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RESEARCH ARTICLE

Vigna mungo var. *gadmalensis* – A New Variety from Madhya Pradesh, Central India

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Abstract

A new taxon, *Vigna mungo* (L.) Hepper var. *gadmalensis* K. Tripathi, Pamarthi & Wankhede (Fabaceae), is reported and described from the Satpura Plateau region of India. It has historical and agricultural significance in the tribal-dominated areas of the Betul district, Madhya Pradesh, owing to its endemic adaptation and distribution. Morpho-anatomical and molecular tools were used to identify the new taxon. Morphologically, it closely resembles *V. mungo* var. *mungo* (L.) Hepper, but can be readily distinguished by its purple-colored stems, longer pod hair, brownish-grey seed colour, and smooth seed texture. Phylogenetic analysis of the Internal Transcribed Spacer (ITS) region confirms its distinctiveness and indicates its relationship with the typical variety. This study presents a comprehensive description, comparative analysis, identification key, and notes on the species distribution.

Keywords: Betul, Endemic, Gadmal, Madhya Pradesh, Pulse crop, *Vigna mungo* var. *gadmalensis*

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Introduction

The pantropical genus *Vigna* Savi belongs to the family Fabaceae and comprises 106 species (POWO, 2025), distributed among seven subgenera: *Ceratotropis, Haydonia, Lasiosporon, Macrorhyncha, Plectotropis, Sigmoidotropis*, and *Vigna* (Yadav *et al.,* 2014). In India, the genus is represented by 34 taxa (Babu *et al*., 1985; Sanjappa, 1992, 2020; Jalander and Swamy, 2023), of which 16 taxa are endemic to the country. Crop wild relatives hold significant potential for crop improvement programmes, including the development of resistant lines to address biotic and abiotic stresses and the creation of hybrids (Stolon *et al*., 2006; Pradheep *et al*., 2021; Nallavelli *et al.,* 2026). According to Singh *et al.* (2017), there are 958 crop wild relative species of cereals, millets, legumes, oilseeds, fibres, vegetables, tubers, fruits, spices, condiments, and medicinal and aromatic plants that are related to cultivated species and have great potential for crop improvement. Pradheep *et al.,* (2021) enumerated 861 taxa, including 150 crop species belonging to 14 different crop groups. India serves as a secondary centre of species diversity for the subgenus *Ceratotropis*, also known as Asian *Vigna* (Yadav *et al*., 2014). This subgenus includes eight cultivated species primarily used for their seeds, pods, or forage production, particularly in Asian countries. Taxonomically, *Ceratotropis* is divided into three sections: *Angularis, Aconitifolia*, and *Ceratotropis* (Tomaso *et al*., 2011).

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The genus *Vigna* belongs to the tribe Phaseoleae and is significant within the pulse group, comprising nearly 200 wild and cultivated species (Gore *et al*., 2022a; Tripathi *et al*., 2024). In India, seven crop taxa of *Vigna* are cultivated, namely *V. aconitifolia* (Jacq.) Marechal, *V. angularis* (Willd.) Ohwi & Ohashi, *V. mungo* (L.) Hepper, *V. radiata* (L.) R. Wilczek, *V. unguiculata* (L.) Walp. subsp. *unguiculata*, *V. unguiculata* subsp. *sesquipedalis* (L.) Verdc., and *V. umbellata* (Thunb.) Ohwi & Ohashi. These taxa are cultivated across various states of the country. According to Pradheep *et al.,* (2021), certain *Vigna* species, such as *V. mungo* and *V. radiata*, have been prioritized for future collections in India. Among these, *V. mungo,* commonly known as black gram, urd, urad, or mash, is an important grain legume. *V. mungo* originated and was domesticated in India from its wild progenitor, *V. silvestris* Lukoki, Marechal & Otoul (Chandel *et al*., 1984; Gore *et al*., 2022a). The National Genebank (NGB) at ICAR-NBPGR, New Delhi, India, houses approximately 15,113 accessions of the *genus Vigna, including* wild species (Gore *et al*., 2022b). This study reports a distinct taxon within the genus *Vigna* and attempts to establish its taxonomic identity.

Materials and Methods

Field study

During a field survey conducted in Betul, Madhya Pradesh (Fig. 1), a local landrace named 'Gadmal', cultivated since ancient times, was collected in 2022. A thorough study of all *Vigna* species in India, including protologues, type specimens, and other herbarium specimens from CAL, BSA, BSD, BSI, BSID, MH, and NHCP, along with relevant taxonomic literature (Yadav *et al*., 2014; Sanjappa, 1992, 2020; POWO, 2025), revealed that this taxon is new to science. The specimens were processed, and the type specimens were deposited in the NHCP. Photographic plates of the new taxon were prepared (Fig. 2 and Fig. 3) to illustrate the features of different plant parts. Additionally, an identification key was prepared.

Experimental studies

The collected seeds were grown at the ICAR-NBPGR experimental farm for characterization. For evaluation studies, additional seeds were obtained from the National Genebank, New Delhi. The closely related species *V. mungo* var. *mungo* was used as reference material for comparative studies with the newly described taxon. Field observations were recorded in accordance with the ICAR-NBPGR minimal descriptors for the *Vigna* group (Mahajan *et al*., 2000).

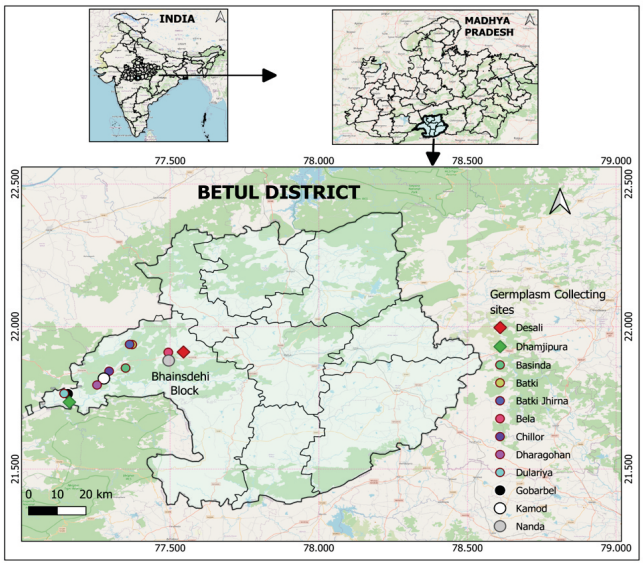


Fig. 1: Occurrence map of *Vigna mungo* var. *gadmalensis* var. nov. in Betul district, Madhya Pradesh, India.
The collecting-site map was prepared using QGIS.

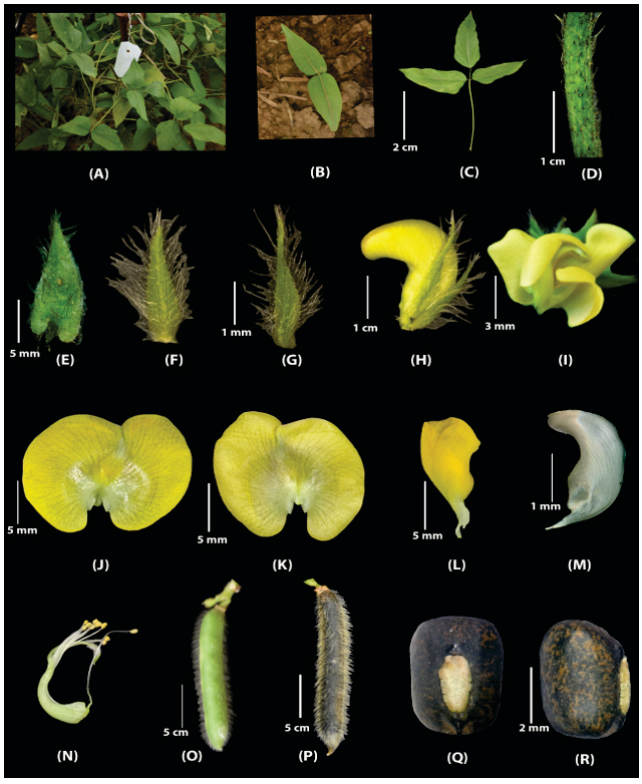


Fig. 2: *Vigna mungo* var. *mungo* (L.) Hepper: (A) Plant; (B) Two leaf stage; (C) Leaflet; (D) Stem; (E) Stipule; (F) Bract; (G) Bracteole; (H) Bud; (I) Flower; (J) Standard petal; (K) Standard petal – back view; (L) Lateral petal; (M) Keel petal; (N) Anthers and ovary; (O) Immature pod; (P) Mature pod; (Q) Single seed – hilum view; (R) Single seed – lateral view.

Morphological descriptors

Morphological observations and measurements were made on both freshly collected and dried specimens. All morphological characters were recorded using a

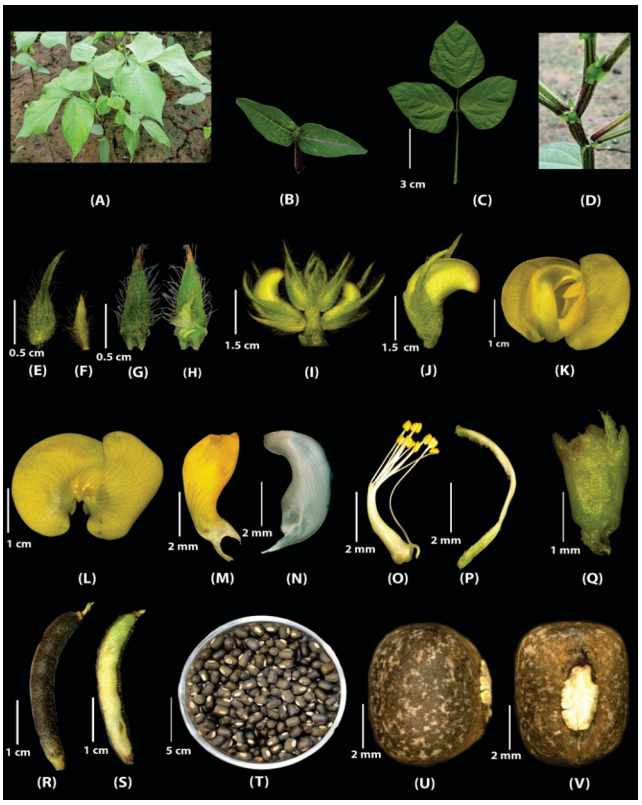


Fig. 3: *Vigna mungo* var. *gadmalensis* var. nov. (A) Plant; (B) Two leaf stage; (C) Leaflet; (D) Stem; (E) Primary bract; (F) Bracteole; (G) Stipule outer view; (H) Stipule-axial view; (I) Inflorescence; (J) Bud; (K) Flower; (L) Standard petal; (M) Lateral petal; (N) Keel petal; (O) Anthers; (P) Style and stigma; (Q) Calyx; (R) Immature pod; (S) Mature pod; (T) Seeds; (U) Single seed – lateral view and (V) Single seed – hilum view.

standard centimetre scale (CS). A Nikon D3500 DSLR camera was used to capture high-quality photographs of various plant parts. High-contrast images of leaves and immature and mature pods were produced using a flatbed scanner (HP Scanjet G3110). Micromorphological observations were made using a dissecting Stereo microscope (Leica S9i), and images were captured with a Leica S9i microscope-mounted camera using LasX software. For scanning electron microscopy (SEM), the seeds were dried and mounted on aluminium stubs using double-sided sticky carbon tape. The samples were then coated with gold/palladium. Images of the seed coat surface were captured at different scales (20 µm and 50 µm) using a Scanning electron microscope (TESCANVEGA3).

Leaf anatomical studies

Leaf samples from the midrib portion were used for anatomical studies. Cross sections were prepared using a microtome (Leica BM2165) after wax fixation. During staining, dried samples were treated with xylene and left for 12 hr. Subsequently, the samples were subjected to repeated washing with different staining solutions in the following sequence: xylene, absolute alcohol (1:1), 95% alcohol, 70% alcohol, A50% alcohol, safranin (45 min), 50% alcohol, 70% alcohol, 95% alcohol, fast green, 95% alcohol, xylene: absolute alcohol (1:1), and pure xylene. The final slides were prepared using the PX mount solution. Permanent slides were observed, and images were captured using a light microscope (Olympus BH-2).

Phylogenetic analysis using the nuclear ribosomal internal transcribed spacer (ITS) sequence

Leaf samples for genomic DNA (gDNA) extraction were collected from one-month-old seedlings raised from single-plant progeny in the Crop wild relative garden. Genomic DNA was extracted using a DNeasy Plant Mini Kit (Qiagen). Initially, the leaf tissue was ground in liquid nitrogen and then processed for DNA isolation according to the manufacturer's instructions. The quality and quantity of purified DNA were assessed by 1% agarose gel electrophoresis and spectrophotometry (Analytik, Jena, Germany). The ITS genomic region (ITS1 and ITS2) of *V. silvestris* and *V. mungo* var. *gadmalensis* was amplified using plant-specific universal primers (NS7: 5'-GAGGCAATAACAGGTCTGTGATGC-3' and 28KJ: 5'-GGACGGAATTTACCGCC-3'). The thermal profile for PCR amplification consisted of one cycle at 94°C for 5 min, followed by 30 cycles of 94°C for 45 s, annealing at 55°C for 45 s, and extension at 74°C for 45 s, with a final extension at 72°C for 7 min. The PCR product was electrophoresed on a 1.2% agarose gel, and the desired product was gel-eluted using a DNA Gel Elution Kit (Qiagen). The purified amplicon was subjected to DNA sequencing on an ABI 3730 DNA sequencer (Applied Biosystems) using forward and reverse PCR primers. Three samples of the eluted PCR product were sequenced separately using forward and reverse primers for comparison and to avoid sequencing errors. The final sequence was constructed by matching all forward and reverse sequences in triplicate using multiple alignments (MultAlin; Corpet, 1988), comparing them with the respective electropherograms, and manually curating them. ITS sequences of other *Vigna* species were downloaded from NCBI. The plant species and their accession numbers are provided. *V. mungo* var. *mungo* (JX233500.1), *V. angularis* (JF430407.1), *V. radiata* (JF430409.1), *V. aconitifolia* (JX233501.1), *V. radiata* var. *sublobata* (MK372017.1), *V. reflexopilosa* var. *glabra* (JN008297.1), *V. reticulata* (KX057911.1), *V. riukiuensis* (LC414525.1), *V. trilobata* (JN008298.1), *V. umbellata* (JF430411.1), and *V. unguiculata* (AY748429.1) were included in the analysis. The ITS sequence of *Cajanus*

cajan (MK253074.1) was used as the outgroup. Multiple pairwise alignments were performed using T-Coffee (Tommaso *et al.*, 2022), and genetic distances and evolutionary history were inferred using the Maximum Likelihood method based on the Jukes-Cantor model in MEGA 11 (Tamura *et al.*, 2021).

Results and Discussion

The morphological description of the collected specimen, locally known as the landrace "Gadmal", did not match any existing taxa of *Vigna*. It showed a close resemblance to *V. mungo* var. *mungo,* but differed in distinct morphological features; therefore, it is proposed here as a new taxon under the species *V. mungo*.

Taxonomic treatment

Vigna mungo (L.) Hepper var. *gadmalensis* K. Tripathi, Pamarthi & Wankhede, var. *nov.* (Fig. 3, Fig. 4 & Fig. 5).

Type: INDIA. Madhya Pradesh: Damjipura, Betul District, *Kuldeep Tripathi* (Holo: [HS27298] NHCP, Iso:[HS27300]: NHCP: CAL, Paratype: [HS27299] NHCP).

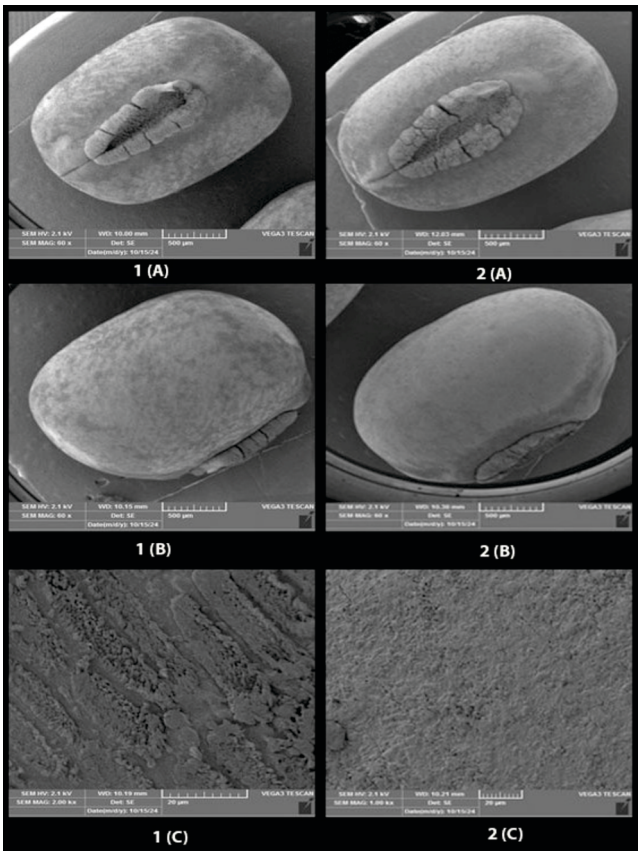


Fig. 4: Comparison of Scanning Electron Microscope (SEM) micrographs of *Vigna mungo* var. *mungo* (1A, B & C) and *V. mungo* var. *gadmalensis* (2A, B & C).

Vigna mungo var. *gadmalensis***,** Tripathi K, Pamarthi & Wankhede, var. nov.

Diagnosis: The new variety is most similar to *V. mungo* var. *mungo* (L.) Hepper (Fig. 2), but differs in its procumbent growth habit (vs. erect and twining habit), the presence of dense tufts of hairs on the stem surface (vs. sparse hairs), and hirsute hairs on the stem surface (vs. stellate hairs).

Procumbent herb, 40–80 cm long, entirely covered with dense whitish-yellow pubescence. Stems solid, woody, slender, green to purple; lateral branches 5–11. Leaves 3-foliolate, pubescent; terminal leaflet obliquely ovate, with purple veins; petioles slightly purple. Stipules elliptic-lanceolate, medifixed, 12–14 × 3–4 mm. Inflorescence 5 - or 6 - flowered; flowers yellow, *c.* 2.5 × 3.5 cm; standard 1.2–1.4 cm; lateral petals *c.* 1.1 × 0.5 cm; keel petals *c.* 1.4 × 2.2 cm; keel pocket present on one side, *c.* 0.4 cm; peduncles 14–16 cm long. Pods cylindrical, 4.9–5.2 cm long, green and densely pubescent when young, slightly curved to straight at maturity, dark brown to slightly black, 5–7-seeded. Seeds oval, 4–5.5 mm long, mottled, dark brown; hilum prominently visible. Flowering begins 38–44 days after sowing, whereas pod maturation occurs in 70–75 days. The morphological comparison between *Vigna mungo* var. *mungo* and *V. mungo* var. *gadmalensis* var. *nov.* is presented in Table 1.

Table 1: Morphological comparison between *Vigna mungo* and *V. mungo* var. *gadmalensis* var. *nov.*

Characters	*Vigna mungo* var. *mungo*	*Vigna mungo* var. *gadmalensis* var. *nov.*
Plant habit		
Growth	Erect	Procumbent
Pubescence on	Moderately	Densely
plant body	pubescent	pubescent
Leaflet		
Terminal leaflet	Acute to obliquely oblong	Oblong
Stem		
Pubescence	Moderately pubescent	Densely pubescent
Nature of hairiness	glabrous on adaxial surface	Hirsute
Colour	Green	Purple
Seed		
Seed surface	Rough	Smooth
Testa texture	Rough	Smooth
Size	Small to medium	Bold seeds
Colour	Black	Brownish grey

Distribution and habitat: The new variety is found exclusively in Betul district, Madhya Pradesh, India, indicating its photo- and thermo-sensitivity. It thrives in loamy soils in dry, open deciduous lands at elevations ranging from 300 to 400 m. Local farmers have cultivated it as a pulse crop for a long time, but only within its niche area.

Etymology: The epithet "*gadmalensis*" is derived from "Gadmal", the local name for this pulse, as used by the people of Betul, Madhya Pradesh.

Phenology: Flowering begins in October and peaks in November and December. Pods are produced from October to November and mature between mid-December and mid-January.

Key to the varieties

1a. Seeds black, surface rough ..... *V. mungo* var. *mungo*

1b. Seeds brownish grey, surface smooth ..... *V. mungo* var. *gadmalensis*

Leaf anatomy

In *Vigna mungo* var. *gadmalensis*, the transverse section (TS) of the leaf shows a dorsiventral structure. The epidermis consists of small cubical cells covered by a thick cuticle. The mesophyll is composed of small spongy tissue cells. Vascular bundles containing xylem and phloem are present, with individual bundles arranged in the midrib region for the efficient transport of nutrients and minerals (Fig. 5).

Seed morphology

External seed morphology is an important taxonomic feature in *Vigna* species (Nath and Dasgupta, 2015). Kumar and Rangaswamy (1984) studied the seed surfaces of several cultivated and wild *Vigna* species. The puncticulate seed-surface type is found in both *V. mungo* and *V. silvestris* (Nath and Dasgupta, 2015). The seeds of *V. silvestris* are small, rough, and prominently striated, ranging in colour from brown to maroon (Yadav *et al*., 2014). A study on seed-coat morphology in 21 Indian *Vigna* species highlighted its taxonomic significance (Umdale *et al*., 2017). The newly described taxon, *V. mungo* var. *gadmalensis*, has bold, oval-shaped seeds measuring 4–5.5 mm, in contrast to the smaller seeds of *V. mungo* var. *mungo*. The seed surface of *V. mungo* var. *gadmalensis* is smooth and mottled dark brown, whereas that of *V. mungo* var. *mungo* is rough (Fig. 4). Additionally, the hilum is prominently visible in the newly described taxon.

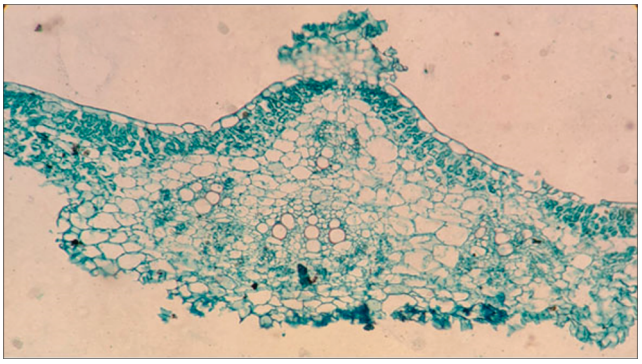


Fig. 5: Transverse section (TS) of the leaf midrib area of *Vigna mungo* var. *gadmalensis* var. nov.

Phylogenetic analysis using ITS1, and ITS2

The phylogenetic tree was constructed using the nuclear ribosomal internal transcribed spacer sequences (ITS1 and ITS2) of the new variety (NCBI GenBank Acc. No. PV083118) and *V. silvestris* (NCBI GenBank Acc. No. PX459862), which were generated in this study, along with sequences of ten other related *Vigna* species and *Cajanus cajan* downloaded from NCBI. Accordingly, the final dataset comprised 12 nucleotide sequences and 1023 positions. Evolutionary analysis was performed in MEGA11 (Tamura *et al*., 2021). The Maximum Likelihood method and the Jukes-Cantor model (Jukes and Cantor, 1969) were used to infer evolutionary history. The tree with the highest log-likelihood (-3866.20) is shown in Fig. 6. The percentage of trees in which the associated taxa clustered together is shown next to the branches.

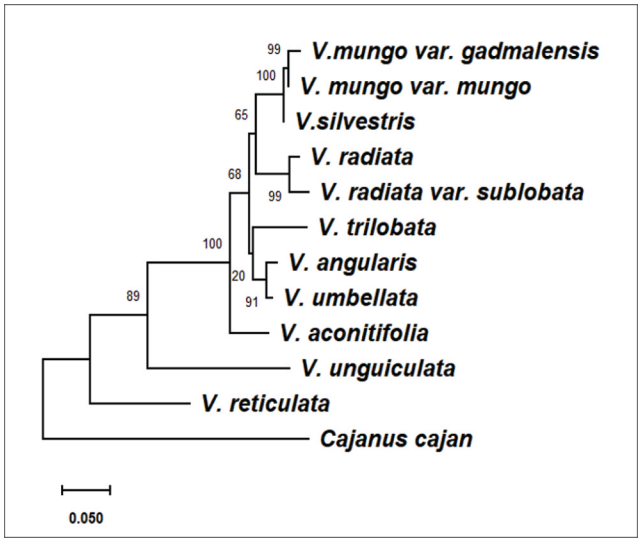


Fig. 6: Molecular phylogeny analysis using the Maximum Likelihood method using the multiple sequence alignment of nuclear ribosomal ITS1 and ITS2 sequences of 12 taxa, showing the distinctness of the newly described taxon *Vigna mungo* var. *gadmalensis*. *Cajanus cajan* (L.) Huth was used as an out-group.

The phylogenetic tree of the studied *Vigna* species showed that *V. reticulata* formed the first major clade, separating from the other *Vigna* species. The next split separated the subgenus *Vigna* (*V. unguiculata*, cowpea) from *Ceratotropis* (other *Vigna* species). The *Ceratotropis* branch further diverged into *V. aconitifolia* (moth bean), *V. trilobata*, and a subgroup comprising *V. umbellata* (rice bean) and *V. angularis* (adzuki bean), with high bootstrap support (94%). The topmost cluster contained *V. radiata* var. sublobata and *V. radiata* (mung bean), which were closely related with 99% bootstrap support. *Vigna mungo* var. *mungo* (black gram), *V. mungo* var. *gadmalensis* (Gadmal), and *V. silvestris* showed a very close relationship with 100% bootstrap support. *Cajanus cajan* (pigeon pea) served as the outgroup in the phylogenetic tree. Thus, based on ITS sequence analysis, the newly described taxon, *Vigna mungo* var. *gadmalensis*, is closely clustered with *Vigna mungo* var. *mungo* (black gram). However, its clear morphological distinctiveness supports its recognition; therefore, it has been categorised as a new taxon.

Traditional use and conservation status

Locally referred to as Gadmal, this pulse is commonly cultivated by tribal farmers in Betul district, Madhya Pradesh. Gadmal is used in various forms, including as a split pulse and in the preparation of chapatis and local vada. Recipes prepared from this pulse are also commonly served by tribal communities on religious occasions (Tripathi *et al*., 2024). *Vigna mungo* var. *gadmalensis* var. nov. is known from its type locality in Betul district, Madhya Pradesh, India. During plant surveys and explorations conducted in 2022 and 2023, approximately 12 locations were documented. Some anthropogenic threats have been observed in this area due to the expansion of cultivated land.

Although Gadmal is regarded as an important traditional pulse, its cultivation area is rapidly declining due to its high susceptibility to yellow mosaic disease (YMD) (Tripathi *et al*., 2024). ICAR-NBPGR has collected seed samples and deposited them at the National Genebank (NGB), New Delhi, India. In addition, herbarium specimens (HS27298, HS27299 & HS27300) have been deposited in the National Herbarium of Cultivated Plants (NHCP), ICAR-NBPGR, New Delhi.

Conclusion

Vigna mungo var. *gadmalensis* is described here as a new variety based on morphological features derived from both live specimens and herbarium collections, complemented by molecular characterization. This new variety is reported as the first of its kind and is endemic to Madhya Pradesh. Samples of this taxon collected during field explorations will be designated under this new name and conserved as seeds in the National Genebank (NGB) in New Delhi for future crop improvement programmes.

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