ICAR

PULSES
NEWSLETTER
ICAR-Indian Institute of Pulses Research, Kanpur

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Annual Group Meet of *Kharif* Pulses organized at UAS, GKVK, Bengaluru

The University of Agricultural Sciences (UAS), Bengaluru, successfully hosted the Annual Group Meet (AGM) of *Kharif* Pulses at its GKVK campus from May 5–7, 2026 to review research progress and design a comprehensive future roadmap for India's *kharif* pulses sector. The three-day event drew

over 220 researchers, policymakers and diverse agricultural stakeholders from across the nation to deliberate on emerging issues surrounding crucial crops like pigeonpea, mungbean, urdbean, rajmash, cowpea, mothbean and clusterbean. The inaugural session was chaired by Dr. M.L. Jat, Secretary, DARE and Director General of ICAR, with Dr. S.V. Suresha, Vice-Chancellor of UAS, Bengaluru, serving as the Chief Guest. The session was co-chaired by Dr. D.K. Yadava, Deputy Director General (Crop Science) while Sh. Sanjay Agarwal, Joint Secretary, National Pulses Mission (DAFW, GoI) attended as the Guest of Honour.

In his inaugural address, Dr. M.L. Jat stressed on the vital need to transition towards pulse-based agri-food systems to enhance environmental sustainability and climate resilience, ensuring these systems align closely with market trends and value chains. He endorsed the widespread adoption of raised-bed sowing in farmers' fields and the implementation of combined yield-enhancement practices, such as using biologicals for pest and disease management and specialized seed treatment agents to boost productivity. Emphasizing translational research, Dr. Jat called for the wide adoption of newly released crop varieties tailored to optimize potential yields across diverse agroclimatic zones noting that a curated portfolio of the best practices is essential to bridge existing on-farm yield gaps. Furthermore, he highlighted the urgency of advancing seed system research and envisioned a modern data ecosystem for the precise prediction of crop pests and disease infestations. Complementing this vision, Dr. S.V. Suresha drew attention to the low productivity of pulses in Karnataka, urging the scientific community to develop profitable and sustainable production models that directly elevate local farmers' income.

Detailing the scientific trajectory, Dr. D.K. Yadava reviewed the national status of *kharif* pulses and highlighted recent research milestones. Given current geopolitical challenges and India's heavy reliance on imported Di-Ammonium Phosphate (DAP) fertilizer, Dr. Yadava strongly advocated for integrating Nutrient

Use Efficiency (NUE) directly into breeding programmes. He suggested focusing on high-yielding varieties that possess robust resistance or tolerance to multiple biotic and abiotic stresses. To modernize operations, the DDG instructed plant breeders to adopt product-profile-oriented breeding approaches, integrate predictive breeding tools, and digitize real-time field data collection. He also proposed expanding the number of testing locations per zone to accelerate the overall process of varietal identification and release. The meet also featured key administrative updates and strategic overviews from other senior officers. Sh. Sanjay Agarwal updated the audience on the National Pulses Mission's target of

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achieving a 15% yield enhancement to reduce the country's import dependency, while Dr. Sanjeev Jha, ADG (O&P) at ICAR, prioritized keeping a farmer-centric focus in all upcoming research methodologies. Additionally, Dr. G.P. Dixit, Director, ICAR-IIPR, Kanpur, outlined the long-term research framework for *kharif* pulses. The inaugural session had started with the presentation of a comprehensive Coordinator's report by Dr. Aditya Pratap, Project Coordinator for the All India Coordinated Research Project (AICRP) on *Kharif* Pulses who detailed the research advancements achieved during 2025–26, immediate roadblocks, and future strategic interventions. Dr. Mudalagiriyappa, Director of Research at UAS, Bengaluru, emphasized driving productivity alongside expanding pulse cultivation into new agro-ecological niches.

To mark the occasion, the dignitaries also unveiled a series of new research publications and presented the prestigious Best Center Awards. Following a formal vote of thanks delivered by Dr. Lohithaswa HC, Principal Scientist (Plant Breeding) for AICRP on *Kharif* Pulses at UAS, Bengaluru, the programme concluded on a high note. The successful gathering ultimately reinforced a shared commitment among National Agricultural Research System (NARS) partners and global collaborators from the CG system to rapidly elevate *kharif* pulse productivity through technological innovation and collective efforts.

Research Highlights

Identification of high-yielding chickpea genotypes suitable for mechanical harvesting

Mechanization in chickpea cultivation, mainly during harvesting, is an essential for reducing labour dependency and minimizing harvest losses. However, most of presently cultivated chickpea varieties possess a spreading growth habit, shorter plant stature, and low first pod height, which makes them unsuitable for mechanical harvesting. Therefore, developing and identifying genotypes with erect growth habit, greater plant height, higher pod clearance, and superior yield performance is crucial. A field experiment was conducted during *rabi* 2025–26 at IIPR-Regional Centre, Dharwad to evaluate 25 advanced breeding lines of chickpea amenable for mechanical harvesting. The genotypes were assessed for

Chickpea genotypes suitable for mechanical harvesting

important agronomic traits including days to maturity, plant height, test weight, and seed yield to identify high-yielding and mechanically harvestable entries. Variations were observed among the genotypes for the traits studied. Among the entries, IPC 23-320 revealed the highest seed yield (2600 kg/ha) along with maximum plant height (55.4 cm) and test weight (25.83 g) along with erect growth habit indicating its suitability for mechanical harvesting. IPC 23-40 and IPC 23-315 also revealed promising performance with seed yields of 2400 kg/ha and 2339 kg/ha, respectively. The check variety JG 11 recorded comparatively lower seed yield (1800 kg/ha) and shorter plant height (35.2 cm). The results indicated that genotypes with higher plant height along with higher yield were better suited for mechanical harvesting. Therefore, genotypes such as IPC 23-320 with taller plant stature and higher yield are promising for mechanized cultivation under Dharwad conditions.

Revanappa SB, Manu B, Yogesh Kumar, Srivastav AK, Mondal B, Uday, Saabale PR, Kodandaram MH

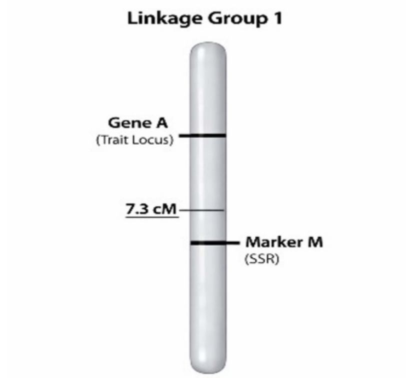
QTL mapping for Powdery Mildew Disease resistance in urdbean (*Vigna mungo* L. Hepper)

Urdbean or blackgram varieties are regularly infected with powdery mildew disease resulting in significant losses for farmers if susceptible varieties are grown. ICAR-IIPR developed urdbean varieties over the years have shown a high degree of genetic resistance in farmers' fields to this deadly disease. This study was designed to identify genomic regions controlling genetic resistance to this disease in urdbean. A RIL population of urdbean was phenotyped over six years in ICAR-IIPR, Kanpur and ICAR-NEH, Tripura and genotyped with genotyping-by-sequencing technique. QTL analysis of these data resulted into the dentification of 4 QTLs for PMW resistance distributed across four chromosomes and phenotypic variation explained ranging from 8.17 to 19.60 per cent. The major QTLs explaining >10 per cent phenotypic variation or detected in multiple environments were identified on chromosomes 4 (*qPMW_IPU 4.787*), chromosome 5 (*qPMW_IPU 5.471*), chromosome 9 (*qPMW_IPU 9.285*) and chromosome 10 (*qPMW_IPU 10.226)* across different years and locations. These four QTLs explained 19.60, 8.17, 14.94 and 10.12 per cent of phenotypic variation, respectively. Further, QTLs will be analysed to identify candidate genes and development of markers for PMW resistance.

Gupta Debjyoti Sen, Kumar Sachin , Kumar Jitendra, Kumar Shivam, Das S.P. and Banik S.

Genetics and molecular mapping of main stem pod bearing habit and validation of linked markers in urdbean [*Vigna mungo* (L.) Hepper]

The present study was undertaken to find out the inheritance of main stem pod bearing habit, in urdbean and to identify a linked molecular marker suitable for marker-assisted selection in a recombinant inbred population, and to validate the linked marker in a set of urdbean breeding lines and varieties. A set of three populations (KPU 13-21×Mukundra Urd 2, IPU 94-1 × IPU 17-1, IPU 13-1 x PU 12) was studied for the inheritance of the main stem pod bearing habit in urdbean and after analyzing F_1, F_2, $F_{2:3}$ and RIL population phenotypic data for pod bearing habit, a monogenic control was detected for this trait. One RIL population (F_8 generation) derived from KPU 13-21×Mukundra Urd 2 was used for gene tagging and molecular mapping using a set of 237 primers comprising simple sequence repeats markers. One simple sequence repeats marker, CEDG056, was found to be linked to the main-stem pod-bearing habit, with a mapping distance of 7.3 cM. This marker, CEDG056, successfully discriminated main stem pod bearing plant types from the normal pod bearing types in a validation panel of 38 urdbean genotypes comprising both varieties and advanced breeding lines. This identified marker will be useful for marker-assisted selection of main stem pod bearing varieties in urdbean breeding programmes.



Linkage Group 1 showing the relative positions of Gene A (Pod Bearing Habit) and Marker M (SSR), separated by 7.3 centiMorgans (cM). The map illustrates the genetic linkage between the trait locus and the SSR marker within a single linkage group, constructed using recombination frequency data.

Ashok Singh Kharbas, Anuradha, Jitendra Kumar, A. K. Parihar, S. S. Punia, G. P. Dixit, Debjyoti Sen Gupta

Genetics, molecular mapping and validation of linked markers for pod and stem pubescence in urdbean (*Vigna mungo* L. Hepper)

Pubescence (trichome development) on the surface of the stem and pod is an agronomically important trait of urdbean (*Vigna mungo* L. Hepper). In the present study, 130 recombinant inbred lines (F_7) were developed by single seed descent method from a cross KU 3 (pubescent) × MU 2 (glabrous) was used. A set of 206 SSR and INDEL primers were tested for detecting parental polymorphisms. As a result, eight markers were found to be polymorphic between parents, namely, CEDG 097, CEDG 056; BLKGSSR-2, BLKGSSR-20, BLKGSSR-28, BLKGSSR-41 (SSRs) and SCA-164, SCA-166 (INDEL). While testing these markers in bulked DNA samples (pubescent vs. glabrous) two markers, CEDG 056 and the SCA-164 were polymorphic in bulk segregant analysis. Consequently, the RIL population was genotyped with these markers. Single marker analysis revealed strong association between CEDG056 (SSR) and pod pubescence (LOD = 7.97) and stem pubescence (LOD = 5.66), and SCA-164 (INDEL) with pod pubescence (LOD = 5.23) and stem pubescence (LOD = 4.06). The inter-marker linkage analysis confirmed CEDG 056 and SCA-164 to be linked in the same chromosome with an inter-marker (Kosambi) distance of 27.07 cM, with observed RIL recombination frequency of 0.331 and a meiotic recombination fraction of 0.247 (Haldane-Waddington formula) and were placed in one linkage group with an inter-marker LOD value of 3.299. Further, interval mapping identified single QTL for both pod and stem pubescence that co-localized at 12 cM within the interval CEDG 056- SCA-164 with LOD scores of 10.50 and 7.81, respectively, explaining 31.29% and 23.73% of the phenotypic variance. These identified and validated markers can be used for marker assisted selection (MAS) in urdbean breeding programmes.

Anuradha, A. S. Kharbas, Jitendra Kumar, A. K. Parihar, S. K. Jain, G. P. Dixit, Debjyoti Sen Gupta

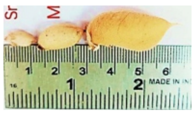
Identification of Distinct and Stable Chickpea Genotypes for morpho-agronomic Traits

Multi-season evaluation of chickpea genotypes was conducted during 2022-23 to 2025-26 to assess the stability of key morphological and agro-economic traits. Nine genotypes viz., ICC 14340 (long pods and seeds), ICC 5712 (flat pods), ICC 5002 (small pods and seeds), ICC 16949 (dwarf and highly branched), ICC 10035 (upright peduncle with single cylindrical pods), along with check varieties RVG 202, RVG 203, JG 16, and JG 14, were evaluated in a randomized block design with three replications across three seasons. Data were recorded for qualitative traits (pod shape, seed shape, and peduncle orientation) and quantitative traits (seed size, plant height and maximum number of branches per plant), and analyzed using combined ANOVA, the Eberhart and Russell stability model, AMMI analysis, and broad-sense heritability estimation.Combined ANOVA revealed a significant seasonal



ICC 14340, Long cylindrical pods and long seeds


ICC 16949; Dwarf (17-20 cm)-highly branched (15-18 secondary branches /plant)



ICC 5002, small pod and seed size (4.3 g per 100-seed weight as compared to seeds of wild species


ICC 5712, Flat pods


ICC 10035, Long Upright peduncle

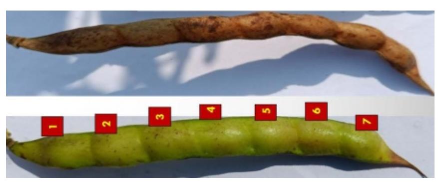
Stable distinct germplasm lines evaluated over four seasons (2022-23 to 2025-26) at IIPR RS, Bhopal, highlighting variation in pod morphology, seed size, plant architecture, and peduncle orientation.

effect on plant height and maximum number of branches per plantin ICC 16949, whereas seed size in ICC 5002 remained unaffected. Stability analysis following Eberhart and Russell indicated that ICC 5002 exhibited a regression coefficient (bi ≈ 1) with non-significant deviation from regression, demonstrating wide adaptability and stability across environments. In contrast, ICC 16949 showed bi> 1, indicating greater responsiveness to environmental changes. The negligible G×E interaction for seed size further confirmed its stability.AMMI analysis supported these findings, positioning ICC 5002 near the origin, indicating high stability (93%) with minimal seasonal variation. Conversely, ICC 16949 exhibited moderate environmental sensitivity (77%). High heritability estimates for seed size (0.85–0.92) suggested strong additive gene action, while the moderate environmental influence on plant height and highly branched genotype indicated partial non-additive genetic control.Overall, the consistent expression of morphological traits across seasons highlights their reliability as diagnostic descriptors and underscores their potential as stable donor traits in chickpea improvement programs.

Archana Singh, Gayacharan, Bhojraj Parmar and Yogesh Kumar

Seven-seeded pod trait in pigeonpea (*Cajanus cajan* L.): A novel genetic resource for yield enhancement and breeding

A unique pigeonpea genotype IC 525760-1 exhibited stable expression ofseven well-developed seeds per pod, across five consecutive cropping seasons (2021-22 to 2025-26), indicating a strong genetic basis for the trait. The pods are elongated and well filled, accommodating seven fully developed seeds. The genotype maintains normal plant architecture, flowering behaviour, and pod setting, suggesting that increased seed



number does not adversely affect reproductive development. Such expression indicates efficient assimilate partitioning and enhanced sink capacity during pod filling. The occurrence of seven seeds per pod substantially exceeds the normal seed number (3-5) observed in cultivated pigeonpea and therefore represents a rare phenotypic variant worthy of conservation and utilization.

Archana Singh, Padmawati G. Gore, Bhojraj Parmar, P.K. Katiyar and G. P. Dixit

Multi-environment evaluation of green gram genotypes for seed yield and adaptability in Karnataka

Green gram is an important short duration pulse crop, known for its nutritional quality and wider adaptability to diverse agro-climatic conditions. Evaluation of advanced genotypes across the environments helps in identification of stable, high-yielding varieties. GGE biplot analysis provides an effective approach to study genotype × environment interaction and select superior green gram genotypes for cultivation. A field evaluation of 12 green gram genotypes was


Evaluation of green gram genotypes in different locations of Karnataka

conducted across four agro-climatic zones of Karnataka, namely Akkialur, Mugad, Mundgod, and Malagi during summer seasons of 2023-2025. GGE biplot analysis can be used to assess the performance of 12 genotypes across four environments. Significant variation in seed yield was observed among genotypes and locations, indicating the influence of genotype and environment. Among the tested entries, IPM 1711-1 recorded the highest mean seed yield (712.5 kg/ha), followed by IPM 1707-1 and IPM 4-10. Karihesaru (local cultivar) showed the lowest mean yield (379.0

kg/ha). The “which-won-where” pattern identifies the best-performing genotype in each environment. Based on mean yield values, IPM 1711-1 showed superior and stable performance across locations, suggesting broad adaptability. The study identified promising high-yielding genotypes suitable for wider cultivation in Karnataka.

Revanappa SB, Manu B, Saabale PR, MD Patil, Gurupad Balol, Mondal B, Kodandaram MH and Patil SL

Characterization of morphological diversity in wild relatives of pigeonpea (*Cajanus* and *Rhynchosia* species)

Understanding the phenotypic variability of wild crop relatives is essential for identifying traits conducive to climate resilience and yield improvement. This study evaluated the morphological diversity of eight accessions belonging to the genera *Cajanus* and *Rhynchosia*, including *C. scarabaeoides* (C_4), *R. suaveolens* (E_2, I_4), *R. rufescens* (E_3), *R. densiflora* (I_5, K_4, E_6), and *R. minima* (I_6). Quantitative and qualitative traits were recorded to establish phenotypic profiles for these accessions. The results revealed significant variation in vegetative and reproductive architecture. Plant height ranged from 78.8 cm (*R. suaveolens* E_2) to 178.1 cm (*R. minima* I_6). *R. minima* exhibited the most distinct floral morphology, characterized by the smallest flower size (0.5 mm) and a unique flower color red, whereas *C. scarabaeoides* displayed the highest number of seeds per pod (5). Stem thickness varied drastically, with *R. suaveolens* I_4 reaching a maximum of 20.54 mm compared to only 1.71 mm in *R. minima*.Qualitative assessments indicated high uniformity in leaf arrangement and margin type across all taxa, while traits such as growth habit, leaf pubescence, and flower scent presence provided clear differentiation between species. Notably, *R. densiflora* accessions exhibited consistent receme lengths ranging from 2.76 to 4.7 cm. These findings highlight the extensive morphological breadth within these wild accessions, particularly regarding pod characteristics and plant vigor, suggesting their potential utility as genetic donors in pigeonpea improvement programmes. Extensive trichome (adaxial/abaxial, glandular/non glandular), petiole and foliar anatomy were also studied among the accessions.

Manu B, Apoorva, Saabale PR, Revanappa SB, Parihar A K and Kodandaram M H

Characterization and morpho-agronomic evaluation of wild *Vigna* germplasm

The genus *Vigna* encompasses a diverse group of wild relatives that harbor essential genetic traits for crop improvement, particularly for biotic and abiotic stress resistance. This study presents a systematic characterization and evaluation of various wild *Vigna* accessions, including *V. stipulaceae*, *V. trilobata*, *V. vexillata*, and other wild relatives of *V. unguiculataV. mungo* and *V. radiata*. The wild *Vigna* (42) germplasm was evaluated based on a comprehensive set of qualitative and quantitative descriptors covering vegetative, floral, and pod-related traits. Qualitative analysis revealed significant variability in growth habit, terminal leaflet shape, and leaf pubescence. Notably, accessions displayed diverse corolla colours and pod attachment angles, ranging from erect to pendant. Quantitative assessment focused on phenological traits and yield components. Days to first flowering varied significantly, with early types maturing around 78 days, while late-maturing accessions extended beyond 120 days. Morphological parameters such as terminal leaflet length, petiole length, and plant height (ranging from 35 cm to over 345 cm in climbing types) highlighted the structural diversity within the collection. Reproductive traits were equally diverse; pod length, number of seeds per pod, and number of pods per peduncle was recorded to identify high-yielding wild progenitors. Seed characteristics, including shape, size, and colour, were documented to aid in taxonomic classification and evolutionary studies. This characterization provides a foundational database for breeders to identify promising wild accessions for pre-breeding programmes, aiming to introgress resilient traits into cultivated pulse varieties to ensure food security under changing climatic conditions.

Manu B, Apoorva, Revanappa SB, Saabale PR, Parihar A K and Kodandaram M H

Occurrence of powdery mildew disease in pigeonpea at Dharwad, Karnataka

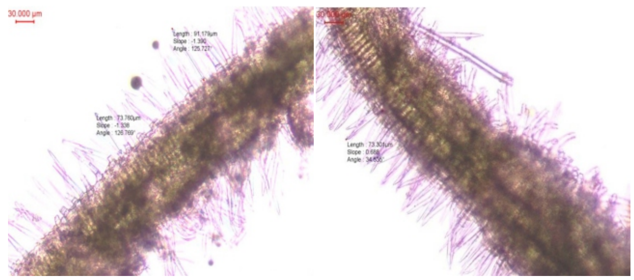
Powdery mildew caused by *Leveillulataurica* (Lev.) G. Arnaud is an important foliar disease of pigeonpea (*Cajanus cajan* L. Millsp.). The disease generally appears during the flowering and pod development stages and can cause considerable yield losses when weather conditions are favourable. Infected plants develop white powdery growth on leaves and other

Field view of PM infected pigeonpea crop (a); *Leveillulataurica* spores (b) aerial plant parts, leading to premature drying of foliage, reduced photosynthetic activity and poor seed development. During the cropping season 2025-26, severe powdery mildew incidence was observed during the last week of December 2025 and the first week of January 2026. The weather during this period was favourable for disease development, with maximum temperatures ranging from 26.0 to 30.0°C, minimum temperatures from 9.2 to 17.0°C and morning relative humidity between 73 and 89 per cent. No rainfall was recorded throughout the observation period. The combination of moderate temperatures, cool nights, high humidity and dry weather conditions created an ideal environment for the development and spread of the pathogen.Out of 278 lines pigeonpea genotypes, ICP 8863, ICPL 23233, ICPL 19060, ICPV 21333, IPAE 23-02, LRG 589, PA 810, Pant Arhar 6, TJT 501, IPAM 24-8, PT 2107, and LRG 616 recorded 100 per cent disease severity. The absence of rainfall during this period may also have favoured the survival and dispersal of fungal spores, resulting in rapid disease spread. These observations indicate that the prevailing weather conditions during late December and early January were highly favourable for powdery mildew development in pigeonpea and can be considered critical periods for disease monitoring and management.

Saabale PR, Veeresh P, Kodandaram MH, Manu B, Revanappa SB, and Nikhil

Cluster analysis and correlation of leaf morpho-anatomical traits with sterility mosaic disease in Pigeonpea

Hierarchical clustering using Ward's method and K-means clustering grouped the 59 pigeonpea genotypes into four distinct clusters based on leaf morpho-anatomical traits and pigeonpeasterility mosaic disease (SMD) reaction. Cluster 2 was the largest, comprising 25 genotypes, followed by Cluster 4 (16 genotypes), Cluster 1 (10 genotypes), and Cluster 3 (8 genotypes). Genotypes within a cluster exhibited greater similarity for trichome characteristics, cuticle thickness and disease response, whereas those belonging to different clusters were more divergent. Cluster 3 contained genotypes with comparatively distinct morpho-anatomical features and SMD reaction, suggesting their potential utility as diverse parents in resistance breeding programmes.



View of leaf morphological traits

Correlation analysis revealed varying associations between leaf morpho-anatomical traits and SMD incidence. Trichome number on the upper surface (TNUS) showed a significant negative correlation with SMD (r = -0.329), while trichome number on the lower surface (TNLS) exhibited a stronger significant negative correlation (r=-0.474). These results indicate that higher trichome density, particularly on the lower leaf surface may contribute to reduced disease incidence by affecting vector movement. In contrast, leaf trichome length, cuticle thickness on both leaf surfaces, and trichome length on the upper surface showed non-significant correlations with SMD. The findings suggest that trichome density may serve as an important morphological trait associated with resistance to sterility mosaic disease in pigeonpea.

Saabale PR, Veeresh P, Kodandaram MH, Manu B, Revanappa SB, and Nikhil

Validation of greengram genotypes against powdery mildew disease resistance

A set of 41 greengram genotypes, comprised local germplasm, advanced breeding lines and released varieties, were screened against powdery mildew disease resistance at IIPR-Regional Station, Phanda, Bhopal. Crop was sown on 03.10.2025 in RBD design with 3 replications and observations were recorded periodically at one week interval. Among the screened genotypes, per cent Disease Severity Index (DSI %) ranged from 20.0 to 81.7%; Area under Disease Progress Curve (AUDPC) varied from 1312 to 5550; and yield ranged from 48.1 to 796.1 kg/ha. DSI % and AUDPC of two resistant genotypes namely, Black Moong Khari 2 (DSI; 20.0% and AUDPC; 1312) and IC 653143 (DSI; 38.09%, AUDPC; 2678) were significantly lower than the susceptible genotype Virat (DSI; 73.33% and AUDPC; 5657). The yield of two resistant genotypes *viz.* Black Moong Khari 2 (796.1 kg/ha) and IC 653143 (779.2 kg/ha) were significantly higher than susceptible genotype Virat (59.7 kg/ha).

Germplasm IC 653143 and BM Khari 2 screening against powdery mildew disease

Surendra Ghritlahre, D. Datta, Nidhi Kumari, Nainika Nagar and Gitanjali Sahay

प्रौद्योगिकी हस्तांतरण

Schedule Caste-Sub Plan

Under the Schedule Caste Sub-Plan, the following activities were conducted :

- Distribution of small equipments by ICAR-IIPR, Kanpur (220 Nos.)

- Quality seed Distribution of mungbean and urdbean seed by ICAR-IIPR, Kanpur (88.00 q.)

- Distribution of NPK Fertilizer Mixture by ICAR-IIPR, Kanpur (550 kg.)
- Farmer's Training at ICAR-IIPR, Kanpur and ICAR-IIPR, RRC Bikaner : 03 Nos.

Miscellaneous

संस्थान में अन्तर्राष्ट्रीय योग दिवस मनाया गया

अन्तर्राष्ट्रीय योग दिवस 21 जून, 2026 को भारतीय दलहन अनुसंधान संस्थान के प्रांगण में बड़े उत्साह के साथ मनाया गया। प्रातः 6:30 बजे आयोजित इस योग कार्यक्रम में संस्थान के वैज्ञानिकों, तकनीकी व प्रशासनिक वर्ग के कर्मचारियों ने भाग लिया। इस अवसर पर संस्थान के निदेशक डॉ. जी.पी. दीक्षित ने जीवन में योग के महत्व पर प्रकाश डाला। उन्होंने कहा कि आज के इस प्रदूषित वातावरण में योग को जीवन में अपनाकर ही स्वस्थ रहा जा सकता है और तनावमुक्त जीवन जिया जा सकता है। योगक्रियांए, आयुष मंत्रालय के प्रोटोकाल के अनुरूप पूर्ण करवाई गईं, बताया गया कि कौन से आसनों का नियमित अभ्यास करके कौन से रोगों से मुक्ति पाई जा सकती है। इस अवसर पर संस्थान के वरिष्ठ पदाधिकारी, परियोजना समन्वयक, विभागाध्यक्ष, वरिष्ठ प्रशासनिक अधिकारी, वरिष्ठ वित एवं लेखाधिकारी आदि मौजूद थे।

PERSONNEL

Promotions, Appointments, Transfers *etc.*

Promotions

Sl.	Name	Promoted to	w.e.f.
1	Sh. Mayank Mishra, UDC	Assistant	30.06.2026 (AN)
2	Sh. Sanjay Kumar Sharma, UDC	Assistant	30.06.2026 (AN)

Transfers

Sl.	Name	Designation	From	To	Date
1	Sh. Ashutosh Tiwari	DD (OL)	ICAR-IIHR, Bengaluru	ICAR-IIPR, Kanpur	01.04.2026 (FN)
2.	Sh. Sunil Kumar Kannaujia	Technical Assistant (T-3)	ICAR-NISST, Mau	ICAR-IIPR, Kanpur	08.06.2026 (FN)
3	Sh. Ranjeet Kumar	Sr. Technician (T-2)	ICAR-IVRI, Izatnagar	ICAR-IIPR, Kanpur	20.06.2026 (FN)
4	Sh. Ravin Umrao	Sr. Technician (T-2)	ICAR-IVRI, Izatnagar	ICAR-IIPR, Kanpur	20.06.2026 (FN)
5	Sh. Ankit Sahu	Sr. Technician (T-2)	ICAR-IVRI, Izatnagar	ICAR-IIPR, Kanpur	20.06.2026 (FN)

Retirements

Sl.	Name	Post held	Date of retirement
1	Sh. Har Govind Rathore	PA	30.06.2026
2	Sh. Sarvesh Kumar Kanaujia	SSS	30.06.2026

Director's Desk

Dear Readers,

Growing geopolitical uncertainty and regional conflicts are causing disruptions in global trade and fluctuations in the supply of critical agricultural inputs. Recent developments in West Asia have once again highlighted the vulnerability of global supply chains for energy, fertilizers, and food commodities. For a country like India where a substantial proportion of phosphatic fertilizers and their raw materials are sourced through imports, these developments reinforce the need to build agricultural systems that are productive, resilient and less dependent on external inputs.

In this context, pulse-based agri-food systems remain the promising alternative. Pulses are unique in their ability to biologically fix atmospheric nitrogen, thereby reducing dependence on synthetic fertilizers, improving soil health, enhancing biodiversity, conserving natural resources, and lowering the environmental footprint of agriculture. They simultaneously contribute to nutritional security, climate resilience, and sustainable intensification of farming systems.

Recognizing their strategic importance, the Government of India has launched the Mission for *Aatmanirbharta* in Pulses (*Dalhan Aatmanirbharta* Mission), which aims to scale up domestic pulses production to 350 lakh tonnes and expand the cultivation area to 310 lakh hectares by 2030–31 through promoting improved production technologies, strengthen seed systems, and ultimately reducing the nation's dependence on pulse imports. Achieving self-reliance in pulses is no longer only an agricultural objective; it is an important component of India's food security, nutritional security, and economic resilience. Strengthening indigenous pulse production will insulate the country from global market volatility while ensuring availability of affordable and protein-rich food for millions of consumers.

The Annual Group Meet of *Kharif* Pulses held at UAS, Bengaluru from May 5–7, 2026, reaffirmed this

national vision. Scientists, policymakers, and stakeholders attending the meeting, collectively emphasized on a renewed focus on developing pulse-based agri-food systems that integrate higher productivity with climate resilience, efficient nutrient management, improved seed systems, predictive breeding, and farmer-centric technologies. The deliberations clearly underscored that sustainable growth in pulse production will be instrumental in achieving the objectives of the Dalhan Aatmanirbharta Mission while simultaneously supporting environmental sustainability.

ICAR–Indian Institute of Pulses Research (IIPR), Kanpur continues to play a pivotal role in realizing this vision. Through cutting-edge research in genomics-assisted breeding and gene-editing technologies development of climate-resilient and disease-resistant varieties, machine-harvestable cultivars, efficient seed systems, and conservation of valuable pulse genetic resources, the Institute is generating technologies that enhance productivity while mitigating production risks and input dependency.

The Institute is equally committed to advancing the nationwide agricultural awareness initiatives such as '*Khet Bachao Abhiyaan*'. Healthy soils are the cornerstone of sustainable agriculture, and pulses are among the most effective biological tools for restoring soil fertility. Their integration into cropping systems naturally enriches soil nitrogen, reduces fertilizer requirements, improves soil microbial activity, enhances carbon sequestration, and supports diversified farming systems. Increasing the area and productivity of pulses will contribute not only to healthier soils and higher farmer incomes but also to reduce India's reliance on imported fertilizers and imported pulses.

By strengthening domestic pulse production through science-led innovations and farmer-centric technologies, India can move decisively towards achieving the twin goals of *Atmanirbhar Bharat* and *Viksit Bharat*. ICAR-IIPR remains steadfast in supporting the National Pulses Mission and advancing pulse-based agri-food systems. With coordinated research efforts, strengthened institutional linkages, and greater synergy among stakeholders, we shall continue to transform scientific innovations into field-level impact, ensuring prosperous farmers, healthy soils, nutritional security and a resilient agricultural future for the nation.

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