habit

(d) Plant height

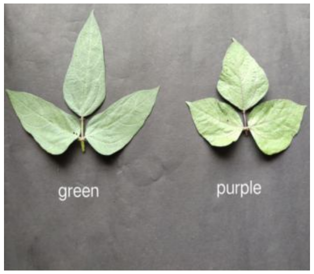
(e)Stem colour

(f)Stem Pubescence

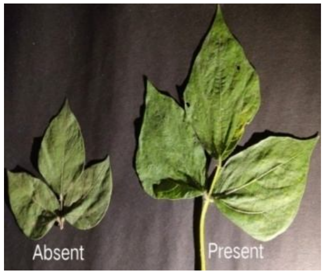


(g)Leaf shape

(h) Foliage Colour

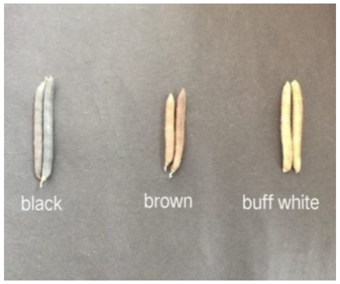


(i)Leaf vein colour



(j) Leaf pubescence

(k)Pod intensity(Premature)

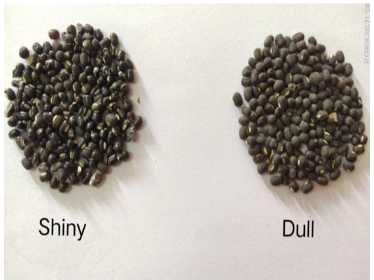


(l) Pod colour

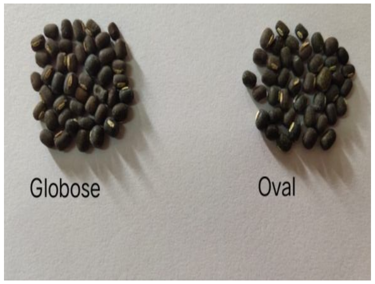
(m) Peduncle length

(n) Pod length

(o)Seed colour



(p)Seedlusture



(q)Seed shape

3.3 Plant Characters

Observations were made on characteristics such as petiole colour, plant habit, growth habit, and height at the stage of 50% flowering and completely grown green pod. These observations can be used as criteria for maintaining and identifying varietal purity. The genotypes were classified into three categories based on the color of their petioles. Out of the total genotypes, one genotype exhibited a green color, 72 genotypes displayed a green color with purple splashes, and 21 genotypes were categorized as purple as shown in Fig. 2(b) and Table 2. Inhis study, (Devi et al., 2019) [4] found that genotypes exhibiting purple petiole pigmentation and purple splashes displayed a resistant to moderately resistant response to Mung bean Yellow Mosaic Virus (MYMV) infection. Conversely, genotypes with green petioles were found to be susceptible to highly susceptible to MYMV infection. The genotypes were categorized into three categories based on the difference in plant growth patterns. There were 4 genotypes classified as erect type, 29 genotypes classified as semi-erect type, and 63 genotypes classified as spreading type as shown in Fig. 2(c) and Table 2. The growth habit of a plant is a distinctive characteristic used in plant classification. The genotypes for this trait in mungbean show similarities, as indicated by (Rai et al., 2024). Erect growth habits are preferred in certain cropping systems, while semi-erect habit balances plant density and air circulation. Spreading growth habits are advantageous in low-input or organic farming systems, but may require more spacing between plants. Genetic differences in factors like internode length, branching patterns, and stem strength could be exploited in breeding programs to develop cultivars with desired growth habits. Typically, plants with an erect growth habit are favored because they receive ample sunlight and effectively produce food for their growth and development. The genotypes were categorized into two categories, determinate and indeterminate, based on variations in plant behaviors. It was observed that all the genotypes belonged to the indeterminate category. Indeterminate genotypes may have a longer growing period and higher yields, but may require more intensive management practices. Determinate genotypes have more predictable growth and better suited for mechanized harvesting. Therefore, selecting genotypes with determinate habit could be appreciated in plant breeding. The attribute of plant height is valuable, and the genotypes were categorized into three groups depending on their plant height: short (45 cm), medium (45-60 cm), and long (> 60 cm). The 95 genotypes exhibited a reduced height, while the 1 genotype had a medium height as shown in Fig. 2(d) and Table 2. No long-statured genotypes were recorded. Genetic differences in factors like internode length, stem strength, and plant architecture contribute to this variation. Short-statured genotypes are preferred in cropping systems or environments with lodging, while medium-height plants may balance yield potential and lodging resistance. The absence of long-statured genotypes suggested either limited genetic diversity or their exclusion from evaluation. This could guide breeding efforts and crop management strategies to develop cultivars better adapted to specific environmental conditions and production systems.

3.4Stem Characters

The color of the stem is a crucial and readily noticeable characteristic for diversity assessment. It is extensively utilized as a genetic marker in genetic research and breeding endeavors. The stem's morphological characteristics, including color and pubescence, were documented when the plant reached the stage of 50% flowering. The genotypes were categorizedinto four classes based on their stem color. One genotype had a green stem, 21 genotypes had green stems with purple splashes, 74 genotypes had purple stems with green splashes, and no genotypes with purely purple stems were detected as mention in Table2 and Fig.2(e).The difference is from pigment biosynthesis and accumulation influenced by genetic factors, environmental conditions, and interactions. Purple pigmentation may offer protection against stress and influence light absorption. Stem may take part in non-foliar photosynthesis contributing up to four percent of total photosynthetic activity(Simkin et al., 2020).This trait can well be used as a marker for varietal identification and registration. The presence of pubescence on the stem is a beneficial characteristic that enhances the plant's resistance to some insect infestations. The classification of Stem Pubescence resulted in two categories: 94 genotypes exhibited pubescence, while pubescence was absent in 2 genotypes as shown in Table2 and Fig.2(f)(Kumar et al., 2024),(Rahangdale et al., 2022)achieved a comparable outcome regarding stem pubescence (Kumari et al., 2022).

3.5Leaf Characters

Leaf morphological characteristics, such as the form of the leaflets, the color of the foliage, the color of the leaf veins, the presence of hair on the leaf, and the color of the petiole, were observed at two specific stages of the plant's growth: when it reached 50% flowering and when the green pods were fully developed. The genotypes' producing ability is significantly influenced by these traits, as the leaves serve as the primary sites for food synthesis and transpiration in plants. The morphology of the leaflets, exhibited significant diversity and was classified into four categories: deltoid, ovate, lanceolate, and cuneate as shown in Table2 and Fig. 2(g).Among the genotypes examined, 19 exhibited a deltoid leaf form, 33 exhibited a lanceolate leaf shape, 31 exhibited an ovate leaf shape, and 13 were found to have a cuneate leaf shape.The presence of plants with lanceolate leaf shape, characterized by narrow leaves, has been found to be linked to drought resistance. Therefore, these plants could potentially be used in the breeding of Urdbean cultivars that are well-suited for rainfed and moisture stress environments (Ghafoor et al., 2001),(Prathyusha et al., 2017),(Soharu et al., 2022),(Tariq et al., 2024).

Differences were noted in features such as foliage color, nine genotypes have green foliage and eighty seven genotypes have dark green foliage colour as shown in Fig. 2(h)and leaf vein color, eighty two genotypes have green leaf vein colour and fourteen genotypes have purple colour, as shown in Fig. 2(i), leaf vein colour is not a primary target trait in blackgram breeding programs, it offers insights into plant health, photosynthetic efficiency, stress tolerance, and genetic marker identification; making it necessary to consider this trait alongside key agronomic characteristics for varietal improvement. The presence of pubescence on the leaf is a significant characteristic that enhances the plant's ability to withstand biotic stressors. In the current investigation, leaf pubescence was found to be absent in 2 genotypes and present in 94 genotypes as shown in Fig. 2(j)(Mallikarjuna et al., 2022),(Chakraborty et al., 2022) in mung.

3.6Pod Characters

The properties of black gram pods are extremely valuable for identifying different genotypes. During the completely grown green pod stage, we noticed characteristics such as the intensity of green color and the presence of fine hairs on the pod. At the harvest maturity stage, we measured the length of the stem that supports the pod, the length of the pod itself, and the color of the mature pod. There was observed variation in all of the traits. By assessing the saturation of the green colour in immature pods. The genotypes were categorized into three classes: 33 genotypes exhibited a yellowish green colour, 35 genotypes had a green colour, and 28 genotypes demonstrated a dark green colour as mention in Table 2 and Fig. 2(k). The dark green color of immature pods contributes to overall crop yield through non-foliar photosynthesis and regulating seed growth and timely maturation (Cho et al., 2023). As a result, dark green pods are favored in yield optimization programs. The genotypes were classified into two categories based on pod pubescence: 15 genotypes had no pubescence, whereas the remaining 81 genotypes had pubescence as mention in Table 2.Genotypes with dense pod pubescence are often preferred for their enhanced tolerance to biotic and abiotic stresses compared to sparsely pubescent or hairless genotypes. A comparable outcome was achieved by (Fukah et al., 2024),(Kumar et al., 2022). During the harvest maturity stage, conducted observations on the length of the peduncle, the length of the pod, and the color of the mature pod. The genotypes were categorized into three classes based on the length of peduncle. Out of the total genotypes, 62 were classified as short, 32 were classified as medium, and only 2 genotypes were classified as long as shown in Fig. 2(m).Peduncle length exhibits a highly significant positive correlation with seed yield (Kumar et al., 2022), suggesting that longer peduncles are advantageous for yield optimization programs.The genotypes were classified into two groups according to pod length: small (5 cm) with 89 genotypes and medium (7 cm) with 7 genotypes as shown in Fig. 2(n). Pod length shows high significant positive correlation with seed yield (Kumari et al.2022) and negatively correlated with pod shattering (Gawhane et al., 2022). Hence, variation in this character may rightly be utilized to select genotypes for various breeding objectives. The genotypes were classified into three categories, namely buff, brown, and black, based on the color of their mature pods. There were 2 genotypes with a buff color (off white), 12 genotypes with a brown color, and 82 genotypes with a black colour as shown in Fig. 2(l). The selection of mature pod color may be influenced by consumer preferences or traditional beliefs, with certain pod colors favored for culinary uses or cultural practices.

3.7Seed Characters

The cost of premium genotypes and customer acceptability of a variety are determined by the features of black gram seeds, such as their color, luster, size, and form. The present experiment include the observation of seed morphological characteristics such as color, luster, size, and form at the mature seed stage of the plant. The key morphological characteristic utilized to distinguish between greengram and Urdbean is the color of their seeds. The current experimental material may be categorized into five classes based on seed colour: green, greenish brown, brown, black, and mottled. Among the genotypes, no mottled and brown type seed color was detected, while there were 2 genotypes with greenish brown seed color, and 93 genotypes with black seed color and 1 genotype with green as shown in Fig. 2(o). The consumer preference for attractive seed color is driven by its ability to command a higher market price along with thisseed coat color serves as an important genetic marker for identifying genotypes. It is determined by the accumulation of anthocyanin in the outer layer of the seed coat. Studies reveal that only black and dark brown seeds contain three variants of anthocyanin pigments, while two are absent in other seeds. The lack of anthocyanin pigments could suggest an imbalance between their biosynthesis and degradation.Therefore, breeders may prefer black-seeded genotypes that can accumulate high levels of anthocyanin, highlighting the plant's capacity to withstand biotic and abiotic stresses due to the antioxidant properties of anthocyanins.The genotypes were categorized into two groups based on seed lustre: shining, consisting of 2 genotypes, and dull, consisting of the remaining 94 genotypes as shown in Fig. 2(p). The genotypes were categorized into three classes based on seed form: globose (3 genotypes), oval (93 genotypes), and no genotypes were discovered with a drum shape as mention in Table 2 and Fig.2(q).A shiny seed surface is the result of monogenic dominant gene action, contrasting with dull seed luster(Nair et al., 2023)and (Gupta et al., 2023).The deposit on the seed surface may be undesirable, as it generates 'seed dust' that can trigger allergies. The relationship between seed luster and seed quality remains unexplored.Sometime, the present genotypes were categorized into three groups according to seed size: small (<3 g) with 1 genotype, medium (3-5 g) with 78 genotypes, and large (>5g) with 17 genotypes. Additional research was conducted by (Singh et al., 2020) on urdbean genotypes, and by (Tripathy et al., 2011).DUS testing serves multiple purposes, including the identification of varieties, registration of varieties under the Plant Variety Protection (PVP) Act, establishment of a varietal information system, classification of varieties into distinct groups, and preservation of genetic resources. The observed diversity in the existing genetic resources must be conserved to safeguard the intellectual property rights of the genetic information in the species. consisting of 96 different genotypes. DUS testing is valuable for the identification, registration, and protection of plant varieties under the Plant Variety Protection (PVP) Act. It is also utilized for the establishment of a varietal information system, classification of varieties into distinct groups, and the preservation of genetic resources. The observed diversity in the existing genetic resources must be conserved to safeguard the intellectual property rights of the genetic material in the species.

4.CONCLUSION

The study conducted on 96 Urdbean genotypes has uncovered substantial morphological variation, which is essential for enhancing genetic traits and developing breeding plans. The key findings reveal that anthocyanin pigmentation is universally present in the hypocotyl, suggesting its usefulness in genetic study. The majority of genotypes displayed early flowering, indicating possible resistance to environmental pressures. Distinct differences in the color of the petiole, the presence of hair on the stem, and the way the plant grows are indicative of features that play a crucial role in resisting diseases and adapting to the environment. The shape and hairiness of leaves, particularly the shape of leaflets and the presence of fine hairs, have a notable impact on the production of food and the ability to withstand stress. The properties of the pod, including as its color and pubescence, serve as significant indicators for distinction. Seed characteristics such as color, shine, and dimension are crucial for the marketability and consumer choice. In summary, this work highlights the significance of these morphological traits in improving the utilization, identification, and preservation of germplasm, which is crucial for the future advancement of Urdbean cultivars.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Please write this section

Option 1:

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

Option 2:

Author(s) hereby declare that generative AI technologies such as Large Language Models, etc have been used during writing or editing of this manuscript. This explanation will include the name, version, model, and source of the generative AI technology and as well as all input prompts provided to the generative AI technology.

Details of the AI usage are given below:

1.
2.
3.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

Chakraborty, A., Bordolui, S. K., & Nandi, D. (2022). Characterization of the green gram (*Vigna radiata* L.) genotypes through both morphological and biochemical parameters. *Environment Conservation Journal, 23*(3), 1–7.

Cho, Y. B., Stutz, S. S., Jones, S. I., Wang, Y., Pelech, E. A., & Ort, D. R. (2023). Impact of pod and seed photosynthesis on seed filling and canopy carbon gain in soybean. *Plant Physiology, 193*(2), 966–979.

Dar, S. A., Khan, M. H., Hussain, J., Dar, N. A., Alie, B. A., Mehvish, S., &Fayaz, U. (2024). Association and variability of morphological, yield, and yield attributing traits in mung bean (*Vigna radiata* L.) Wilezek. *Indian Journal of Plant Genetic Resources, 37*(03), 494–501.

Devi, H. C., Kumari, V. P., & Devi, P. S. (2019). Morphological and phenotypic variability in Urdbean genotypes with varying reaction to mungbean yellow mosaic virus infection. *Journal of Pharmacognosy and Phytochemistry, 8*(4), 1606–1610.

Dhanraj, D., Sruthi, S. R., &Anbuselvam, Y. (2024). DUS characterization of Urdbean (*Vigna mungo* L.) Hepper genotypes using morphological characters and clustering them using Mahalanobis D2 analysis. *Indian Journal of Natural Sciences, 15*.

Fukah, F. K., Magubika, A. J., Tryphone, G. M., &Nassary, E. K. (2024). Meta-analysis of legumes and groundnut production trends and variability in the Global South. *Journal of Agriculture and Food Research*, 101–501.

Gawhane, A. B., Girase, V. S., &Andhali, G. R. (2022). Evolution of Urdbean local germplasm for seed shattering resistance. *The Pharma Innovation Journal, 11*(10), 95–98.

Ghafoor, A., Sharif, A., Ahmad, Z., Zahid, M. A., & Rabbani, M. A. (2001). Genetic diversity in Urdbean (*Vigna mungo* L. Hepper). *Field Crops Research, 69*(2), 183–190.

Gupta, D., Kumar, J., Lamichaney, A., Parihar, A. K., Das, S. P., Kumar, A., & Gupta, S. (2023). Genetics for seed traits and mungbean yellow mosaic India virus reaction in urdbean (*Vigna mungo* L. Hepper). *Legume Science, 5*(2), e180.

International Board for Plant Genetic Resources (IBPGR). (1985). Descriptors for *Vigna mungo* and *Vigna radiata* (Revised). Rome.

Jayamani, P., Srimathy, M., & Sathya, M. (2014). Characterization of Urdbean genotypes based on qualitative traits (*Vigna mungo* L. Hepper). *Madras Agricultural Journal, 101*(1-3), 12–15.

Jegadeesan, S., Raizada, A., Dhanasekar, P., &Suprasanna, P. (2021). Draft genome sequence of the pulse crop Urdbean (*Vigna mungo* L. Hepper) reveals potential R-genes. *Scientific Reports, 11*(1), 11247.

Kumar, P., Singh, S. K., Shukla, R. S., Elahi, T., Prajapati, S. S., &Rahangdale, S. (2022). Morphological characterization for important breeding traits in Urdbean(*Vigna mungo* L. Hepper). *Biological Forum – An International Journal, 14*(2), 1323–1330.

Kumar, V., Rana, L., Ram, S., Salam, J. L., & Kumar, P. (2024). Morphological characterization and assessment of genetic variability in black gram (*Vigna mungo* L.) germplasm at Bastar plateau.

International Journal of Advanced Biochemistry Research, 8(6), 101–110.

Kumari, G., Shanmugavadivel, P. S., Lavanya, G. R., Tiwari, P., Singh, D., Gore, P. G., & Pratap, A. (2022). Association mapping for important agronomic traits in wild and cultivated *Vigna* species using cross-species and cross-genera simple sequence repeat markers. *Frontiers in Genetics, 13*, 1000440.

Mallikarjuna, G., Rao, K. N., Srinivas, T., Ramesh, D., &Tushara, M. (2022). Morphological characterization and genetic diversity studies in Urdbean. *Environment and Ecology, 40*(2C), 1028–1035.

Nair, R. M., Chaudhari, S., Devi, N., Shivanna, A., Gowda, A., Boddepalli, V. N., &Somta, P. (2024). Genetics, genomics, and breeding of black gram (*Vigna mungo* L. Hepper). *Frontiers in Plant Science, 14*, 1273363.

Prathyusha, V. B., Rao, Y. K., Rao, G. P., Prasanthi, L., Hari, Y., Mallikarjuna, G., &Bentur, J. S. (2017). SSR polymorphism and distinctiveness, uniformity and stability (DUS) features in selected genotypes of Urdbean (*Vigna mungo* L. Hepper). *Journal of Food Legumes, 30*(2), 1–8.

Rahangdale, S., Singh, S. K., Lakhani, J. P., Prajapati, S. S., & Kumar, P. (2022). Morphological characterization and new variation in compound leaf of mungbean (*Vigna radiata* L. Wilczek) genotypes. *Electronic Journal of Plant Breeding, 13*(4), 1354–1364.

Rai, N. K., Yadav, R., & 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: An International Journal, 47*(3).

Rajasekhar, D., & Lal, G. M. (2020). Genetic diversity studies of Urdbean genotypes growing in northern India. *Journal of Experimental Biology and Agricultural Sciences, 8*(3), 265–268.

Simkin, A. J., Faralli, M., Ramamoorthy, S., & Lawson, T. (2020). Photosynthesis in non-foliar tissues: Implications for yield. *The Plant Journal, 101*(4), 1001–1015.

Singh, A. K., Biswas, U., Kumar, R. R., Swain, S., &Swarnam, T. P. (2020). Morphological diversity among farmers' varieties of Urdbean (*Vigna mungo* L.) of Andaman and Nicobar Islands agro-ecosystem. *Legume Research: An International Journal, 43*(2), 2–8.

Soharu, A., Mittal, R. K., Sood, V. K., & Kaur, N. (2022). Morphological characterization and evaluation of Himalayan landraces of Urdbean (*Vigna mungo* L.) from North-Western plain zone for yield and its component traits. *Himachal Journal of Agricultural Research, 48*(2), 157–165.

Tariq, K., Ali, G., Dar, Z. A., Shikari, A., & Hamid, A. (2024). DUS characterization of Rajmash (*Phaseolus vulgaris* L.) genotypes for morpho-physiologicaltraits under rainfed conditions.*Legume Research: An International Journal*, 1–13.

Tripathy, S. K., Sardar, S. S., Lenka, D., Rajesh, R., & Mishra, D. R. (2011). Identification of germplasm lines for stable morphological marker traits and selection strategy for high productivity in mungbean (*Vigna radiata* L. Wilczek). *Environment and Ecology, 29*(3A), 1376–1379.
